

RESULT 1  
US-09-738-274-24  
; Sequence 24, Application US/09738274  
; Patent No. 6664981  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: TUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; ~~THE~~ ~~SEQUENCE~~ ~~REFERENCE~~ MYCOBACTERIUM SPECIES  
; CURRENT APPLICATION NUMBER: GP107-02.UT  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 19

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; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-738-274-22

Query Match          94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
Db 7 GAACGGAAGGCGCTTTTCG 24

RESULT 4
US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUGKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/112,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-738-274-21

Query Match          94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18
Db 8 GAACGGAAGGCGCTTTTCG 25

RESULT 5
US-08-485-602-56
; Sequence 56, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Ribosomal RNA Precursors
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-485-602-56

Query Match          86.3%; Score 16.4; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 3;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCG 19
Db 1 GAACGGAAGGCGCTTTTCG 19

RESULT 6
US-08-757-180-55
; Sequence 55, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: SD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000

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Matches      15;  Conservative      2;  Misses
Qy      1  GAACGGAAGGCTTTCGG  19
      |||||
Db      1  GAACGGAAGNCCCUUOGG  19
      |||||

Search completed: May 26, 2006, 14:31:32
Job time : 0.001 secs

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; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-757-180-55

Query Match 86.3%; Score 16.4; DB 1; Length 23;
Best Local Similarity 78.9%; Pred. No. 3;
Matches 15; Conservative 2; Mismatches 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19
||||||| ||:||||
DB 1 GAACGGAAAGNCCCUCCG 19

RESULT 7
US-08-745-638-56
; Sequence 56, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-745-638-56

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[illegible]

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OM nucleic - nucleic search, using sw model  
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(without alignments)  
12.768 Million cell updates/sec

Title: us-10-665-708-24  
Perfect score: 19  
Sequence: 1 gaacgaaagccttcgg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 0.5

Searched: 15 seqs, 336 residues

Total number of hits satisfying chosen parameters: 30

Minimum DB seq length: 18  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 15 summaries

Database : rngdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1 AAD11274	Mycobacterium 16S
2	19	100.0	19	1 ADG88355	Mycobacterium ampl
3	19	100.0	19	1 AEA08230	Mycobacterium xeno
4	19	100.0	22	1 AAD11273	Mycobacterium 16S
5	19	100.0	22	1 ADG88354	Mycobacterium ampl
6	19	100.0	22	1 AEA08229	Mycobacterium cela
7	18	94.7	24	1 AAD11272	Mycobacterium 16S
8	18	94.7	24	1 ADG88353	Mycobacterium ampl
9	18	94.7	24	1 AEA08228	Mycobacterium cela
10	18	94.7	25	1 AAD11271	Mycobacterium 16S
11	18	94.7	25	1 ADG88352	Mycobacterium ampl
12	18	94.7	25	1 AEA08227	Mycobacterium cela
13	16.4	86.3	23	1 AAV24413	Target sequence #2
14	16.4	86.3	23	1 AAV13021	Mycobacterium intr
15	14	73.7	20	1 AAT75816	Corynebacterium pr

## ALIGNMENTS

RESULT 1  
AAD11274  
ID AAD11274 standard; DNA; 19 BP.  
XX  
AC AAD11274;  
XX  
DT 24-SEP-2001 (first entry)  
XX  
DE Mycobacterium 16S rRNA amplifying primer #18.  
XX  
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

OS Mycobacterium sp.  
XX WO200144510-A2.  
PN  
XX 21-JUN-2001.  
PD  
XX 17-DEC-1999; 99WO-US030346.  
XX  
PF 17-DEC-1999; 99WO-US030346.  
PR  
XX (GENP) GEN-PROBE INC.  
PA (INMR) BIOMERIEUX SA.  
XX  
PI Brentano/ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX WPI; 2001-398170/42.  
DR  
XX  
XX Detecting Mycobacterium species, involves in vitro amplification of 16S  
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
PT specific primers, and detecting the amplified nucleic acid.  
XX  
XX Claim 1; Page 36; 44pp; English.  
XX  
XX The invention relates to a method of detecting Mycobacterium species,  
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
CC comprising a polymerase, and at least two primers, and then detecting the  
CC amplified nucleic acid. The method is relatively simple and useful for  
CC detecting the presence of various Mycobacterium species in a biological  
CC sample, and thus important for diagnosis of infections resulting from  
CC them. The method is especially important for screening opportunistic  
CC infections caused by M. tuberculosis or a Mycobacterium other than  
CC tuberculosis (MOTT). The present sequence is a PCR primer used for  
CC amplifying Mycobacterium 16S rRNA  
XX  
SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAACGGAAGCCTTCGG 19  
|||||  
Db 1 GAACGGAAGCCTTCGG 19  
|||||  
  
RESULT 2  
ADG88355  
ID ADG88355 standard; DNA; 19 BP.  
XX  
AC ADG88355;  
XX  
XX 11-MAR-2004 (first entry)  
DT  
XX Mycobacterium amplifying PCR primer #24.  
DE  
XX In vitro amplification; PCR; primer; ss.  
XX  
OS Mycobacterium xenopi.  
XX  
PN US2003165824-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 15-DEC-2000; 2000US-00738274.  
XX  
PR 17-DEC-1999; 99US-0172190P.  
XX  
PA (BREN/) BRENTANO S T.  
PA (JUCK/) JUCKER M T.  
PA (DELG/) DELGADO-F D.  
PA (CLEU/) CLEUZIAZ P.  
PA (RODR/) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX WPI; 2003-898044/82.  
XX  
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
XX in a biological sample comprises performing in vitro nucleic acid  
XX amplification and detection of amplified products.  
XX  
XX Claim 1; SEQ ID NO 24; 20pp; English.  
XX  
XX The present invention relates to a method of detecting Mycobacterium  
XX species present in a biological sample comprises performing an in vitro  
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
XX detecting the amplified Mycobacterium nucleic acid. The present sequence  
XX is Mycobacterium amplifying PCR primer.  
XX  
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAACGGAAGGCTTTTCGG 19  
Db 1 GAACGGAAGGCTTTTCGG 19  
RESULT 3  
AEA08230  
ID AEA08230 standard; DNA; 19 BP.  
XX  
XX AEA08230;  
XX  
XX 14-JUL-2005 (first entry)  
XX  
XX Mycobacterium xenopi 16S rRNA amplifying non-T7 primer, SEQ ID NO: 24.  
XX  
XX DNA amplification; microorganism detection; 16S ribosomal RNA; 16S rRNA;  
XX PCR; primer; ss.  
XX  
XX Mycobacterium xenopi; ATCC 19250.  
XX  
XX US2005100915-A1.  
XX  
XX 12-MAY-2005.  
XX  
XX 18-SEP-2003; 2003US-00665708.  
XX  
XX 17-DEC-1999; 99US-0172190P.  
XX  
XX 15-DEC-2000; 2000US-00738274.  
XX  
XX (BREN/) BRENTANO S T.  
XX (JUCK/) JUCKER M T.  
XX (DELG/) DELGADO F D.  
XX (CLEUZ/) CLEUZAT P.  
XX (RODR/) RODRIGUE M.  
XX  
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX WPI; 2005-345392/35.  
XX  
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
XX in a biological sample, comprises using in vitro nucleic acid  
XX amplification and detection of amplified products.  
XX  
XX Claim 1; SEQ ID NO 24; 21pp; English.  
XX  
XX The present invention relates to a method of detecting Mycobacterium  
XX species present in a biological sample. The method involves using in  
XX vitro nucleic acid amplification and detection of amplified products. The  
XX invention is useful for diagnostic detection of pathogenic bacteria such  
XX as Mycobacterium species. The present sequence is the Mycobacterium

CC xenopi (ATCC 19250) 16S ribosomal RNA (16S-rRNA) amplifying non-T7 PCR  
CC primer.  
XX  
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAACGGAAGGCTTTTCGG 19  
Db 1 GAACGGAAGGCTTTTCGG 19  
RESULT 4  
AAD11273  
ID AAD11273 standard; DNA; 22 BP.  
XX  
XX AAD11273;  
XX  
XX 24-SEP-2001 (first entry)  
XX  
XX Mycobacterium 16S rRNA amplifying primer #17.  
XX  
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.  
XX  
XX Mycobacterium sp.  
XX  
XX WO200144510-A2.  
XX  
XX 21-JUN-2001.  
XX  
XX 17-DEC-1999; 99WO-US030346.  
XX  
XX 17-DEC-1999; 99WO-US030346.  
XX (GENP-) GEN-PROBE INC.  
XX (INNR) BIOMERIEUX SA.  
XX  
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX WPI; 2001-398170/42.  
XX  
XX Detecting Mycobacterium species, involves in vitro amplification of 16S  
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
XX specific primers, and detecting the amplified nucleic acid.  
XX  
XX Claim 1; Page 36; 44pp; English.  
XX  
XX The invention relates to a method of detecting Mycobacterium species,  
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
XX comprising a polymerase, and at least two primers, and then detecting the  
XX amplified nucleic acid. The method is relatively simple and useful for  
XX detecting the presence of various Mycobacterium species in a biological  
XX sample, and thus important for diagnosis of infections resulting from  
XX them. The method is especially important for screening opportunistic  
XX infections caused by M. tuberculosis or a Mycobacterium other than  
XX tuberculosis (MOTT). The present sequence is a PCR primer used for  
XX amplifying Mycobacterium 16S rRNA  
SQ  
Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAACGGAAGGCTTTTCGG 19  
Db 4 GAACGGAAGGCTTTTCGG 22

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RESULT 5
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX AC ADG88354;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #23.
XX KW In vitro amplification; PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2003165824-A1.
XX PD 04-SEP-2003.
XX PF 15-DEC-2000; 2000US-00738274.
XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPT-2003-898044/82.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 23; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample. The method involves using in
XX CC vitro nucleic acid amplification and detection of amplified products.
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCTTTCCG 19
Db 4 GAACGGAAGGCTTTCCG 22
RESULT 6
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX AC AEA08229;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGAAGGCTTTCCG 19
Db 4 GAACGGAAGGCTTTCCG 22
RESULT 7
AAD11272
ID AAD11272 standard; DNA; 24 BP.
XX AC AAD11272;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #16.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (ENMR-) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPT-2004-398170/42.
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using

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PT specific primers, and detecting the amplified nucleic acid.

PS Claim 1; Page 36; 4pp; English.

XX The invention relates to a method of detecting Mycobacterium species, CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture CC comprising a polymerase, and at least two primers, and then detecting the CC amplified nucleic acid. The method is relatively simple and useful for CC detecting the presence of various Mycobacterium species in a biological CC sample, and thus important for diagnosis of infections resulting from CC them. The method is especially important for screening opportunistic CC infections caused by M. tuberculosis or a Mycobacterium other than CC tuberculosis (MOTT). The present sequence is a PCR primer used for CC amplifying Mycobacterium 16S rRNA

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 8

ADG88353  
ID ADG88353 standard; DNA; 24 BP.

AC ADG88353;

DT 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #22.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium celatum.

XX US2003165824-A1.

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN//) BRENTANO S T.

XX (JUCK//) JUCKER M T.

XX (DELG//) DELGADO F D.

XX (CLEU//) CLEUZIAT P.

XX (RODR//) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
in a biological sample comprises performing in vitro nucleic acid  
amplification and detection of amplified products.

XX Claim 1; SEQ ID NO 22; 20pp; English.

XX The present invention relates to a method of detecting Mycobacterium  
species present in a biological sample comprises performing an in vitro  
amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
detecting the amplified Mycobacterium nucleic acid. The present sequence  
is Mycobacterium amplifying PCR primer.

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 9

AEA08228

ID AEA08228 standard; DNA; 24 BP.

AC AEA08228;

DT 14-JUL-2005 (first entry)

XX Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.

XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;  
PCR; primer; ss.

XX Mycobacterium celatum.

XX US2005100915-A1.

XX 12-MAY-2005.

XX 18-SEP-2003; 2003US-00665708.

XX 17-DEC-1999; 99US-0172190P.

XX 15-DEC-2000; 2000US-00738274.

XX (BREN//) BRENTANO S T.

XX (JUCK//) JUCKER M T.

XX (DELG//) DELGADO F D.

XX (CLEU//) CLEUZIAT P.

XX (RODR//) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2005-345392/35.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
in a biological sample, comprises using in vitro nucleic acid  
amplification and detection of amplified products.

XX Claim 8; SEQ ID NO 22; 21pp; English.

XX The present invention relates to a method of detecting Mycobacterium  
species present in a biological sample. The method involves using in  
vitro nucleic acid amplification and detection of amplified products. The  
invention is useful for diagnostic detection of pathogenic bacteria such  
as Mycobacterium species. The present sequence is the Mycobacterium  
celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)  
amplifying non-T7 PCR primer.

XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
Db 7 GAACGGAAGGCTTTTCG 24

RESULT 10

AAD11271

ID AAD11271 standard; DNA; 25 BP.

XX AAD11271;

```

XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #15.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (LINR-) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2001-398170/42.
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX PS Claim 1; Page 36; 44pp; English.
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25

RESULT 11
ADG88352
ID ADG88352 standard; DNA; 25 BP.
AC ADG88352;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #21.
XX KW In vitro amplification; PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2003165824-A1.
XX PD 04-SEP-2003.
XX PF 15-DEC-2000; 2000US-00738274.

Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25

RESULT 12
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX AC AEA08227;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAZ P.
XX PA (RODR/) RODRIGUE M.
XX PT Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample, comprises using in vitro nucleic acid
XX PT amplification and detection of amplified products.

```

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XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAZ P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2003-898044/82.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 21; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25

RESULT 12
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX AC AEA08227;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZIAZ P.
XX PA (RODR/) RODRIGUE M.
XX PT Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample, comprises using in vitro nucleic acid
XX PT amplification and detection of amplified products.

```

XX PS Claim 8; SEQ ID NO 21; 21bp; English.

XX CC The present invention relates to a method of detecting Mycobacterium

XX CC species present in a biological sample. The method involves using in

XX CC vitro nucleic acid amplification and detection of amplified products. The

XX CC invention is useful for diagnostic detection of pathogenic bacteria such

XX CC as Mycobacterium species. The present sequence is the Mycobacterium

XX CC cellatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)

XX CC amplifying non-T7 PCR primer.

XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 1; Length 25;

Best Local Similarity 100.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 18

Db 8 GAACGGAAGGCGCTTCG 25

RESULT 13

AAV24413

ID AAV24413 standard; preRNA; 23 BP.

XX AC AAV24413;

XX DT 24-AUG-1998 (first entry)

XX DE Target sequence #2 for M. intracellulare specific probe.

XX KW Probe; target sequence; hybridisation; mycobacterial cell sensitivity;

XX KW antimicrobial agent; pre-rRNA detection; ss.

XX OS Synthetic.

OS Mycobacterium intracellulare.

PN US5770373-A.

XX PD 23-JUN-1998.

XX PF 08-NOV-1996; 96US-00745638.

PR 16-JUN-1994; 94US-00261068.

PR 07-JUN-1995; 95US-00485602.

XX (BECT ) BECTON DICKINSON & CO.

XX Cangelosi GA, Britschgi TB;

XX WPI; 1998-376792/32.

XX Mycobacterial sensitivity and drug screening assays - involving release

XX of pre-rRNA by lysis.

XX Example 4; Col 17-18; 50pp; English.

XX This sequence represents a target sequence for mycobacterial probes. This

XX sequence represents a precursor RNA fragment that is released during the

XX method of the invention. The method is for the determination of

XX mycobacterial cell sensitivity to an antimicrobial agent, and comprises:

XX (a) culturing the cells in the presence of the antimicrobial agent; (b)

XX treating the cells by enzymatic or mechanical means to expose the cell

XX membrane to lysis reagents, and contacting the cells with a lysis reagent

XX under conditions such that pre-rRNA is released from the cells but not

XX degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe

XX capable of hybridizing to a region of the pre-rRNA that is not present in

XX mature mycobacterial RNA, where sensitivity to the antimicrobial agent

XX is indicated by an increase or decrease in pre-rRNA levels for cells

XX exposed to the antimicrobial agent compared with mycobacterial cells not

XX exposed to the antimicrobial agent. The lysis method, unlike known

XX methods, results in detectable levels of pre-rRNA

XX SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;

Query Match 86.3%; Score 16.4; DB 1; Length 23;

Best Local Similarity 78.9%; Pred. No. 7.9;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19

Db 1 GAACGGAAGGCGCTTCGG 19

RESULT 14

AAV13021

ID AAV13021 standard; rRNA; 23 BP.

XX AC AAV13021;

XX DT 18-MAY-1998 (first entry)

XX DE Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.

XX KW Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;

XX KW hybridisation; antibiotic resistance; cell lysis; ss.

XX OS Mycobacterium intracellulare.

XX PN US5712095-A.

XX PD 27-JAN-1998.

XX PF 07-JUN-1995; 95US-00485602.

XX PR 16-JUN-1994; 94US-00261068.

XX (BECT ) BECTON DICKINSON CO.

XX Cangelosi GA, Britschgi TB;

XX WPI; 1998-119975/11.

XX Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation

XX with specific probes after cell lysis.

XX Disclosure; Col 18; 54pp; English.

XX The present sequence represents a mycobacterial mature ribosomal RNA

XX target sequence. The present invention describes a method for detecting

XX pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)

XX treating the cells to release pre-rRNA by: (i) pretreating the cells by

XX enzymatic degradation using both lysozyme and protease until their cell

XX walls are rendered porous to expose their cell membranes, making the

XX cells susceptible to lysis; (ii) contacting the pretreated cells with a

XX combination of a magnesium chelator, a nonionic detergent and an anionic

XX detergent; and (iii) heating the cells to 75-99 degrees Celsius until the

XX mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at

XX least one oligonucleotide probe which is capable of selectively

XX hybridizing to a region of the pre-rRNA that is not present in a mature

XX mycobacterial rRNA. The probes can be used to identify many Mycobacterium

XX spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,

XX M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.

XX intracellulare. The probes may also be used to measure mycobacterial

XX response to inhibitors of RNA and protein synthesis and may therefore be

XX used to screen new antimycobacterial drugs. Mycobacteria have a slow

XX growth rate. By using the probes, drug developers can now identify

XX compounds that are more effective, but less stable than those previously

XX identified

XX SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;

Query Match 86.3%; Score 16.4; DB 1; Length 23;

Best Local Similarity 78.9%; Pred. No. 7.9;

Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;



QY 1 GAACGAAAGGCCTTTCGG 19  
Db 1 GAACGAAAGGCCCUUCGG 19

RESULT 15  
AAT75816  
ID AAT75816 standard; rRNA; 20 BP.  
XX  
AC AAT75816;  
XX  
DT 10-SEP-1997 (first entry)  
XX  
DE Corynebacterium propinquum 16S rRNA (from region 72-100).  
XX  
KW Ribosomal RNA; species specific; detection; reverse transcription;  
KW primer; hybridisation probe; identification; ss.  
XX  
OS Corynebacterium propinquum.  
XX  
PN FR273755-A1.  
XX  
PD 08-NOV-1996.  
XX  
PF 03-MAY-1995; 95FR-00005494.  
XX  
PR 03-MAY-1995; 95FR-00005494.  
XX  
PA (INMR ) BIO MERIEUX.  
XX  
PI Mabilat C, Ruimy R;  
XX  
DR WPI; 1997-001738/01.  
XX  
PT Fragments of Corynebacterium 16S RNA - useful as probes and primers for  
PT identifying Corynebacterium spp.  
XX  
PS Claim 2; Page 14; 60pp; French.  
XX  
CC Fragments covering 90 % of the sequence of 16S ribosomal RNA were  
CC amplified from 28 strains of 25 different species of Corynebacterium by  
CC PCR using primers specific for eubacteria. The amplification products  
CC were sequenced and the sequences were aligned for comparison. It was  
CC found that certain regions, i.e. those corresponding to nucleotides 72-  
CC 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S  
CC ribosomal RNA of C. diphtheriae, vary considerably between different  
CC species. Probes and primers comprising at least 5 nucleotides from one of  
CC these species-specific sequences, including the present sequence, or  
CC their complements, are useful to distinguish between different  
CC Corynebacterium species. DNA versions of the probes and primers are also  
CC included  
XX  
SQ Sequence 20 BP; 5 A; 4 C; 7 G; 0 T; 4 U; 0 Other;

Query Match 73.7%; Score 14; DB 1; Length 20;  
Best Local Similarity 78.6%; Pred. No. 20;  
Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTTT 16  
Db 1 ACGGAAAGGCCUUU 14

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 14:29:31 ; Search time 0.001 seconds  
(without alignments)  
8.588 Million cell updates/sec

Title: us-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaagccctttcgg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 10 seqs, 226 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 18

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 10 summaries

Database : rgedb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	AR438656
2	19	100.0	19	1	AX166858
3	19	100.0	22	1	AR438655
4	19	100.0	22	1	AX166857
5	18	94.7	24	1	AR438654
6	18	94.7	24	1	AX166856
7	18	94.7	25	1	AR438653
8	18	94.7	25	1	AX166855
9	16.4	86.3	23	1	I82017
10	16.4	86.3	23	1	I91705

# ALIGNMENTS

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RESULT 1
AR438656
LOCUS AR438656 19 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 24 from patent US 6664081.
ACCESSION AR438656
VERSION AR438656.1 GI:42663580
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 24 16-DEC-2003;
FEATURES Gen-Probe incorporated and Bio Merieux S.A.; San Diego, CA
source 1..19

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/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 100.0%; Score 19; DB 1; Length 19;  
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19

Db 1 GAACGGAAGCCCTTTTCGG 19

## RESULT 2

AX166858

LOCUS AX166858

DEFINITION Sequence 24 from Patent WO0144510.

ACCESSION AX166858

VERSION AX166858.1 GI:14596461

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..19

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db xref="taxon:32630"

/note="primer oligonucleotide"

Location/Qualifiers

1..19

Query Match 100.0%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19

Db 1 GAACGGAAGCCCTTTTCGG 19

## RESULT 3

AR438655

LOCUS AR438655

DEFINITION Sequence 23 from patent US 6664081.

ACCESSION AR438655

VERSION AR438655.1 GI:42663579

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..22

/organism="unknown"

/mol\_type="genomic DNA"

Query Match 100.0%; Score 19; DB 1; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19

Db 4 GAACGGAAGCCCTTTTCGG 22

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RESULT 4
AXI166857
LOCUS AXI166857 22 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 23 from Patent WO0144510.
ACCESSION AXI166857
VERSION AXI166857.1 GI:14596460
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 100.0%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 19
Db 4 GAACGGAAGGCCCTTTCG 22

RESULT 5
AXI166854
LOCUS AXI166854 24 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 22 from patent US 6664081.
ACCESSION AXI166854
VERSION AXI166854.1 GI:42663578
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.1; 0; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 19
Db 4 GAACGGAAGGCCCTTTCG 22

RESULT 6
AXI166856
LOCUS AXI166856 24 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 22 from Patent WO0144510.
ACCESSION AXI166856
VERSION AXI166856.1 GI:14596459
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Query Match 100.0%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 7 GAACGGAAGGCCCTTTCG 24

RESULT 7
AXI166855
LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.8; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 8 GAACGGAAGGCCCTTTCG 25

RESULT 8
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LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 2.8; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 8 GAACGGAAGGCCCTTTCG 25

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REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: WO 0144510-A 22 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Query Match 94.7%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 7 GAACGGAAGGCCCTTTCG 24

RESULT 7
AXI166853
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
Location/Qualifiers
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/mol_type="genomic DNA"

Query Match 94.7%; Score 18; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.8; 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCCCTTTCG 18
Db 8 GAACGGAAGGCCCTTTCG 25

RESULT 8
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LOCUS AXI166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AXI166855
VERSION AXI166855.1 GI:14596458
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
Nucleic acid amplification and detection of mycobacterium species
Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
Location/Qualifiers
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/note="primer oligonucleotide"

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Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAACGGAAGGCTTTCG 18  
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Db 8 GAACGGAAGGCTTTCG 25

RESULT 9  
I82017  
LOCUS I82017 23 bp DNA linear PAT 10-JUN-1998  
DEFINITION Sequence 56 from patent US 5712095.  
ACCESSION I82017  
VERSION I82017.1 GI:3210314  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Britschgi,T.B. and Cangelosi,G.A.  
TITLE Rapid and sensitive detection of antibiotic-resistant mycobacteria  
using oligonucleotide probes specific for ribosomal RNA precursors  
JOURNAL Patent: US 5712095-A 56 27-JAN-1998;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 86.3%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 5.4;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GAACGGAAGGCTTTCG 19  
|||||  
Db 1 GAACGGAAGGCTTTCG 19

RESULT 10  
I91705  
LOCUS I91705 23 bp DNA linear PAT 01-DEC-1998  
DEFINITION Sequence 55 from patent US 5726021.  
ACCESSION I91705  
VERSION I91705.1 GI:3936175  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Britschgi,T.B. and Cangelosi,G.A.  
TITLE Rapid and sensitive detection of antibiotic-resistant mycobacteria  
using oligonucleotide probes specific for ribosomal RNA precursors  
JOURNAL Patent: US 5726021-A 55 10-MAR-1998;  
FEATURES Location/Qualifiers  
source 1..23  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 86.3%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 5.4;  
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OY 1 GAACGGAAGGCTTTCG 19  
|||||  
Db 1 GAACGGAAGGCTTTCG 19

Search completed: May 26, 2006, 14:29:31  
Job time : 0.001 secs

**this Page Blank (uspto)**

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 14:32:49 ; Search time 0.001 Seconds  
(without alignments)  
12.616 Million cell updates/sec

Title: us-10-665-708-24  
Perfect score: 19  
Sequence: 1 gaacggaaggccttcgg 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 16 seqs, 332 residues

Total number of hits satisfying chosen parameters: 32

Minimum DB seq length: 18  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 16 summaries

Database : rnpbmdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	1	US-09-738-274-24
2	19	100.0	19	1	US-10-665-708-24
3	19	100.0	22	1	US-09-738-274-23
4	19	100.0	22	1	US-10-665-708-23
5	18	94.7	24	1	US-09-738-274-22
6	18	94.7	24	1	US-10-665-708-22
7	18	94.7	25	1	US-09-738-274-21
8	18	94.7	25	1	US-10-665-708-21
9	14.8	77.9	20	1	US-10-831-286A-38180
10	14.2	74.7	19	1	US-11-083-784-811277
11	14.2	74.7	19	1	US-11-101-244-811277
12	13.8	72.6	19	1	US-11-083-784-811307
13	13.8	72.6	19	1	US-11-101-244-811307
c 14	13.4	70.5	19	1	US-11-083-784-31921
c 15	13.4	70.5	19	1	US-11-101-244-31921
16	12.8	67.4	18	1	US-10-310-914A-193761

ALIGNMENTS

RESULT 1  
US-09-738-274-24  
; Sequence 24, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES

FILE REFERENCE: GP107-02.UT  
CURRENT APPLICATION NUMBER: US/09/738,274  
CURRENT FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: 60/172,190  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
OTHER INFORMATION: oligonucleotide  
US-09-738-274-24

Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19  
|||||  
Db 1 GAACGGAAGGCCTTCGG 19

RESULT 2  
US-10-665-708-24  
; Sequence 24, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
FILE REFERENCE: GP107-02.UT  
CURRENT APPLICATION NUMBER: US/10/665,708  
CURRENT FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: US/09/738,274  
PRIOR FILING DATE: 2000-12-15  
PRIOR APPLICATION NUMBER: 60/172,190  
PRIOR FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 24  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: primer  
OTHER INFORMATION: oligonucleotide  
US-10-665-708-24

Query Match 100.0%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTCGG 19  
|||||  
Db 1 GAACGGAAGGCCTTCGG 19

RESULT 3  
US-09-738-274-23  
; Sequence 23, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe

; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-23

Query Match 100.0%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCGCTTTTCG 19  
Db 4 GAACGGAAGGCGCTTTTCG 22

## RESULT 4

US-10-665-708-23  
; Sequence 23, Application US/10665708  
; Publication No. US20050100915A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-23

Query Match 100.0%; Score 19; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.8; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCGCTTTTCG 19  
Db 4 GAACGGAAGGCGCTTTTCG 22

## RESULT 5

US-09-738-274-22  
; Sequence 22, Application US/09738274  
; Publication No. US20030165824A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.

; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-22

Query Match 94.7%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18  
Db 7 GAACGGAAGGCGCTTTTCG 24

## RESULT 6

US-10-665-708-22  
; Sequence 22, Application US/10665708  
; Publication No. US20050100915A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-22

Query Match 94.7%; Score 18; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0;

Qy 1 GAACGGAAGGCGCTTTTCG 18  
Db 7 GAACGGAAGGCGCTTTTCG 24

## RESULT 7

US-09-738-274-21  
; Sequence 21, Application US/09738274



Publication No. US20030165824A1  
 GENERAL INFORMATION:  
 APPLICANT: BRENTANO, Steven T.  
 APPLICANT: JUCKER, Markus T.  
 APPLICANT: DELGADO, Francisco D.  
 APPLICANT: CLEUZIAT, Philippe  
 APPLICANT: RODRIGUE, Marc  
 TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
 FILE REFERENCE: GP107-02.UT  
 CURRENT APPLICATION NUMBER: US/09/738,274  
 CURRENT FILING DATE: 2000-12-15  
 PRIOR APPLICATION NUMBER: 60/172,190  
 PRIOR FILING DATE: 1999-12-17  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 21  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: primer  
 OTHER INFORMATION: oligonucleotide  
 US-09-738-274-21

Query Match 94.7%; Score 18; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
 |||||  
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 8  
 US-10-665-708-21  
 Sequence 21, Application US/10665708  
 Publication No. US20050100915A1  
 GENERAL INFORMATION:  
 APPLICANT: BRENTANO, Steven T.  
 APPLICANT: JUCKER, Markus T.  
 APPLICANT: DELGADO, Francisco D.  
 APPLICANT: CLEUZIAT, Philippe  
 APPLICANT: RODRIGUE, Marc  
 TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
 FILE REFERENCE: GP107-02.UT  
 CURRENT APPLICATION NUMBER: US/10/665,708  
 CURRENT FILING DATE: 2003-09-18  
 PRIOR APPLICATION NUMBER: US/09/738,274  
 PRIOR FILING DATE: 2000-12-15  
 PRIOR APPLICATION NUMBER: 60/172,190  
 PRIOR FILING DATE: 1999-12-17  
 NUMBER OF SEQ ID NOS: 42  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 21  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: primer  
 OTHER INFORMATION: oligonucleotide  
 US-10-665-708-21

Query Match 94.7%; Score 18; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.3;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
 |||||  
 Db 8 GAACGGAAGGCTTTTCG 25

RESULT 9  
 US-10-831-286A-38180  
 Sequence 38180, Application US/10831286A  
 Publication No. US20060046246A1  
 GENERAL INFORMATION:  
 APPLICANT: ZENG, QIANDONG  
 APPLICANT: CHATELLIER, SONIA  
 APPLICANT: MOIR, DONALD T.  
 APPLICANT: LACROIX, BRUNA  
 APPLICANT: CHILDRESS, DARRELL  
 TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
 FILE REFERENCE: 032796-174.001  
 CURRENT APPLICATION NUMBER: US/10/831,286A  
 CURRENT FILING DATE: 2004-04-26  
 PRIOR APPLICATION NUMBER: 60/464,955  
 PRIOR FILING DATE: 2003-04-24  
 NUMBER OF SEQ ID NOS: 48788  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 38180  
 LENGTH: 20  
 TYPE: DNA  
 ORGANISM: Corynebacterium jeikeium  
 US-10-831-286A-38180

Query Match 77.9%; Score 14.8; DB 1; Length 20;  
 Best Local Similarity 88.9%; Pred. No. 9.4;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 18  
 |||||  
 Db 1 GAACGGAAGGCTTTTCG 18

RESULT 10  
 US-11-083-784-811277  
 Sequence 811277, Application US/11083784  
 Publication No. US20050245475A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmakon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/083,784  
 CURRENT FILING DATE: 2005-03-18  
 PRIOR APPLICATION NUMBER: US/10/714,333  
 PRIOR FILING DATE: 2003-11-14  
 PRIOR APPLICATION NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIOR APPLICATION NUMBER: 60/426,137  
 PRIOR FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO 811277  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-083-784-811277

Query Match 74.7%; Score 14.2; DB 1; Length 19;  
 Best Local Similarity 68.4%; Pred. No. 12;  
 Matches 13; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTTCG 19  
 |||||  
 Db 1 GAACGGAAGGCTTTTCG 19

RESULT 11  
 US-11-101-244-811277

; Sequence 811277, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101.244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 811277  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-811277

Query Match 74.7%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 68.4%; Pred. No. 12;  
Matches 13; Conservative 3; Mismatches 0; Gaps 0; Indels 3; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTCG 19  
||||||| |:::|  
Db 1 GAACGGAACGCCUUCAG 19

## RESULT 12

US-11-083-784-811307  
; Sequence 811307, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083.784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 811307  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-811307

Query Match 72.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 70.6%; Pred. No. 14;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Indels 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTC 17  
||||||| |:::|  
Db 2 GAACGGAACGCCUUC 18

## RESULT 13

US-11-101-244-811307  
; Sequence 811307, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101.244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 811307  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-811307

Query Match 72.6%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 70.6%; Pred. No. 14;  
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTC 17  
||||||| |:::|  
Db 2 GAACGGAACGCCUUC 18

## RESULT 14

US-11-083-784-31921/c  
; Sequence 31921, Application US/11083784  
; Publication No. US20050245475A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/083.784  
; CURRENT FILING DATE: 2005-03-18  
; PRIOR APPLICATION NUMBER: US/10/714,333  
; PRIOR FILING DATE: 2003-11-14  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 31921  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-083-784-31921

Query Match 70.5%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 15;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Indels 0; Gaps 0;

Qy 5 GGAAAGGCCTTTCGG 19  
||||||| |:::|  
Db 15 GGGAAGGCCTTTCGG 1

RESULT 15  
US-11-101-244-31921/c  
; Sequence 31921, Application US/11101244  
; Publication No. US20050246794A1  
; GENERAL INFORMATION:  
; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khvorova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William  
; APPLICANT: Scaringe, Stephen  
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
; FILE REFERENCE: 13499US  
; CURRENT APPLICATION NUMBER: US/11/101,244  
; CURRENT FILING DATE: 2005-04-07  
; PRIOR APPLICATION NUMBER: 60/502,050  
; PRIOR FILING DATE: 2003-09-10  
; PRIOR APPLICATION NUMBER: 60/426,137  
; PRIOR FILING DATE: 2002-11-14  
; NUMBER OF SEQ ID NOS: 1591911  
; SOFTWARE: Proprietary  
; SEQ ID NO 31921  
; LENGTH: 19  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-11-101-244-31921

Query Match 70.5%; Score 13.4; DB 1; Length 19;  
Best Local Similarity 93.3%; Pred. No. 15;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 5 GGAAAGGCCTTCGG 19  
Db 15 GGAAAGGCCTTCGG 1

RESULT 16  
US-10-310-914A-193761  
; Sequence 193761, Application US/10310914A  
; Publication No. US20060003322A1  
; GENERAL INFORMATION:  
; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shlier, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 193761  
; LENGTH: 18  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-193761

Query Match 67.4%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 68.8%; Pred. No. 19;  
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GAACGGAAGGCCTTT 16  
Db 2 GAACAGAAAGGCAUUU 17

Search completed: May 26, 2006, 14:32:50  
Job time : 1 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 259.361 Seconds  
(without alignments)  
591.412 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22  
Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : N\_Geneseq\_8.\*

1: Geneseqn1980s.\*  
2: Geneseqn1990s.\*  
3: Geneseqn2000s.\*  
4: Geneseqn2001as.\*  
5: Geneseqn2001bs.\*  
6: Geneseqn2002as.\*  
7: Geneseqn2002bs.\*  
8: Geneseqn2003as.\*  
9: Geneseqn2003bs.\*  
10: Geneseqn2003cs.\*  
11: Geneseqn2003ds.\*  
12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*  
15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	4	AD11275 Mycobacte
2	22	100.0	22	10	ADG88356
3	22	100.0	22	14	AEA08231 Mycobacte
4	22	100.0	25	4	AD11276 Mycobacte
5	22	100.0	25	10	ADG88357 Mycobacte
6	22	100.0	25	14	AEA08232 Mycobacte
7	18.8	85.5	23	2	AAK32480 Probe CNB
8	18.8	85.5	166	2	AAK32481 Preferred
9	17.8	80.9	110000	11	ADM27081 Hyperther
10	17.8	80.9	487	11	ADP65654 Human per
11	17.8	80.9	40491	11	ACN4798 Human gen
12	17.4	79.1	74849	11	ACN44932_3
13	17.2	78.2	569	4	ABA59963 Human foe
14	17.2	78.2	569	4	AAI39835 Probe #85
15	17.2	78.2	569	4	ABA28379 Probe #68
16	17.2	78.2	569	4	AAK34112 Human bon
17	17.2	78.2	569	4	AAK08233 Human bra
18	17.2	78.2	569	4	ABS33911 Human liv

19	17.2	78.2	569	6	ABS08880	
20	17.2	78.2	1440	8	ACA36105	
21	17.2	78.2	58822	9	ADA02540	
22	17.2	78.2	58822	10	ADB72278	
23	17.2	78.2	58822	10	ADG95788	
24	17.2	78.2	63686	11	ACN44158	
25	16.8	76.4	276	11	ABD17022	
C	26	16.8	601	13	ACN53618	
C	27	16.8	2107	8	ACA31638	
28	16.8	76.4	110000	14	AD213575_1	
29	16.8	76.4	289190	13	ABD33143	
30	16.4	74.5	309	4	AAH36786	
31	16.4	74.5	521	13	ACN47886	
C	32	16.4	47804	10	ADC86176	
C	33	16.2	73.6	420	4	AAK76977
C	34	16.2	73.6	420	4	AAK76978
35	16.2	73.6	426	11	ADL96630	
36	16.2	73.6	511	12	ACH76350	
C	37	16.2	73.6	590	4	AAH31560
C	38	16.2	73.6	607	12	ADO36603
C	39	16.2	73.6	771	11	ABD02872
40	16.2	73.6	828	11	ABD03097	
41	16.2	73.6	909	7	ADS31309	
42	16.2	73.6	909	7	ADY36697	
C	43	16.2	1218	4	AAI23344	
C	44	16.2	1218	4	ABA68451	
C	45	16.2	1218	4	AAI48666	
C	46	16.2	1218	4	ABA50502	
C	47	16.2	1218	4	ABA35441	
C	48	16.2	1218	4	AAK42594	
C	49	16.2	1218	4	AAK16823	
C	50	16.2	1218	4	ABS42209	
C	51	16.2	1218	5	AAI08981	
C	52	16.2	1218	6	ABS16646	
C	53	16.2	1239	11	ABD02999	
54	16.2	73.6	1377	8	ACA38376	
55	16.2	73.6	1380	8	ACA40722	
C	56	16.2	1704	6	AAS94778	
C	57	16.2	1740	4	AAC85094	
C	58	16.2	1740	11	ADM29578	
C	59	16.2	1954	4	AAI14134	
C	60	16.2	1954	4	ABA55860	
C	61	16.2	1954	4	AAI35517	
C	62	16.2	1954	4	ABA45372	
C	63	16.2	1954	4	ABA25535	
C	64	16.2	1954	4	AAK29561	
C	65	16.2	1954	4	AAK04079	
C	66	16.2	1954	4	ABS29189	
C	67	16.2	1954	5	AAI03983	
C	68	16.2	1954	6	ABS04116	
C	69	16.2	2772	6	ABQ54935	
70	16.2	73.6	3135	13	ADV35075	
71	16.2	73.6	4258	11	ADP65658	
72	16.2	73.6	4395	3	AAK77830	
C	73	16.2	4415	11	ADL96632	
74	16.2	73.6	4670	14	AEA20710	
75	16.2	73.6	4738	14	ADY91665	
76	16.2	73.6	4758	10	ABX93240	
77	16.2	73.6	4831	10	ADK41009	
78	16.2	73.6	4831	13	ADRI5723	
79	16.2	73.6	5970	2	AAK26546	
80	16.2	73.6	5994	10	ADB80558	
81	16.2	73.6	5994	10	ADB79896	
82	16.2	73.6	5994	12	ADQ19074	
83	16.2	73.6	6315	14	AEA19724	
84	16.2	73.6	6332	4	ABA09565	
85	16.2	73.6	8411	12	ADL12831	
86	16.2	73.6	8412	12	ADE77058	
87	16.2	73.6	14063	4	AAK82933	
88	16.2	73.6	14063	4	AAK82934	
89	16.2	73.6	25759	11	ADM22177	
90	16.2	73.6	104932	14	ABS96542	
C	91	16.2	106664	13	ADV35021	

ABS08880	Human gen
ACA36105	Prokaryot
ADA02540	Human TCO
ADB72278	Human TCO
ADG95788	Human TCO
ACN44158	Human gen
ABD17022	Pseudomon
ACA31638	Prokaryot
AD213575_1	Continuation (2 of
ABD33143	Murine ca
AAH36786	Human col
ACN47886	Cotton pr
ADC86176	Human imm
AAK76977	Human imm
AAK76978	Human imm
ADL96630	M. paratu
ACH76350	Human gen
AAH31560	Human olf
ADO36603	Isoquinol
ABD02872	Pseudomon
ABD03097	Pseudomon
ADS31309	Human gen
ADY36697	HIRA geno
AAI23344	Probe #13
ABA68451	Human foe
AAI48666	Probe #17
ABA50502	Human bre
ABA35441	Probe #13
AAK42594	Human bon
AAK16823	Human bra
ABS42209	Human liv
AAI08981	Probe #89
ABS16646	Human gen
ABD02999	Pseudomon
ACA38376	Prokaryot
ACA40722	Prokaryot
AAS94778	Human DNA
AAC85094	Atheroscl
ADM29578	Human ath
AAI14134	Probe #40
ABA55860	Human foe
AAI35517	Probe #42
ABA45372	Human bre
ABA25535	Probe #40
AAK29561	Human bon
AAK04079	Human bra
ABS29189	Human liv
AAI03983	Probe #39
ABS04116	Human gen
ABQ54935	Human ova
ADV35075	Human cdN
ADP65658	Human mit
AAK77830	Human can
ADL96632	M. paratu
AEA20710	Novel hum
ADY91665	Human pro
ABX93240	Full-leng
ADK41009	Novel hum
ADRI5723	Kinase 69
AAK26546	Nucleic a
ADB80558	Ovarian c
ADB79896	Human put
ADQ19074	Human sof
AEA19724	Novel hum
ABA09565	Human car
ADL12831	Human ste
ADE77058	Human cdN
AAK82933	Human imm
AAK82934	Human imm
ADM22177	Rat hepat
ABS96542	Human STA
ADV35021	Murine cd

C 92	16.2	73.6	110000	4	AAI99682_30	Continuation (31 o	C 165	15.6	70.9	487	6	ABS02690	Abso2690 Human gen
C 93	16.2	73.6	110000	4	AAI99682_31	Continuation (32 o	C 166	15.6	70.9	502	4	ABA08675	ABA08675 Human R31
C 94	16.2	73.6	110000	4	AAI99683_30	Continuation (31 o	C 167	15.6	70.9	502	10	ADF60129	ADF60129 Human con
C 95	16	72.7	287	9	ADB82110	ADB82110 Human cdn	C 168	15.6	70.9	516	12	ACH77191	ACH77191 Human gen
C 96	16	72.7	331	6	ABQ89167	ABQ89167 Human gen	C 169	15.6	70.9	597	12	ACH68923	ACH68923 Human gen
C 97	15.8	71.8	132	8	ABX64840	ABX64840 Human gen	C 170	15.6	70.9	641	4	AAH31571	AAH31571 Human oif
C 98	15.8	71.8	362	13	ADQ50381	ADQ50381 Novel can	C 171	15.6	70.9	651	4	AAH31541	AAH31541 Human oif
C 99	15.8	71.8	579	9	ADA28874	ADA28874 DNA encod	C 172	15.6	70.9	701	4	AAH92121	AAH92121 Human cdn
C 100	15.8	71.8	665	8	ABZ54797	ABZ54797 Aspergill	C 173	15.6	70.9	701	4	AAK93385	AAK93385 Human cdn
C 101	15.8	71.8	859	5	ABV03387	ABV03387 Human pro	C 174	15.6	70.9	701	12	ADL28548	ADL28548 5' end of
C 102	15.8	71.8	900	14	ADY26912	ADY26912 Vimentin	C 175	15.6	70.9	701	12	ADL29812	ADL29812 5' end of
C 103	15.8	71.8	2000	12	ADJ40830	ADJ40830 Plant cdn	C 176	15.6	70.9	729	12	ACH87086	ACH87086 Human gen
C 104	15.8	71.8	2001	14	ADY26869	ADY26869 Vimentin	C 177	15.6	70.9	777	3	ACAC78029	ACAC78029 Human can
C 105	15.8	71.8	3789	12	ADQ64482	ADQ64482 Novel hum	C 178	15.6	70.9	783	6	ABQ45189	ABQ45189 Oligonuc
C 106	15.8	71.8	5328	4	AAK76010	AAK76010 Human imm	C 179	15.6	70.9	783	6	ABQ45188	ABQ45188 Oligonuc
C 107	15.8	71.8	5328	4	AAK76011	AAK76011 Human imm	C 180	15.6	70.9	820	5	ABV11138	ABV11138 Human pro
C 108	15.8	71.8	6279	4	ABL09332	ABL09332 Drosophi	C 181	15.6	70.9	875	4	AAK94431	AAK94431 Human ful
C 109	15.8	71.8	9661	4	ABL09504	ABL09504 Drosophi	C 182	15.6	70.9	875	12	ADL31179	ADL31179 Full leng
C 110	15.8	71.8	48300	5	AAF61281	AAF61281 N. magada	C 183	15.6	70.9	893	2	AAZ40786	AAZ40786 Secreted
C 111	15.8	71.8	118544	12	ADQ97100	ADQ97100 Human can	C 184	15.6	70.9	893	11	ADM77763	ADM77763 Human cdn
C 112	15.8	71.8	159400	6	ABQ88126	ABQ88126 Human ost	C 185	15.6	70.9	893	12	ADP19084	ADP19084 Human sec
C 113	15.8	71.8	172984	8	ACF62733	ACF62733 Cancer ba	C 186	15.6	70.9	893	14	ADZ89223	ADZ89223 Secreted
C 114	15.8	71.8	172984	8	ADB20848	ADB20848 MRP1 base	C 187	15.6	70.9	933	4	AAH00857	AAH00857 Leishmani
C 115	15.8	71.8	172984	10	ADB87937	ADB87937 Human UGT	C 188	15.6	70.9	948	4	AAH31841	AAH31841 Human oif
C 116	15.8	71.8	172984	10	ADB96930	ADB96930 Human MDR	C 189	15.6	70.9	948	4	AAH32188	AAH32188 Human oif
C 117	15.8	71.8	172984	10	ADB92111	ADB92111 Human MDR	C 190	15.6	70.9	948	4	AAH32375	AAH32375 Human oif
C 118	15.6	70.9	114	4	ABA70662	ABA70662 Human foe	C 191	15.6	70.9	951	6	ABZ43029	ABZ43029 Human gpc
C 119	15.6	70.9	114	4	AAI50828	AAI50828 Probe #19	C 192	15.6	70.9	960	6	ABL99835	ABL99835 Human sec
C 120	15.6	70.9	114	4	AAK44852	AAK44852 Human bon	C 193	15.6	70.9	967	6	ABT04182	ABT04182 Human G-p
C 121	15.6	70.9	114	4	AAK18908	AAK18908 Human bra	C 194	15.6	70.9	967	6	ABT04183	ABT04183 Human G-p
C 122	15.6	70.9	114	4	ABS44514	ABS44514 Human liv	C 195	15.6	70.9	967	12	ADH30905	ADH30905 Human G-p
C 123	15.6	70.9	114	6	ABS19093	ABS19093 Human gen	C 196	15.6	70.9	967	12	ADH30903	ADH30903 Human G-p
C 124	15.6	70.9	208	8	ABX35037	ABX35037 Bovine ES	C 197	15.6	70.9	1015	3	AAZ87206	AAZ87206 Human NTA
C 125	15.6	70.9	221	12	ACH82623	ACH82623 Human gen	C 198	15.6	70.9	1057	10	ADL21845	ADL21845 Novel hum
C 126	15.6	70.9	329	2	AAK40619	AAK40619 Human sec	C 199	15.6	70.9	1057	6	ABL40538	ABL40538 Basidiomy
C 127	15.6	70.9	367	6	ABK15957	ABK15957 Human lun	C 200	15.6	70.9	1247	2	AAQ90650	AAQ90650 Rat galec
C 128	15.6	70.9	367	10	ADB95920	ADB95920 Human lun	C 201	15.6	70.9	1247	10	ADD90597	ADD90597 Rat galec
C 129	15.6	70.9	366	9	ACH18348	ACH18348 Human adu	C 202	15.6	70.9	1247	12	ADL13480	ADL13480 Rat galec
C 130	15.6	70.9	386	4	ABA58058	ABA58058 Human foe	C 203	15.6	70.9	1263	6	ABQ50083	ABQ50083 Oligonuc
C 131	15.6	70.9	386	4	AAI37658	AAI37658 Probe #63	C 204	15.6	70.9	1263	6	ABQ50082	ABQ50082 Oligonuc
C 132	15.6	70.9	396	4	AAK31783	AAK31783 Human bon	C 205	15.6	70.9	1265	6	ABQ28517	ABQ28517 Oligonuc
C 133	15.6	70.9	396	4	AAK06130	AAK06130 Human bra	C 206	15.6	70.9	1265	6	ABQ28516	ABQ28516 Oligonuc
C 134	15.6	70.9	396	4	ABS31469	ABS31469 Human liv	C 207	15.6	70.9	1325	12	ADK14124	ADK14124 Human aut
C 135	15.6	70.9	396	6	ABS06541	ABS06541 Human gen	C 208	15.6	70.9	1325	12	ADN14333	ADN14333 Human hom
C 136	15.6	70.9	405	4	AAI02356	AAI02356 Human iep	C 209	15.6	70.9	1325	13	ADR25738	ADR25738 Breast ca
C 137	15.6	70.9	407	4	AAI14836	AAI14836 Probe #47	C 210	15.6	70.9	1325	14	ADW80340	ADW80340 Human typ
C 138	15.6	70.9	407	4	ABA56566	ABA56566 Human foe	C 211	15.6	70.9	1343	12	ACH90897	ACH90897 Human gen
C 139	15.6	70.9	407	4	AAI36194	AAI36194 Probe #48	C 212	15.6	70.9	1388	3	AAAC59295	AAAC59295 Human sec
C 140	15.6	70.9	407	4	ABA46028	ABA46028 Human bre	C 213	15.6	70.9	1400	14	AED73400	AED73400 Human pla
C 141	15.6	70.9	407	4	ABA26185	ABA26185 Probe #46	C 214	15.6	70.9	1410	6	ABK73375	ABK73375 Bacillus
C 142	15.6	70.9	407	4	AAK30233	AAK30233 Human bon	C 215	15.6	70.9	1429	11	ADL31363	ADL31363 Human cdn
C 143	15.6	70.9	407	4	AAK04717	AAK04717 Human bra	C 216	15.6	70.9	1429	13	ADS83430	ADS83430 Human lym
C 144	15.6	70.9	407	5	AAI04622	AAI04622 Probe #46	C 217	15.6	70.9	1449	11	ACH96943	ACH96943 Klebsiell
C 145	15.6	70.9	407	6	ABS04821	ABS04821 Human gen	C 218	15.6	70.9	1596	12	ADN98896	ADN98896 Novel hum
C 146	15.6	70.9	422	10	ADC31993	ADC31993 Human nov	C 219	15.6	70.9	1596	12	ADO00465	ADO00465 Novel hum
C 147	15.6	70.9	436	9	ACH47589	ACH47589 Human inf	C 220	15.6	70.9	1746	2	AAK58059	AAK58059 Canine GA
C 148	15.6	70.9	459	9	ACH28774	ACH28774 Human adu	C 221	15.6	70.9	1761	8	ACA26579	ACA26579 Prokaryot
C 149	15.6	70.9	477	10	ADA19380	ADA19380 Human lns	C 222	15.6	70.9	1862	10	ADB62746	ADB62746 Human cdn
C 150	15.6	70.9	477	13	ACF85952	ACF85952 Human SIR	C 223	15.6	70.9	1917	10	ADL21386	ADL21386 Novel hum
C 151	15.6	70.9	479	3	AAZ43020	AAZ43020 Human 5'	C 224	15.6	70.9	1918	4	AAH98371	AAH98371 Human EST
C 152	15.6	70.9	479	13	ADU72182	ADU72182 Signal pe	C 225	15.6	70.9	1934	10	ADC29972	ADC29972 Human nov
C 153	15.6	70.9	479	14	ADZ73173	ADZ73173 Human 5'	C 226	15.6	70.9	1990	10	ACA56458	ACA56458 Human sig
C 154	15.6	70.9	485	13	ACF89723	ACF89723 Human SIR	C 227	15.6	70.9	1990	12	ADL56254	ADL56254 Human pol
C 155	15.6	70.9	486	2	AAZ33493	AAZ33493 Human pro	C 228	15.6	70.9	2120	13	ADL561102	ADL561102 Bacterial
C 156	15.6	70.9	487	4	AAI12753	AAI12753 Probe #26	C 229	15.6	70.9	2129	10	ABZ79877	ABZ79877 Human nuc
C 157	15.6	70.9	487	4	ABA54448	ABA54448 Human foe	C 230	15.6	70.9	2130	13	ADR07764	ADR07764 Full leng
C 158	15.6	70.9	487	4	AAI34102	AAI34102 Probe #27	C 231	15.6	70.9	2287	10	ADC30627	ADC30627 Human nov
C 159	15.6	70.9	487	4	ABA43994	ABA43994 Human bre	C 232	15.6	70.9	2297	10	ADA52853	ADA52853 Human cod
C 160	15.6	70.9	487	4	ABA24230	ABA24230 Probe #26	C 233	15.6	70.9	2304	14	AED30768	AED30768 Human pos
C 161	15.6	70.9	487	4	AAK28180	AAK28180 Human bon	C 234	15.6	70.9	2708	4	ABU12610	ABU12610 Drosophil
C 162	15.6	70.9	487	4	AAK02739	AAK02739 Human bra	C 235	15.6	70.9	2895	2	AAK58058	AAK58058 Canine GA
C 163	15.6	70.9	487	4	ABS27785	ABS27785 Human liv	C 236	15.6	70.9	3205	13	ADV41710	ADV41710 Rat cardl
C 164	15.6	70.9	487	5	AAI02663	AAI02663 Probe #26	C 237	15.6	70.9	3568	3	AAAC76411	AAAC76411 Human ORF

c 238	15.6	70.9	3995	6	ABK35489	Abk35489 Human end	XX	24-SEP-2001	(first entry)
c 239	15.6	70.9	3995	6	ABK35548	Abk35548 Gene DLG4	DT		
c 240	15.6	70.9	3995	6	ABV78023	ABV78023 Hypoxia-r	XX		
c 241	15.6	70.9	3995	9	ACC85074	Acc85074 Human MBC	DE		
c 242	15.6	70.9	4857	10	ACC42643	Acc42643 Maize dek	XX		
c 243	15.6	70.9	4928	4	ABL12611	ABL12611 Drosophila	KW		
c 244	15.6	70.9	5514	4	ABL12193	ABL12193 Drosophila	KW		
c 245	15.6	70.9	5862	4	AAL04675	Aal04675 Human rep	XX		
c 246	15.6	70.9	5862	4	ABL97582	Ab197582 Human tes	OS		
c 247	15.6	70.9	6065	4	AAL06964	Aal06964 Human rep	XX		
c 248	15.6	70.9	6831	10	ADC24898	Adc24898 Human bre	PN		
c 249	15.6	70.9	7110	10	ACC42659	Acc42659 Maize dek	XX		
c 250	15.6	70.9	7110	13	ADT16606	Adt16606 Plant con	PD		
c 251	15.6	70.9	15762	4	ABL06916	Ab106916 Drosophila	XX		
c 252	15.6	70.9	22970	10	ADK70082	Adk70082 Mutant hu	PF		
c 253	15.6	70.9	22970	10	ADK70081	Adk70081 Wild type	XX		
c 254	15.6	70.9	25411	10	ACC42660	Acc42660 Maize dek	XX		
c 255	15.6	70.9	32249	4	AAL04676	Aal04676 Human rep	XX		
c 256	15.6	70.9	32249	4	ABL97583	Ab197583 Human tes	PA		
c 257	15.6	70.9	32548	4	ABL29482	Ab129482 Drosophila	PA		
c 258	15.6	70.9	33634	11	ACN45028	Acn45028 Mouse gen	XX		
c 259	15.6	70.9	34115	8	AAL56708	Aal56708 Rhesus mo	PI		
c 260	15.6	70.9	34115	14	ADM42639	Adm42639 Chimpanze	XX		
c 261	15.6	70.9	34471	13	ADR66979	Adr66979 Mouse can	DR		
c 262	15.6	70.9	34471	14	ADZ12758	Adz12758 Murine ca	XX		
c 263	15.6	70.9	38726	4	AAS59513	Aas59513 Propionib	PT		
c 264	15.6	70.9	38726	8	ACF64442	Acf64442 Propionib	PT		
c 265	15.6	70.9	41400	10	ABX77189	Abx77189 Mouse BAC	XX		
c 266	15.6	70.9	47988	10	ADR86070	Adr86070 Streptomy	XX		
c 267	15.6	70.9	52659	9	AAL60188	Aal60188 Paederus	PS		
c 268	15.6	70.9	82615	9	ACA60905	Ac60905 Human tra	XX		
c 269	15.6	70.9	82615	14	AEA04986	Aea04986 Human tra	CC		
c 270	15.6	70.9	94001	13	ADJ33491	Adj33491 Human LAR	CC		
c 271	15.6	70.9	94941	15	AEF80170	Aef80170 Cancer-as	CC		
c 272	15.6	70.9	110000	13	ABD32629_2	Abd32629_2	CC		
c 273	15.6	70.9	110000	14	ADQ12821_3	Adq12821_3	CC		
c 274	15.6	70.9	114771	12	ADQ17641	Adq17641 Human sof	CC		
c 275	15.6	70.9	127222	12	ADQ97301	Adq97301 Human can	CC		
c 276	15.6	70.9	142299	10	ADP50651	Adp50651 BAC seque	CC		
c 277	15.6	70.9	142299	14	ADV77909	Adv77909 Human BAC	CC		
c 278	15.6	70.9	227246	13	ABD33272	Abd33272 Human can	CC		
c 279	15.4	70.0	23	12	ADH09470	Adh09470 Propionib	CC		
c 280	15.4	70.0	383	12	ADF13121	Adf13121 Hypermeth	XX		
c 281	15.4	70.0	383	12	ADJ37267	Adj37267 Hypermeth	XX		
c 282	15.4	70.0	668	13	AAF12059	Aaf12059 Aspergill	XX		
c 283	15.4	70.0	668	13	ADU56100	Adu56100 Aspergill	XX		
c 284	15.4	70.0	668	14	ADZ94103	Adz94103 Aspergill	XX		
c 285	15.4	70.0	911	6	ABN73985	Abn73985 Bovine em	XX		
c 286	15.4	70.0	1463	15	AEF24215	Aef24215 16S rRNA	XX		
c 287	15.4	70.0	3198	5	AAH81777	Aah81777 Human dif	XX		
c 288	15.4	70.0	3198	6	AAI67787	Aai67787 Human lys	XX		
c 289	15.4	70.0	3198	6	ABQ88184	Abq88184 Human ost	XX		
c 290	15.4	70.0	3198	6	ABX04181	Abx04181 Human mRN	XX		
c 291	15.4	70.0	3432	12	ADQ85032	Adq85032 Human tum	XX		
c 292	15.4	70.0	3573	13	ACN43163	Acn43163 Human dia	XX		
c 293	15.4	70.0	3594	13	ACN43162	Acn43162 Human dia	XX		
c 294	15.4	70.0	3609	13	ACN43161	Acn43161 Human dia	XX		
c 295	15.4	70.0	3630	13	ACN43160	Acn43160 Human dia	XX		
c 296	15.4	70.0	3723	13	ACN43159	Acn43159 Human dia	XX		
c 297	15.4	70.0	3804	13	ACN43158	Acn43158 Human dia	XX		
c 298	15.4	70.0	8653	5	ABAI5780	Abai5780 Human ner	XX		
c 299	15.4	70.0	61710	4	AAK83782	Aak83782 Human imm	XX		
c 300	15.4	70.0	61710	4	AAK83782	Aak83782 Human imm	XX		

ALIGNMENTS

RESULT 1  
AAD11275  
ID AAD11275 standard; DNA; 22 BP.  
XX  
AC AAD11275;

Query Match 100.0%; Score 22; DB 4; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.7;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAAGGCCTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | |  
Db 1 GAAAGGCCTTCGGGGTGCTC 22  
RESULT 2  
ADG88356  
ID ADG88356 standard; DNA; 22 BP.  
XX  
AC ADG88356;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Mycobacterium amplifying PCR primer #25.  
XX  
KW In vitro amplification; PCR; primer; ss.  
XX  
OS Mycobacterium celatum.  
XX  
PN US2003165824-A1.  
XX  
PD 04-SEP-2003.  
XX  
PF 15-DEC-2000; 2000US-00738274.

Claim 1; Page 37; 44pp; English.  
Detecting Mycobacterium species, involves in vitro amplification of 16S rRNA or DNA encoding RNA in nucleic acid amplification mixture using specific primers, and detecting the amplified nucleic acid.  
The invention relates to a method of detecting Mycobacterium species, that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA encoding 16S rRNA in an in vitro nucleic acid amplification mixture comprising a polymerase, and at least two primers, and then detecting the amplified nucleic acid. The method is relatively simple and useful for detecting the presence of various Mycobacterium species in a biological sample, and thus important for diagnosis of infections resulting from them. The method is especially important for screening opportunistic infections caused by M. tuberculosis or a Mycobacterium other than tuberculosis (MOTT). The present sequence is a PCR primer used for amplifying Mycobacterium 16S rRNA

24-SEP-2001 (first entry)  
Mycobacterium 16S rRNA amplifying primer #19.  
Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.  
Mycobacterium sp.  
WO200144510-A2.  
21-JUN-2001.  
17-DEC-1999; 99WO-US030346.  
17-DEC-1999; 99WO-US030346.  
(GENP)-GEN-PROBE INC.  
(INMR ) BIOMERIEUX SA.  
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
WFI; 2001-398170/42.  
Detecting Mycobacterium species, involves in vitro amplification of 16S rRNA or DNA encoding RNA in nucleic acid amplification mixture using specific primers, and detecting the amplified nucleic acid.

```

XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 25; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 3 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGTGCTC 22
XX
RESULT 4
ID AAD11276 standard; DNA; 25 BP.
XX
XX AAD11276;
XX
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying primer #20.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 37; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX the method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 4; Length 25;

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Best Local Similarity 100.0%; Pred. No. 0.71; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 5
ADG88357
ID ADG88357 standard; DNA; 25 BP.
XX
AC ADG88357;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #26.
XX
XX In vitro amplification; PCR; primer; ss.
KW Mycobacterium celatum.
XX
OS
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 26; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 6
AEA08232
ID AEA08232 standard; DNA; 25 BP.
XX
AC AEA08232;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 26.
XX

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KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
PR 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Example 3; SEQ ID NO 26; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
XX amplifying non-T7 PCR primer.
XX
XX Sequence 25 BP; 4 A; 5 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.71;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGGTGCTC 22

RESULT 7
AAX32480
ID AAX32480 standard; DNA; 23 BP.
XX
AC AAX32480;
XX
XX 22-JUN-1999 (first entry)
DE
DE Probe CNB-ESP derived from a variable region of 16S rRNA.
XX
XX 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
XX
XX Synthetic.
XX
XX Streptomyces ambofaciens.
XX
XX WO9914361-A1.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-EP006038.
XX
XX 18-SEP-1997; 97US-0059295P.
XX
XX 16-DEC-1997; 97US-0069748P.
XX

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PA (MERI ) MERCK SHARP & DOHME ESPANA SAE.
XX
XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
XX WPI; 1999-229548/19.
DR
XX
XX New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.
PT
XX
XX Claim 5; Page 13; 22pp; English.
PS
XX
XX The invention relates to a novel nucleic acid probe hybridises to a
CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
CC under hybridisation conditions, and does not hybridise to nucleic acids
CC encoding a portion of 16S rRNA of streptomycetes under identical
CC hybridisation conditions. The probes can be used for detecting the
CC presence of maduromycetes bacteria in a sample and for differentiating
CC between maduromycetes and streptomycetes bacteria in a sample. The
CC present sequence represents a probe derived from a highly variable region
CC of 16S rRNA molecule
XX
XX Sequence 23 BP; 4 A; 6 C; 9 G; 4 T; 0 U; 0 Other;
SQ
Query Match 85.5%; Score 18.8; DB 2; Length 23;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 1 GAAAGGCCTTTCGGGGTGACTC 22
RESULT 8
AA32481
ID AAX32481 standard; DNA; 166 BP.
XX
XX AAX32481;
AC
XX
XX 22-JUN-1999 (first entry)
DT
XX
XX Preferred probe of the invention.
DE
XX
XX 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.
KW
XX
XX Synthetic.
OS
XX Streptomycetes ambofaciens.
XX
XX WO9914361-A1.
PN
XX
XX 25-MAR-1999.
PD
XX
XX 16-SEP-1998; 98WO-EP006038.
PF
XX
XX 18-SEP-1997; 97US-0059295P.
PR
XX 16-DEC-1997; 97US-0069748P.
XX
XX (MERI ) MERCK SHARP & DOHME ESPANA SAE.
PA
XX
XX Genilloud O, Mellado RP, Parro V, Rodriguez V;
PI
XX
XX WPI; 1999-229548/19.
DR
XX
XX New probes used for detection of maduromycetes bacteria and to
PT differentiate between maduromycetes and streptomycetes.
PT
XX
XX Disclosure; Fig 1; 22pp; English.
PS
XX
XX The invention relates to a novel nucleic acid probe hybridises to a
CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria
CC under hybridisation conditions, and does not hybridise to nucleic acids
CC encoding a portion of 16S rRNA of streptomycetes under identical
CC hybridisation conditions. The probes can be used for detecting the
CC presence of maduromycetes bacteria in a sample and for differentiating
CC
```

```
CC between maduromycetes and streptomycetes bacteria in a sample. The
CC present sequence represents a preferred probe of the invention
XX
XX Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;
SQ
Query Match 85.5%; Score 18.8; DB 2; Length 166;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
Db 68 GAAAGGCCTTTCGGGGTGACTC 89
RESULT 9
ADM27081_00/c
WP Sequence split into 17 fragments LOCUS ADM27081 Accession Adm27081
WP Fragment Name Begin End
WP ADM27081_00 1 110000
WP ADM27081_01 100001 210000
WP ADM27081_02 200001 310000
WP ADM27081_03 300001 410000
WP ADM27081_04 400001 510000
WP ADM27081_05 500001 610000
WP ADM27081_06 600001 710000
WP ADM27081_07 700001 810000
WP ADM27081_08 800001 910000
WP ADM27081_09 900001 1010000
WP ADM27081_10 1000001 1110000
WP ADM27081_11 1100001 1210000
WP ADM27081_12 1200001 1310000
WP ADM27081_13 1300001 1410000
WP ADM27081_14 1400001 1510000
WP ADM27081_15 1500001 1610000
WP ADM27081_16 1600001 1694968
ID ADM27081 standard; DNA; 1694968 BP.
XX
XX ADM27081;
AC
XX
XX 20-MAY-2004 (first entry)
DT
XX
XX Hyperthermophile Methanopyrus kandleri complete genome.
DE
XX
XX hyperthermophile; protein stability enhancement;
KW
XX protein activity enhancement; ds.
XX
XX Methanopyrus kandleri.
OS
XX
XX WO2003076575-A2.
PN
XX
XX 18-SEP-2003.
PD
XX
XX 04-MAR-2003; 2003WO-US006664.
PF
XX
XX 04-MAY-2002; 2002US-0361742P.
PR
XX 14-MAY-2002; 2002US-0380423P.
XX 16-SEP-2002; 2002US-0410974P.
XX
XX (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY/) MALYKH A.
XX
XX Slesarev AI, Pavlov A, Pavlova N, Kozyavkin S;
PI
XX
XX WPI; 2003-748383/70.
DR
XX
XX New isolated nucleic acids encoding any of about 1700 Methanopyrus
PT kandleri proteins, and the encoded proteins, useful as a medicaments or
PT as diagnostic agents.
XX
XX Claim 17; SEQ ID NO 1693; 1023pp; English.
PS
XX
XX The invention comprises the amino acid sequence of proteins from the
XX hyperthermophile Methanopyrus kandleri, the invention also comprises the
CC
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CC complete genome from Methanopyrus kandleri. The Methanopyrus kandleri  
 CC proteins of the invention are useful for enhancing the stability and/or  
 CC activity of other proteins. The Methanopyrus kandleri genome is useful in  
 CC a variety of diagnostic and analytical methods. The present DNA sequence  
 CC represents the Methanopyrus kandleri complete genome.

XX Sequence 1694968 BP; 329927A; 520759C; 515869G; 328413T; 0U; 0Other;  
 Query Match 85.5%; Score 18.8; DB 11; Length 110000;  
 Best Local Similarity 90.9%; Pred. No. 50;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 54678 GAAAGGCTTTCGGGGTGATC 54657

# RESULT 10

ADP65654

ID ADP65654 standard; DNA; 487 BP.

XX AC ADP65654;

XX 12-AUG-2004 (first entry)

DE Human peripheral benzodiazepine receptor gene, exon 2 DNA.

XX autoimmune disease; arthritis; gene expression analysis;  
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; anti-rheumatic;  
 KW antiarthritis; osteoarthritis; antigout; antiinflammatory; dermatological;  
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;  
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;  
 KW immune; ds; human.

XX Homo sapiens.

XX WO2003072827-A1.

XX 04-SEP-2003.

XX 31-OCT-2002; 2002WO-US035433.

XX 31-OCT-2001; 2001US-0336220P.

XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

XX Hirsch R, Thorton SL;

XX WPI; 2003-712740/67.

XX GENBANK; L21952.

PT Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.

XX Disclosure; Page; 56pp; English.

XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following

CC activities: immunosuppressive, antirheumatic, antiarthritis, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.

XX Sequence 487 BP; 67 A; 168 C; 156 G; 96 T; 0 U; 0 Other;

Query Match 80.9%; Score 17.8; DB 11; Length 487;

Best Local Similarity 90.5%; Pred. No. 1e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21

|||  
 Db 79 GACAGGCTTTCGGGGTGCT 99

# RESULT 11

ACN44798/c

ID ACN44798 standard; DNA; 40491 BP.

XX AC ACN44798;

XX 18-NOV-2004 (first entry)

DE Human genomic sequence hCG41911.

KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.

XX Homo sapiens.

XX WO2003073826-A2.

XX 12-SEP-2003.

XX 28-FEB-2003; 2003WO-US006235.

XX 01-MAR-2002; 2002US-00087192.

XX (SAGR-) SAGRES DISCOVERY.

XX Morris DW;

XX WPI; 2003-328604/31.

PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma  
 PT comprises a nucleotide sequence.

XX Claim 1; SEQ ID NO 1426; 0pp; English.

XX The present invention relates to novel DNA and protein sequences which  
 CC are associated with carcinomas. The sequences are useful for: (i) for  
 CC screening drug candidates; (ii) for screening of bioactive agent capable  
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of  
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;  
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for  
 CC determining Carcinoma Associated (CA) gene copy number. In addition, the  
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
 CC carcinoma including lymphoma. The present sequence is one such CA coding  
 CC sequence. Note: This patent is an equivalent to basic patent  
 CC US2002182586A1, for which no sequence data was published

XX Sequence 40491 BP; 9332 A; 11009 C; 11280 G; 8870 T; 0 U; 0 Other;

Query Match 80.9%; Score 17.8; DB 11; Length 40491;  
Best Local Similarity 90.5%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCGGGGTGCT 21  
DB 37999 GACAGGCCTTCGGGGTGCT 37979

RESULT 12  
ACN44932\_3  
Continuation (4 of 4) of ACN44932 from base 300001 (Mouse genomic sequence MCG5728. )  
WP Sequence split into 4 fragments LOCUS ACN44932 Accession ACN44932  
Fragment Name Begin End  
WP ACN44932\_0 1 110000  
WP ACN44932\_1 100001 210000  
WP ACN44932\_2 200001 310000  
WP ACN44932\_3 300001 374849

Query Match 79.1%; Score 17.4; DB 11; Length 74849;  
Best Local Similarity 94.7%; Pred. No. 2.4e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGCCTTCGGGGTGCT 21  
DB 53594 AAGGCCTTCAGGGTGCT 53612

RESULT 13  
ABA59963  
ID ABA59963 standard; DNA; 569 BP.  
XX AC ABA59963;  
XX AC ABA59963;  
DT 01-FEB-2002 (first entry)  
XX XX  
DE Human foetal liver single exon nucleic acid probe #8268.  
XX Human foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.  
XX Homo sapiens.  
XX WO200157277-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000669.  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-483447/52.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human foetal liver.  
XX Claim 1; SEQ ID NO 8268; 639pp + Sequence Listing; English.  
XX The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a single exon nucleic acid probe of the invention.  
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 4; Length 569;  
Best Local Similarity 86.4%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCGGGGTGCTC 22  
DB 290 GAAAGCCTTCAGGGTGCTC 311

RESULT 14  
AAI39835  
ID AAI39835 standard; DNA; 569 BP.  
XX AC AAI39835;  
XX AC AAI39835;  
DT 17-OCT-2001 (first entry)  
XX XX  
DE Probe #8521 used to measure gene expression in human placenta sample.  
XX Probe; microarray; human; placenta; antenatal diagnosis;  
XX genetic disorder; ss.  
XX Homo sapiens.  
XX WO200157272-A2.  
XX 09-AUG-2001.  
XX 30-JAN-2001; 2001WO-US000663.  
XX 04-FEB-2000; 2000US-0180312P.  
XX 26-MAY-2000; 2000US-0207456P.  
XX 30-JUN-2000; 2000US-00608408.  
XX 03-AUG-2000; 2000US-00632366.  
XX 21-SEP-2000; 2000US-0234687P.  
XX 27-SEP-2000; 2000US-0236359P.  
XX 04-OCT-2000; 2000GB-00024263.  
XX (MOLE-) MOLECULAR DYNAMICS INC.  
XX Penn SG, Hanzel DK, Chen W, Rank DR;  
XX WPI; 2001-488897/53.  
XX Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.  
XX Claim 25; SEQ ID NO 8521; 654pp; English.  
XX The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders  
XX  
SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 4; Length 569;  
Best Local Similarity 86.4%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCGGGGTGCTC 22  
DB 290 GAAAGCCTTCAGGGTGCTC 311

RESULT 15  
ABA28379

```
ID  ABA28379 standard; DNA; 569 BP.
XX
AC  ABA28379;
XX
DT  23-JAN-2002 (first entry)
XX
DE  Probe #6845 for gene expression analysis in human heart cell sample.
XX
KW  Human; gene expression; heart; microarray; vascular system; probe;
KW  cardiovascular disease; hypertension; cardiac arrhythmia;
KW  congenital heart disease; ss.
XX
OS  Homo sapiens.
XX
PN  WO200157274-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000666.
XX
PR  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
PA  (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR  WPI; 2001-488990/53.
XX
PT  Single exon nucleic acid probes for analyzing gene expression in human
PT  hearts.
XX
PS  Claim 1; SEQ ID NO 6845; 530pp; English.
XX
SS  The present invention relates to single exon nucleic acid probes for
CC  measuring human gene expression in a sample derived from human heart. The
CC  present sequence is one such probe. The probes may be used for
CC  predicting, measuring and displaying gene expression in samples derived
CC  from the human heart via microarrays. By measuring gene expression, the
CC  probes are useful for predicting, diagnosing, grading, staging,
CC  monitoring and prognosing diseases of the human heart and vascular system
CC  e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
CC  congenital heart disease. Note: The sequence data for this patent did not
CC  form part of the printed specification, but was obtained in electronic
CC  format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ  Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;

Query Match      78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GAAAGGCTTTCGGGGTGCTC 22
DB  290 GAAAGGCTCTCAGGGTGCTC 311

RESULT 16
AAK34112
ID  AAK34112 standard; DNA; 569 BP.
XX
AC  AAK34112;
XX
DT  06-NOV-2001 (first entry)
XX
DE  Human bone marrow expressed single exon probe SEQ ID NO: 8669.
XX
KW  Human; bone marrow expressed exon; gene expression analysis; probe;

microarray; cancer; leukaemia; lymphoma; myeloma; ss.
Homo sapiens.
WO200157276-A2.
09-AUG-2001.
30-JAN-2001; 2001WO-US000668.
04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
(MOLE-) MOLECULAR DYNAMICS INC.
Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-488990/53.
Human genome-derived single exon nucleic acid probes useful for analyzing
gene expression in human bone marrow.
Example 4; SEQ ID NO 8669; 658pp + Sequence Listing; English.
The present invention provides a number of single exon nucleic acid
probes which are derived from genomic sequences expressed in the human
bone marrow. They can be used to measure gene expression in bone marrow
samples, which may enable the improved diagnosis and treatment of cancers
such as lymphoma, leukaemia and myeloma. The present sequence is one of
the probes of the invention
Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;

Query Match      78.2%; Score 17.2; DB 4; Length 569;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1 GAAAGGCTTTCGGGGTGCTC 22
DB  290 GAAAGGCTCTCAGGGTGCTC 311

RESULT 17
AAK08233
ID  AAK08233 standard; DNA; 569 BP.
XX
AC  AAK08233;
XX
DT  05-NOV-2001 (first entry)
XX
DE  Human brain expressed single exon probe SEQ ID NO: 8224.
XX
KW  Human; brain expressed exon; gene expression analysis; probe; microarray;
KW  Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW  ss.
XX
OS  Homo sapiens.
XX
PN  WO200157275-A2.
XX
PD  09-AUG-2001.
XX
PF  30-JAN-2001; 2001WO-US000667.
XX
PR  04-FEB-2000; 2000US-0180312P.
PR  26-MAY-2000; 2000US-0207456P.
PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
```

PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 XX  
 XX Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains.  
 PT  
 XX Example 4; SEQ ID NO 8224; 650pp + Sequence Listing; English.  
 PS  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 XX  
 SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;  
 Query Match 78.2%; Score 17.2; DB 4; Length 569;  
 Best Local Similarity 86.4%; Pred. No. 2e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 1 GAAAGGCTTCGGGGTGCTC 22  
 Db 290 GAAAGGCTTCAGGGTGCTC 311  
  
 RESULT 18  
 ABS33911  
 ID ABS33911 standard; DNA; 569 BP.  
 AC ABS33911;  
 XX  
 DT 25-FEB-2003 (first entry)  
 DE Human liver single exon probe, SEQ ID No 8901.  
 XX  
 XX Human; single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US0000664.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2001-488898/53.  
 XX  
 XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 PT gene expression in human adult liver.  
 PT  
 XX

PS Claim 1; SEQ ID NO 8901; 658pp; English.  
 XX  
 CC The invention relates to a single exon nucleic acid probe (SENP) (I) for  
 CC measuring human gene expression in a sample derived from human adult  
 CC liver, comprising one of 13109 defined nucleotide sequences given in the  
 CC specification (or complements/ fragments). The probe hybridises at high  
 CC stringency to a nucleic acid molecule expressed in the human adult liver.  
 CC (I) may be used for predicting, measuring and displaying gene expression  
 CC in samples derived from human adult liver. The genes identified may be  
 CC involved in genetic liver diseases such as cirrhosis,  
 CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is  
 CC associated with coronary heart disease. ABS25011-ABS51005 represent human  
 CC liver single exon nucleic acid probes of the invention. Note: The  
 CC sequence information for this patent does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;  
 Query Match 78.2%; Score 17.2; DB 4; Length 569;  
 Best Local Similarity 86.4%; Pred. No. 2e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
 QY 1 GAAAGGCTTCGGGGTGCTC 22  
 Db 290 GAAAGGCTTCAGGGTGCTC 311  
  
 RESULT 19  
 ABS08880  
 ID ABS08880 standard; DNA; 569 BP.  
 AC ABS08880;  
 XX  
 DT 19-AUG-2002 (first entry)  
 DE Human genome-derived single exon probe from lung SEQ ID No 8871.  
 XX  
 XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200186003-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 30-JAN-2001; 2001WO-US0000665.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 PI WPI; 2002-114183/15.  
 XX  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 PT measure gene expression in human lung samples.  
 PT  
 XX

PS Claim 1; SEQ ID NO 8871; 634pp; English.

XX The invention relates to a spatially-addressable set of single exon

CC nucleic acid probes for measuring gene expression in a sample derived

CC from human lung comprising single exon nucleic acid probes having one of

CC 12614 nucleic acid sequences mentioned in the specification, or their

CC complements or the 12387 open reading frames derived from the 12614

CC probes. Also included are a microarray comprising the novel set of probes

CC; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample

CC derived from human lung, comprising (a) contacting the array with a

CC collection of detectably labeled nucleic acids derived from human lung

CC mRNA, and (b) measuring the label detectably bound to each probe of the

CC array; identifying exons in a eukaryotic genome, comprising (a)

CC algorithmically predicting at least one exon from genomic sequences of

CC the eukaryote; and (b) detecting specific hybridisation of detectably

CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

CC having a fragment identical to the predicted exon, the probe is included

CC in the above mentioned microarray; assigning exons to a single gene,

CC comprising (a) identifying exons from genomic sequence by the method

CC above and (b) measuring the expression of each of the exons in several

CC microarrays having a probe with the exon, where a common pattern of

CC expression of the exons in the tissues and/or cell types indicates that

CC the exons should be assigned to a single gene; a peptide comprising one

CC of 12011 sequences, mentioned in the specification, or encoded by the

CC probes/open reading frames (ORF). The probes are used for gene expression

CC analysis, and for identifying exons in a gene, particularly using human

CC lung derived mRNA and for the study of lung diseases such as asthma, lung

CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung

CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,

CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-

CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary

CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,

CC Karagenes syndrome, fibrocystic pulmonary dysplasia, primary ciliary

CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The

CC present sequence is a single exon probe of the invention. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 569 BP; 144 A; 123 C; 151 G; 151 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 6; Length 569;

Best Local Similarity 86.4%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22

Db 290 GAAAGGCTTCAGGGTGCTC 311

RESULT 20

ACA36105

ID ACA36105 standard; DNA; 1440 BP.

XX

XX ACA36105;

XX

XX 19-JUN-2003 (first entry)

XX

XX Prokaryotic essential gene #17762.

XX

XX Antisense; ds; prokaryotic essential gene; cell proliferation;

XX drug design; gene.

XX

XX Klebsiella pneumoniae.

XX

XX WO200277183-A2.

XX

XX 03-OCT-2002.

XX

XX 21-MAR-2002; 2002WO-US009107.

XX

PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362899P.

XX (ELIT-) ELITRA PHARM INC.

XX

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

PI Wali D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX

XX WPI; 2003-029926/02.

DR P-PSDB; ABU32235.

DR

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX

XX Claim 14; SEQ ID NO 23975; 1766pp; English.

XX

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target

CC prokaryotic essential genes. Note: The sequence data for this patent did

CC not form part of the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 1440 BP; 242 A; 437 C; 464 G; 297 T; 0 U; 0 Other;

Query Match 78.2%; Score 17.2; DB 8; Length 1440;

Best Local Similarity 86.4%; Pred. No. 2.2e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22

Db 141 GAAAGGCTTCGGGGTGCTC 162

RESULT 21

ADA02540

ID ADA02540 standard; DNA; 58822 BP.

XX

XX ADA02540;

XX

XX 06-NOV-2003 (first entry)

XX

XX Human TCOP1 carcinoma associated gene, SEQ ID NO:1058.

XX

KW Human; carcinoma associated; oncogene; carcinoma; cancer; breast;  
 KW prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;  
 KW gene; ds.  
 XX Homo sapiens.  
 OS  
 XX WO2003057146-A2.  
 PN  
 XX 17-JUL-2003.  
 XX  
 XX 26-DEC-2002; 2002WO-US041414.  
 PF  
 XX 26-DEC-2001; 2001US-00035832.  
 XX  
 XX (SAGR-) SAGRES DISCOVERY.  
 PA  
 XX Morris DW;  
 PI  
 XX WPI; 2003-587068/55.  
 DR  
 XX New recombinant nucleic acid encoding carcinoma associated protein,  
 PT useful for preparing compositions for treating carcinomas.  
 PT  
 XX Claim 1; SEQ ID NO 1058; 245pp; English.  
 PS  
 XX The invention relates to recombinant carcinoma associated (CA) nucleic  
 CC acid sequences from mouse and human (ADA01482-ADA03094), and to  
 CC recombinant carcinoma associated proteins (CAP) encoded by them. The  
 CC invention also encompasses expression vectors and host cells comprising a  
 CC CA nucleic acid, a polypeptide (especially an antibody) that specifically  
 CC binds to the protein, and a biochip comprising CA nucleic acid or  
 CC fragments thereof. The sequences of the invention were identified using  
 CC oncogenic retroviruses, which insert into the genome of the host organism  
 CC at random. Many of these do not carry transduced host oncogenes or  
 CC pathogenic trans-acting viral genes, meaning that cancer incidence is a  
 CC direct consequence of the effects of proviral integration into host  
 CC protooncogenes. The CA nucleic acid sequences can be used to diagnose  
 CC carcinoma (especially breast cancer, prostate cancer, lymphoma or  
 CC leukaemia) or a propensity to carcinoma by determination of the sequence  
 CC of a CA gene, or by determination of CA gene expression in particular  
 CC tissues. CA nucleic acids, proteins and antibodies are also useful as  
 CC therapeutic agents and in screening and evaluating drug candidates. The  
 CC present sequence represents a specifically claimed human CA nucleic acid  
 CC sequence of the invention. Note: The complete sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;  
 Query Match 78.2%; Score 17.2; DB 9; Length 58822;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTTCGGGGTGCTC 22  
 DB 26859 GACAGGCCCTTTCGGGGTTCTC 26880  
 RESULT 22  
 ADB72278  
 ID ADB72278 standard; DNA; 58822 BP.  
 XX  
 AC ADB72278;  
 XX  
 XX 04-DEC-2003 (first entry)  
 DT  
 XX Human TCOF1 gene.  
 DE  
 XX human; ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;  
 KW cancer; neoplasm; adenocarcinoma; sarcoma; gene.  
 KW  
 XX Homo sapiens.  
 OS

XX WO2003008583-A2.  
 PN  
 XX 30-JAN-2003.  
 PD  
 XX  
 XX 26-DEC-2001; 2001WO-US051291.  
 PF  
 XX  
 XX 02-MAR-2001; 2001US-00798586.  
 PR  
 XX 23-OCT-2001; 2001US-00004113.  
 PR  
 XX 08-NOV-2001; 2001US-00052482.  
 PR  
 XX 20-DEC-2001; 2001US-00034650.  
 XX  
 XX (SAGR-) SAGRES DISCOVERY.  
 PA  
 XX Morris DW, Engelhard EK;  
 PI  
 XX WPI; 2003-239337/23.  
 DR  
 XX New recombinant nucleic acid, useful for treating carcinomas, lymphomas,  
 PT cancers, neoplasm, adenocarcinoma, or sarcomas.  
 PT  
 XX Claim 1; SEQ ID NO 106; 2304pp; English.  
 PS  
 XX The invention relates to a novel recombinant nucleic acid comprising a  
 CC nucleotide sequence selected from any of the 660 sequences fully defined  
 CC in the specification. A polynucleotide of the invention has cytostatic  
 CC activity, and may have a use in gene therapy, or in a vaccine. The  
 CC recombinant nucleic acids and polypeptides are useful for treating  
 CC carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and  
 CC sarcomas. The present sequence represents a human gene of the invention.  
 XX  
 SQ Sequence 58822 BP; 14199 A; 14875 C; 15625 G; 13656 T; 0 U; 467 Other;  
 Query Match 78.2%; Score 17.2; DB 10; Length 58822;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+02;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTTCGGGGTGCTC 22  
 DB 26859 GACAGGCCCTTTCGGGGTTCTC 26880  
 RESULT 23  
 ADE95788  
 ID ADE95788 standard; DNA; 58822 BP.  
 XX  
 AC ADE95788;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX Human TCOF1 gene genomic DNA sequence.  
 DE  
 XX cancer diagnosis; cancer treatment; carcinoma; cytostatic; gene therapy;  
 KW lymphoma; breast cancer; prostate cancer; leukaemia; ds; human; TCOF1.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2003039484-A2.  
 PN  
 XX 15-MAY-2003.  
 PD  
 XX  
 XX 08-NOV-2002; 2002WO-US036071.  
 PF  
 XX  
 XX 08-NOV-2001; 2001US-00052482.  
 PR  
 XX (SAGR-) SAGRES DISCOVERY.  
 PA  
 XX Morris DW, Engelhard EK;  
 PI  
 XX WPI; 2003-441462/41.  
 DR  
 XX New carcinoma associated nucleic acids and proteins, useful for screening  
 PT



PT drug candidates, or for diagnosing and treating carcinomas, e.g.  
XX lymphoma, breast cancer, prostate cancer or leukemia.  
PS Claim 1; SEQ ID NO 46; 793pp; English.  
XX  
CC This invention relates to novel recombinant nucleic acids for use in  
CC diagnosis and treatment of cancer, especially carcinomas, as well as the  
CC use of compositions in screening methods. The compositions of the  
CC invention may have cytostatic activity whilst the disclosed sequences may  
CC be useful for gene therapy. The carcinoma associated nucleic acids and  
CC proteins are useful for diagnosing and treating carcinomas, for example  
CC lymphoma, breast cancer, prostate cancer or leukemia, or for screening  
CC drug candidates or bioactive agents capable of binding to, or modulating  
CC the activity of, a carcinoma associated protein. The present sequence is  
CC the genomic DNA sequence of the human TCOF1 gene which is a carcinoma  
CC associated gene of the invention.  
XX  
SQ Sequence 58822 BP; 14199 A; 14881 C; 15619 G; 13656 T; 0 U; 467 Other;  
  
Query Match 78.2%; Score 17.2; DB 10; Length 58822;  
Best Local Similarity 86.4%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GAAGGCGCTTCGGGGTGTCTC 22  
Db 26859 GACAGGCGCTTCGGGGTGTCTC 26880  
  
RESULT 24  
ACN44158  
ID ACN44158 standard; DNA; 63686 BP.  
XX  
AC ACN44158;  
XX  
AC ACN44158;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human genomic sequence hCG1783275.  
XX  
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.  
XX  
XX Homo sapiens.  
XX  
XX WO2003073826-A2.  
XX  
PD 12-SEP-2003.  
XX  
XX 28-FEB-2003; 2003WO-US006235.  
XX  
XX 01-MAR-2002; 2002US-00087192.  
XX  
XX (SAGR-) SAGRES DISCOVERY.  
XX  
XX Morris DW;  
XX  
XX WPI; 2003-328604/31.  
XX  
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma  
PT comprises a nucleotide sequence.  
XX  
XX Claim 1; SEQ ID NO 466; opp; English.  
XX  
XX The present invention relates to novel DNA and protein sequences which  
CC are associated with carcinomas. The sequences are useful for: (i) for  
CC screening drug candidates; (ii) for screening of bioactive agent capable  
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of  
CC a bioactive agent capable of modulating the activity of CAP; (iv) for  
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing  
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating  
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;  
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for  
CC determining Carcinoma Associated (CA) gene copy number. In addition, the  
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of  
CC carcinoma including lymphoma. The present sequence is one such CA coding

CC sequence. Note: This patent is an equivalent to basic patent  
CC US2002182586A1, for which no sequence data was published  
XX  
SQ Sequence 63686 BP; 15766 A; 14989 C; 15180 G; 17751 T; 0 U; 0 Other;  
  
Query Match 78.2%; Score 17.2; DB 11; Length 63686;  
Best Local Similarity 86.4%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GAAGGCGCTTCGGGGTGTCTC 22  
Db 45915 GAAAGGCGCTTCAGGGCTGCTC 45936  
  
RESULT 25  
ABD17022/c  
ID ABD17022 standard; DNA; 276 BP.  
XX  
AC ABD17022;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polynucleotide #15626.  
XX  
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
KW antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
XX US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
XX 18-FEB-1999; 99US-00252991.  
XX  
XX 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX  
XX WPI; 2003-615309/58.  
DR P-PSDB; AB083451.  
XX  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 15626; 455pp; English.  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX  
XX  
SQ Sequence 276 BP; 72 A; 82 C; 66 G; 56 T; 0 U; 0 Other;  
  
Query Match 76.4%; Score 16.8; DB 11; Length 276;  
Best Local Similarity 90.0%; Pred. No. 3e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTCGGGGTGCT 21  
 |||||  
 Db 87 AAAGGCTTCGTAGGTGCT 68  
 RESULT 26  
 ACN53618/c  
 ID ACN53618 standard; cDNA; 601 BP.  
 XX  
 AC ACN53618;  
 DT 02-DEC-2004 (first entry)  
 DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-K6-G5, SEQ:8399.  
 DE  
 XX Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium;  
 KW variety Nucotton33B; library LIB3828; molecular tag; molecular marker;  
 KW genetic mapping; molecular mapping; seed germination; plant growth;  
 KW plant quality; plant yield; plant breeding; tissue printing; ss.  
 XX  
 OS Gossypium hirsutum.  
 XX  
 PN US2004123340-A1.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 12-DEC-2001; 2001US-00021323.  
 XX  
 PR 14-DEC-2000; 2000US-0255619P.  
 XX  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 XX  
 PI Daikman J, Feng PCC, Fincher KL, Ziegler TE;  
 XX WPI; 2004-479808/45.  
 DR  
 XX  
 PT New isolated nucleic acid molecule that encodes a plant protein or its  
 PT fragment, useful for isolating a variety of agronomically significant  
 PT genes associated with plant growth, quality or yield, and as molecular  
 PT tags to map genes.  
 XX  
 PS Claim 1; SEQ ID NO 8399; 34pp; English.  
 XX  
 CC The invention relates to 17880 cotton expressed sequence tags (ESTs;  
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
 CC from primed or non-primed seeds from variety DP50B, mature seeds from  
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium  
 CC tissue, developing fibres, carpel walls and septa from variety  
 CC Nucotton33B. The invention also relates to substantially purified  
 CC proteins or their fragments encoded by nucleic acid molecules of the  
 CC invention, and to transformed plants having a nucleic acid construct  
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
 CC molecular tags to isolate genetic regions, to isolate genes, to map  
 CC genes, to determine gene function and to determining whether genes are  
 CC members of a particular gene family. The nucleic acid molecules may be  
 CC used for isolating a variety of agronomically significant genes  
 CC associated with plant growth, quality, yield, and could also serve as  
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
 CC also useful for identifying genes important in initiating and maintaining  
 CC seed germination or that may be used to mitigate stresses encountered  
 CC during seed germination. The ESTs additionally enable the acquisition of  
 CC promoters and cis-regulatory elements which will be useful to express  
 CC agronomically significant genes in these tissues and/or other tissues,  
 CC and also permits the acquisition of molecular markers useful in breeding  
 CC schemes, genetic and molecular mapping, and in cloning of agronomically  
 CC significant genes. The nucleic acid molecules are further useful for  
 CC detecting the expression level or pattern of a protein or mRNA and for  
 CC detecting the presence or quantity of a protein by tissue printing. The  
 CC present sequence represents a specifically claimed EST isolated from a

CC cotton variety Nucotton33B androecium tissue cDNA library (LIB3828). The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the US  
 CC patent office at seqdata.uspto.gov/sequence.html?DocID=US20040123340  
 XX  
 XX Sequence 601 BP; 273 A; 89 C; 106 G; 133 T; 0 U; 0 Other;  
 Query Match 76.4%; Score 16.8; DB 13; Length 601;  
 Best Local Similarity 90.0%; Pred. No. 3.2e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCTTCGGGGTGCT 20  
 |||||  
 Db 525 GAAAGGCTTCGGGGGGGC 506  
 RESULT 27  
 ACN31638  
 ID ACN31638 standard; DNA; 2107 BP.  
 XX  
 AC ACN31638;  
 XX  
 DT 19-JUN-2003 (first entry)  
 DE Prokaryotic essential gene #13295.  
 DE  
 XX Antisense; ds; prokaryotic essential gene; cell proliferation;  
 KW drug design; gene.  
 KW  
 XX Enterobacter cloacae.  
 OS  
 XX WO200277183-A2.  
 PN  
 XX 03-OCT-2002.  
 PD  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 DR WPI; 2003-029926/02.  
 DR P-PSDB; ABU27768.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 14; SEQ ID NO 19508; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target  
CC prokaryotic essential genes. Note: The sequence data for this patent did  
CC not form part of the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2107 BP; 498 A; 511 C; 618 G; 480 T; 0 U; 0 Other;  
  
Query Match 76.4%; Score 16.8; DB 8; Length 2107;  
Best Local Similarity 90.0%; Pred. No. 3.5e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 AAGGCCCTTCGGGGTGCTC 22  
Db 113 AAGCGTTCGGGGTGCTC 132  
  
RESULT 28  
AD213575\_1  
Continuation (2 of 6) of AD213575 from base 100001 (Murine cancer-associated genomic DNA  
WP Sequence split into 6 fragments LOCUS AD213575 Accession Ad213575  
WP Fragment Name Begin End  
WP AD213575\_0 1 110000  
WP AD213575\_1 100001 210000  
WP AD213575\_2 200001 310000  
WP AD213575\_3 300001 410000  
WP AD213575\_4 400001 510000  
WP AD213575\_5 500001 582589  
  
Query Match 76.4%; Score 16.8; DB 14; Length 110000;  
Best Local Similarity 90.0%; Pred. No. 4.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 AAGGCCCTTCGGGGTGCT 21  
Db 16886 AAGGCCCTTCGTGTGCT 16905  
  
RESULT 29  
ABD33143  
ID ABD33143 standard; DNA; 289190 BP.  
XX  
AC ABD33143;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Murine cancer-associated (CA) gene MD07-018.  
XX  
KW Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;  
KW ds; cancer; cytostatic.  
XX  
OS Mus musculus.  
XX  
PN WO2004058146-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 15-DEC-2003; 2003WO-US040081.  
XX  
PR 17-DEC-2002; 2002US-00322281.  
XX  
PA (SAGR-) SAGRES DISCOVERY INC.  
XX

PI Morris DW, Malandro MS;  
XX WPI; 2004-499109/47.  
XX  
XX Novel human cancer associated protein encoded within open reading frame  
PT of cancer associated gene, useful as targets for diagnosing cancer.  
PS  
XX Disclosure; SEQ ID NO 115; 182pp; English.  
XX  
XX The invention relates to cancer-associated proteins (CAP) and the cancer-  
CC associated (CA) nucleic acids encoding them. The invention also relates  
CC to a method for treating cancers involving administering to a patient an  
CC inhibitor of CAP, and a method of screening for anticancer activity in a  
CC potential drug involving providing a cell that expresses a CA gene,  
CC contacting a tissue sample derived from a cancer cell with an anticancer  
CC drug candidate and monitoring the effect of the anticancer drug candidate  
CC on expression of the CA gene. The CAP proteins are useful for detecting  
CC cancer associated with expression of a CAP protein in a test cell sample  
CC and for screening for a bioactive agent capable of modulating the  
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing  
CC cancer, involving determining the expression of a CA nucleic acid in a  
CC tissue. This sequence represents a murine CA gene of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 289190 BP; 79193 A; 58337 C; 57759 G; 83755 T; 0 U; 10146 Other;  
  
Query Match 76.4%; Score 16.8; DB 13; Length 289190;  
Best Local Similarity 90.0%; Pred. No. 5.1e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 2 AAGGCCCTTCGGGGTGCT 21  
Db 116861 AAGGCCCTTCGTGTGCT 116880  
  
RESULT 30  
AAH36786  
ID AAH36786 standard; cDNA; 309 BP.  
XX  
AC AAH36786;  
XX  
DT 03-SEP-2001 (first entry)  
XX  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:3868.  
XX  
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;  
KW colorectal carcinoma; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200122920-A2.  
XX  
PD 05-APR-2001.  
XX  
PF 28-SEP-2000; 2000WO-US026524.  
XX  
PR 29-SEP-1999; 99US-0157137P.  
PR 03-NOV-1999; 99US-0163280P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Birse CE, Rosen CA;  
XX WPI; 2001-235357/24.  
DR P-PSDB; AAG77379.  
XX  
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
PT useful for preventing, diagnosing and/or treating colorectal cancers.  
XX  
PS Claim 1; Page 5728-5732; 9803pp; English.  
XX

CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the  
 CC proteins are collectively known as colon cancer antigens. The colon  
 CC cancer antigens have cytostatic activity and can be used in gene therapy  
 CC and vaccine production. N and P may be used in the prevention, diagnosis  
 CC and treatment of diseases associated with inappropriate P expression. For  
 CC example, N and P may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of P by expressing inactive proteins or to  
 CC supplement the patient's own production of P. Additionally, N may be used  
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids  
 CC into a host cell and culturing the cell to express the proteins. N and P  
 CC can be used in the prevention, diagnosis and treatment of colorectal  
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent  
 CC sequences used in the exemplification of the present invention. N.B.  
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at  
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027  
 CC to 1052, 7921 and 7922  
 XX  
 SQ Sequence 309 BP; 70 A; 94 C; 73 G; 59 T; 0 U; 13 Other;

Query Match 74.5%; Score 16.4; DB 4; Length 309;  
 Best Local Similarity 94.4%; Pred. No. 4.8e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 2 AAAGGCTTTCGGGGGTG 19  
 |||||  
 Db 74 AAAGGCTTTCGGGGGTG 91

RESULT 31  
 ACN47886  
 ID ACN47886 standard; cDNA; 521 BP.  
 XX  
 AC ACN47886;  
 DT 02-DEC-2004 (first entry)  
 XX Cotton primed seed EST Clone ID: LTB3825-016-Q1-N6-D3, SEQ:2667.  
 DE  
 XX Cotton; plant; EST; expressed sequence tag; transgenic plant; seed;  
 KW variety DP50B; library LTB3825; molecular tag; molecular marker;  
 KW genetic mapping; molecular mapping; seed germination; plant growth;  
 KW plant quality; plant yield; plant breeding; tissue printing; ss.  
 XX Gossypium hirsutum.  
 OS  
 XX US2004123340-A1.  
 XX 24-JUN-2004.  
 XX 12-DEC-2001; 2001US-00021323.  
 XX 14-DEC-2000; 2000US-0255619P.  
 XX (DEIK/) DEIKWAN J.  
 PA (FENG/) FENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;  
 PI WPI; 2004-479808/45.  
 XX New isolated nucleic acid molecule that encodes a plant protein or its  
 PT fragment, useful for isolating a variety of agronomically significant  
 PT genes associated with plant growth, quality or yield, and as molecular  
 PT tags to map genes.  
 XX Claim 1; SEQ ID NO 2667; 34pp; English.  
 PS  
 XX The invention relates to 17880 cotton expressed sequence tags (ESTs;  
 CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated

CC from primed or non-primed seeds from variety DP50B, mature seeds from  
 CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium  
 CC tissue, developing fibres, carpel wallis and septa from variety  
 CC Nuctoton3B. The invention also relates to substantially purified  
 CC proteins or their fragments encoded by nucleic acid molecules of the  
 CC invention, and to transformed plants having a nucleic acid construct  
 CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
 CC molecular tags to isolate genetic regions, to isolate genes, to map  
 CC genes, to determine gene function and to determining whether genes are  
 CC members of a particular gene family. The nucleic acid molecules may be  
 CC used for isolating a variety of agronomically significant genes  
 CC associated with plant growth, quality, yield, and could also serve as  
 CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
 CC also useful for identifying genes important in initiating and maintaining  
 CC seed germination or that may be used to mitigate stresses encountered of  
 CC during seed germination. The ESTs additionally enable the acquisition of  
 CC promoters and cis-regulatory elements which will be useful to express  
 CC agronomically significant genes in these tissues and/or other tissues,  
 CC and also permits the acquisition of molecular markers useful in breeding  
 CC schemes, genetic and molecular mapping, and in cloning of agronomically  
 CC significant genes. The nucleic acid molecules are further useful for  
 CC detecting the expression level or pattern of a protein or mRNA and for  
 CC detecting the presence or quantity of a protein by tissue printing. The  
 CC present sequence represents a specifically claimed EST isolated from a  
 CC cotton variety DP50B primed seed cDNA library (LTB3825). The sequence  
 CC data for this patent did not form part of the printed specification, but  
 CC was obtained in electronic format directly from the US patent office at  
 CC seqdata.uspto.gov/sequence.html?DocId=US20040123340  
 XX  
 SQ Sequence 521 BP; 277 A; 32 C; 136 G; 76 T; 0 U; 0 Other;

Query Match 74.5%; Score 16.4; DB 13; Length 521;  
 Best Local Similarity 94.4%; Pred. No. 5e+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 AAAGGCTTTCGGGGGTG 19  
 |||||  
 Db 232 AAAGGCTTTCGGGGGAG 249  
 RESULT 32  
 ADC86176/c  
 ID ADC86176 standard; DNA; 47804 BP.  
 XX  
 AC ADC86176;  
 XX 01-JAN-2004 (first entry)  
 XX Human GPCR gene SEQ ID NO:629.  
 DE ds; gene; human; GPCR;  
 KW guanosine triphosphate-binding protein coupled receptor; gene therapy.  
 XX Homo sapiens.  
 XX EP1270724-A2.  
 XX 02-JAN-2003.  
 XX 18-JUN-2002; 2002EP-00013517.  
 XX 18-JUN-2001; 2001JP-00246789.  
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 XX Suwa M, Asai K, Akiyama Y, Aburatani H;  
 PI WPI; 2003-315783/31.  
 DR P-PSDB; ADC86177.  
 XX New polynucleotide, useful for preparing a composition for treating a  
 PT patient in need of increased or suppressed activity or expression of the

PT guanosine triphosphate-binding protein coupled receptor.  
 XX Claim 1; SEQ ID NO 629; 28pp; English.  
 XX  
 CC The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The  
 CC polynucleotide sequences shown in ADC85548-ADC87616 encode GPCR's of the  
 CC invention.  
 XX  
 SQ Sequence 47804 BP; 13080 A; 10916 C; 11116 G; 12192 T; 0 U; 500 Other;  
 Query Match 74.5%; Score 16.4; DB 10; Length 47804;  
 Best Local Similarity 94.4%; Pred. No. 7.le+02;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 GGCCTTTCGGGGGTC 22  
 Db 47345 GGCCTTTCGGGGGTC 47328  
 RESULT 33  
 AAK76977/c  
 ID AAK76977 standard; DNA; 420 BP.  
 XX  
 AC AAK76977;  
 XX  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31789.  
 XX  
 KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytosstatic; gene therapy; vaccine; metastasis; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157182-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 17-JAN-2001; 2001WO-US001354.  
 XX  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225477P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 06-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 08-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239335P.  
 PR 13-OCT-2000; 2000US-0239337P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.









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XX PD 19-APR-2001.
XX PS
XX PF 06-OCT-2000; 2000WO-US027582.
XX PR 08-OCT-1999; 99US-0158615P.
XX PR 24-FEB-2000; 2000US-0184809P.
XX PA (DIGI-) DIGISCENTS.
XX PA (YEDA ) YEDA RES & DEV CO LTD.
XX PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX DR
XX PT New polynucleotides which encode polypeptides involved in olfactory
XX PT sensation for identifying olfactory agonists and antagonists.
XX PS Claim 1; Fig 2; 1857pp; English.
XX CC The present sequence is one of a number of isolated polynucleotides which
XX CC encode polypeptides involved in olfactory sensation. The polynucleotides
XX CC can be used in screening for olfactory agonists and antagonists. The
XX CC methods allow for the determination of primary scents and the
XX CC identification of the odour receptors used to detect these primary
XX CC scents. The methods also enable determination of secondary scents and the
XX CC identification of combinations of odour receptors that are involved in
XX CC detecting such secondary scents. This enables the construction of a scent
XX CC representation (also called a scent fingerprint or scent profile), which
XX CC may be used to re-create and edit scents. Libraries of olfactory
XX CC receptors are useful for determining the interaction pattern of a
XX CC composition with the receptors, and can be used for determining
XX CC differences in the olfactory faculties of different individuals
XX SQ Sequence 590 BP; 133 A; 124 C; 137 G; 128 T; 0 U; 68 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 590;
Best Local Similarity 81.8%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22
Db 172 GAAAGGCTTTTGACCTGCTC 151

RESULT 38
ADO36603/c
ID ADO36603 standard; DNA; 607 BP.
XX AC
XX AD036603;
XX DT 15-JUL-2004 (first entry)
XX DE Isoquinoline alkaloid biosynthesis protein related EST DNA, SEQ ID No 52.
XX KW biosynthesis; isoquinoline alkaloid; columbamine 7-O-methyltransferase;
XX KW nor coclaurine synthetase; expressed sequence tag; ds.
XX OS Unidentified.
XX PN JP2004121233-A.
XX PD 22-APR-2004.
XX PF 02-SEP-2003; 2003JP-00310660.
XX PR 05-SEP-2002; 2002JP-00260642.
XX PA (KYOU ) UNIV KYOTO.
XX WPI; 2004-322858/30.
XX PT New protein concerned in biosynthesis of isoquinoline alkaloid, and

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PT having columbamine 7-O-methyltransferase and nor coclaurine synthetase
PT activity, useful for producing isoquinoline alkaloid.
XX PS Claim 1; SEQ ID NO 52; 35pp; Japanese.
XX CC The invention relates to a novel protein concerned in biosynthesis of an
XX CC isoquinoline alkaloid. The protein has a fully defined sequence of 351 or
XX CC 352 amino acids as given in the specification, or a sequence in which one
XX CC or more amino acids are deleted, added, or substituted in the protein,
XX CC and having columbamine 7-O-methyltransferase, and nor coclaurine
XX CC synthetase activity. The protein and a transformed host are useful for
XX CC producing isoquinoline alkaloid. The isoquinoline alkaloid biosynthesis
XX CC protein encoding polynucleotide and cDNA library are useful for isolating
XX CC a full length gene concerned in biosynthesis of an isoquinoline alkaloid.
XX CC The alkaloid biosynthesis protein encoding polynucleotide is useful as a
XX CC probe for isolating a full length gene concerned in biosynthesis of an
XX CC isoquinoline alkaloid which is useful as a pharmaceutical raw material.
XX CC This polynucleotide sequence represents the DNA of an expressed sequence
XX CC tag relating to the isoquinoline alkaloid biosynthesis protein of the
XX CC invention.
XX SQ Sequence 607 BP; 169 A; 122 C; 140 G; 173 T; 0 U; 3 Other;

Query Match 73.6%; Score 16.2; DB 12; Length 607;
Best Local Similarity 85.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 76 AAAGGCTTTTGCGGTGTC 56

RESULT 39
ABD02872/c
ID ABD02872 standard; DNA; 771 BP.
XX AC ABD02872;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polynucleotide #1476.
XX KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
XX KW antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
XX DR P-PSDB; ABO69301.
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 1476; 455pp; English.
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a

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CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
 CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 CC  
 XX  
 SQ Sequence 771 BP; 120 A; 270 C; 259 G; 122 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 11; Length 771;  
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCTTTCGGGGTGCT 21  
 ||| ||||| |||||  
 Db 615 GAAGGCGCTTTCGGCGTGCT 595  
 RESULT 40  
 ABD03097  
 ID ABD03097 standard; DNA; 828 BP.  
 XX  
 AC ABD03097;  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX  
 DE Pseudomonas aeruginosa polynucleotide #1701.  
 XX  
 KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
 KW antibacterial.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US651795-B1.  
 XX  
 PD 22-APR-2003.  
 XX  
 PF 18-FEB-1999; 99US-00252991.  
 XX  
 PR 18-FEB-1998; 98US-0074788P.  
 PR 27-JUL-1998; 98US-0094190P.  
 XX  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 WPI; 2003-615309/58.  
 DR P-PSDB; ABO69526.  
 XX  
 XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 PS Disclosure; SEQ ID NO 1701; 455pp; English.  
 XX  
 CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences ABD01397-

CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 CC  
 XX  
 SQ Sequence 828 BP; 127 A; 282 C; 284 G; 135 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 11; Length 828;  
 Best Local Similarity 85.7%; Pred. No. 6.4e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCTTTCGGGGTGCT 21  
 ||| ||||| |||||  
 Db 226 GAAGGCGCTTTCGGCGTGCT 246  
 RESULT 41  
 ADS31309  
 ID ADS31309 standard; DNA; 909 BP.  
 XX  
 AC ADS31309;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human genome high complexity repeat found in the HIRA gene #342.  
 XX  
 KW Human; ds;  
 KW histone cell cycle regulation defective, S. cerevisiae homologue A; HIRA;  
 KW high complexity repeat; in situ hybridisation; Southern blot;  
 KW chromosome breakpoint; inherited genetic disease; neoplastic disorder;  
 KW chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003224356-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 14-MAY-2001; 2001US-00854867.  
 XX  
 PR 16-MAY-2000; 2000US-00573080.  
 XX  
 PA (KNOLL/) KNOLL J H M.  
 PA (ROGA/) ROGAN P K.  
 XX  
 PI Knoll JHM, Rogan PK;  
 XX  
 DR WPI; 2002-062378/08.  
 XX  
 XX Single copy genomic hybridization probes for detecting specific nucleic  
 PT acid sequences in sample by in situ hybridization useful for detection of  
 PT acquired or inherited genetic diseases.  
 XX  
 PS Example 1; SEQ ID NO 342; 30pp; English.  
 XX  
 CC The invention relates to a nucleic acid hybridisation probe comprising a  
 CC labelled, single copy nucleic acids of at least 50 nucleotides, which  
 CC will hybridise to a deduced single copy sequence interval in target  
 CC nucleic acid (TNA) of known sequence. The single copy sequence is deduced  
 CC by comparing the target nucleic acid (e.g. a disease causing gene) with a  
 CC collection of high and low complexity repeat sequences as found in the  
 CC genome of the organism from containing the target nucleic acid. The probe  
 CC is generated by PCR on the target sequence. The probe is essentially free  
 CC of blocking nucleic acid sequences which will hybridise to repeat  
 CC sequences within the genome of which the TNA is a part, and is labelled  
 CC with a label selected from fluorochrome-responsive labels, fluorochromes,  
 CC calorimetric chemical, conjugated proteins, antibodies, antigens and  
 CC their mixtures. The probe is useful in a hybridisation method, where the  
 CC hybridisation method is from in situ hybridisation, Southern blot, and  
 CC other methods in which nucleic acid is immobilised, where the method  
 CC further comprises selecting a single copy nucleic acid which will  
 CC hybridise to a duplicon or triplicon sequence domain. The probe is useful  
 CC for determining the existence of previously unknown repeat sequence

will hybridize to a deduced single copy sequence interval in target nucleic acid (TNA) of known sequence. (I) is useful in a hybridization method which comprises preparing a reaction mixture comprising TNA and (I) which hybridizes to TNA, and causing (I) to hybridize to TNA, where the hybridization method is from in situ hybridization, Southern blot, and other methods in which nucleic acid is immobilized, where the method further comprises selecting a single copy nucleic acid which will hybridize to a duplcon or triplicon sequence domain. (I) is useful for determining the existence of previously unknown repeat sequence families in a genome; determining a chromosome breakpoint and in the fields of cytogenetics and molecular genetics for determining the presence of specific nucleic acid sequences in a sample of eukaryotic origin, e.g. the probes may be used to analyze specific chromosomal locations by in situ hybridization as a detection of acquired or inherited genetic diseases especially for detection of genetic or neoplastic disorders. Unlike prior art techniques, (I) permits more precise chromosomal breakpoint determinations by in situ hybridization. Hybridization techniques utilizing (I), have made it possible to obtain reliable, easily detectable signals with relatively small probes. A readily detectable signal was obtained with a probe on the order of 2 kb in length, using fluorescent in situ hybridization (FISH) technology. This sensitivity of (I) is improved compared to the prior art, because the probes of (I) are homogeneous single copy sequences. However, smaller amplified segments, each comprising non-repetitive sequences, may also be used in combination as probes to achieve adequate signals for in situ hybridization. Complex single copy probes that hybridize to duplicated or triplicated targets can also increase hybridization signals. This sequence represents a human HIRA genomic sequence that shows homology to a known high-complexity repeat sequence family of the human genome and is used in the creation of an HIRA gene probe.

CC used in combination as probes to achieve adequate signals for  
CC hybridization. Complex single copy probes that hybridize to  
CC triplicated targets can also increase hybridization signals.  
CC sequence represents a human HIRA genomic sequence that show  
CC a known high-complexity repeat sequence family of the human  
CC used in the creation of an HIRA gene probe.  
XX  
SQ Sequence 909 BP; 353 A; 160 C; 162 G; 215 T; 0 U; 19 Other;

CC triplicated targets can also increase hybridization signals.  
CC sequence represents a human HIRA genomic sequence that shows  
CC a known high-complexity repeat sequence family of the human  
CC used in the creation of an HIRA gene probe.  
XX  
SQ Sequence 909 BP; 353 A; 160 C; 162 G; 215 T; 0 U; 19 Other;  
Query Match 73.6%; Score 16.2; DB 7; Length 909;

CC sequence represents a human HIRA genomic sequence that shows homology  
 CC to a known high-complexity repeat sequence family of the human genome  
 CC used in the creation of an HIRA gene probe.  
 XX  
 SQ Sequence 909 BP; 353 A; 160 C; 162 G; 215 T; 0 U; 19 Other;  
 Query Match 73.6%; Score 16.2; DB 7; Length 909;  
 Best Local Similarity 85.7%; Pred. No. 6.5e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

[illegible]

Sequence	909 BP; 353 A; 160 C; 162 G	Score	73.6%;	Score	73.6%;
Query Match		Best Local Similarity	85.7%;	Pred.	85.7%;
Matches	18; Conservative	Matches	0; Conservative	0; Conservative	0; Conservative
Qy	1	GAAGGCGCTTTTCGGGGGTGCT	21		
Db	762	GAGAGGGCTTTTCGGGGGTCT	782		

Qy

Db

RESULT 43

[illegible]

Db                      762

RESULT 43  
AAI23344/c  
ID    AAI23344  
XX  
AC    AAI23344;

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RESULT 43
AAI23344/C
ID AAI23344 standard; DNA; 1218 BP.
XX
XX
XX AAI23344;
XX
XX
DT 12-OCT-2001 (first entry)

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Accession	AAI23344.1	
ID	AAI23344	standard; DNA; 1218 BP.
XX	AAI23344;	
XX	AC	
XX	AC	
DT	12-OCT-2001	(first entry)
DE	Probe #13277	for gene expression
XX		

ID	AAI23344	StandardIQ; DNA; 1210 bp.
XX		
XX	AAI23344;	
AC		
XX		
XX	12-OCT-2001	(first entry)
DT		
XX		
XX	Probe #13277	for gene expression analysis in human cervical cell sample.
DE		

XX 12-OCT-2001 (first entry) DT

Probe #13277 for gene expression analysis in human cervical cell sample.  
 XX DE  
 XX DE  
 XX DE  
 KW KW  
 KW KW

XX probe: human: microa

XX	cervical cancer; ss.
KW	
OS	Homo sapiens.
XX	
XX	
PN	W0200157278-A2.
XX	
XX	
PD	09-AUG-2001.
XX	
PF	30-JAN-2001; 2001WO-US000670.

XX	Homo sapiens.
OS	
XX	WO200157278-A2.
PN	
XX	09-AUG-2001.
PD	
XX	30-JAN-2001: 2001WO-US0000670.
PF	

AA	
PN	WO200157278-A2.
XX	
XX	09-AUG-2001.
PD	
XX	
PF	30-JAN-2001: 2001WO-US000670.

XX 09-AUG-2001.  
PD  
XX  
PF 30-JAN-2001: 2001WO-US000670.

XX  
PF 30-JAN-2001: 2001WO-US0000670.

XX  
PP 04-FEB-2000. 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.  
PR 30-JUN-2000; 2000US-00608408.  
PR 03-AUG-2000; 2000US-00632366.  
PR 21-SEP-2000; 2000US-0234687P.  
PR 27-SEP-2000; 2000US-0236359P.  
PR 04-OCT-2000; 2000GB-00024263.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC. XX

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PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX Claim 25; SEQ ID NO 13277; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENP). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging of
CC diseases of the cervix, notably cervical cancer. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119

RESULT 44
ABA68451/c
ID ABA68451 standard; DNA; 1218 BP.
XX ABA68451;
XX 01-FEB-2002 (first entry)
XX Human foetal liver single exon nucleic acid probe #16756.
XX Human; foetal liver; gene expression; single exon nucleic acid probe; es.
XX Homo sapiens.
XX WO200157277-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000669.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234587P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX Claim 25; SEQ ID NO 17352; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119

RESULT 45
AAI48666/c
ID AAI48666 standard; DNA; 1218 BP.
XX AAI48666;
XX 17-OCT-2001 (first entry)
XX Probe #17352 used to measure gene expression in human placenta sample.
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder; ss.
XX Homo sapiens.
XX WO200157272-A2.
XX 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US000663.
XX 04-FEB-2000; 2000US-0180312P.
XX 26-MAY-2000; 2000US-0207456P.
XX 30-JUN-2000; 2000US-00608408.
XX 03-AUG-2000; 2000US-00632366.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX Claim 25; SEQ ID NO 17352; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for
CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119
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RESULT 46
ABA50502/c
ID ABA50502 standard; DNA; 1218 BP.
XX AC ABA50502;
XX AC ABA50502;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9197.
XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX KW cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX PS Claim 4; SEQ ID NO 9197; 327pp + Sequence Listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and Bt 474 cells. The method involves contacting the
XX CC probes with a collection of detectably labelled nucleic acids derived
XX CC from mRNA of human breast, and then measuring the label bound to each
XX CC probe of the microarray. The probes are useful for verifying the
XX CC expression of regions of genomic DNA predicted to encode proteins. They
XX CC are useful for gene discovery, and for determining predisposition and/or
XX CC prognosing breast disease. Gene expression analysis is useful for
XX CC assessing the toxicity of chemical agents on cells. The microarray of
XX CC this invention presents a far greater diversity of probes for measuring
XX CC gene expression, with far less bias than expressed sequence tag
XX CC microarrays. The method is suitable for rapid production of functional
XX CC information from genomic sequence. The present sequence is a single exon
XX CC nucleic acid probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AAAGCGCTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119
RESULT 47
ABA50502/c
ID ABA50502 standard; DNA; 1218 BP.
XX AC ABA50502;
XX AC ABA50502;
XX DT 01-FEB-2002 (first entry)
XX DE Human breast cell single exon nucleic acid probe #9197.
XX KW Human; microarray; single exon probe; gene expression; breast; disease;
XX KW cancer; ss.
XX OS Homo sapiens.
XX PN WO200157271-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000662.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-496933/54.
XX PT New spatially-addressable set of single exon nucleic acid probes, useful
XX PT for measuring gene expression in sample derived from human breast,
XX PT comprises number of single exon nucleic acid probes.
XX PS Claim 4; SEQ ID NO 9197; 327pp + Sequence Listing; English.
XX CC The invention relates to a spatially-addressable set of single exon
XX CC nucleic acid probes for measuring gene expression in a sample derived
XX CC from human breast and Bt 474 cells. The method involves contacting the
XX CC probes with a collection of detectably labelled nucleic acids derived
XX CC from mRNA of human breast, and then measuring the label bound to each
XX CC probe of the microarray. The probes are useful for verifying the
XX CC expression of regions of genomic DNA predicted to encode proteins. They
XX CC are useful for gene discovery, and for determining predisposition and/or
XX CC prognosing breast disease. Gene expression analysis is useful for
XX CC assessing the toxicity of chemical agents on cells. The microarray of
XX CC this invention presents a far greater diversity of probes for measuring
XX CC gene expression, with far less bias than expressed sequence tag
XX CC microarrays. The method is suitable for rapid production of functional
XX CC information from genomic sequence. The present sequence is a single exon
XX CC nucleic acid probe of the invention. Note: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1218;
Best Local Similarity 85.7%; Pred. No. 6.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 AAAGCGCTTCGGGGTGCTC 22
Db 139 AAATGCCTTTGGGAGTGCTC 119
RESULT 48
ABA42594/c
ID ABA42594 standard; DNA; 1218 BP.
XX AC ABA42594;
XX AC ABA42594;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 17151.
XX
```

KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157276-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US000668.  
 XX

PR 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488900/53.  
 XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human bone marrow.  
 PT  
 XX Example 4; SEQ ID NO 17151; 659pp + Sequence Listing; English.  
 XX

CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow  
 CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is one of  
 CC the probes of the invention  
 XX

SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 4; Length 1218;  
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGCTTTCGGGGTGCTC 22  
 ||| ||||| ||||| |||||  
 Db 139 AAATGCTTTGGGAGTGCTC 119

RESULT 49  
 AAK16823/c  
 ID AAK16823 standard; DNA; 1218 BP.  
 XX  
 AC AAK16823;  
 XX  
 DT 05-NOV-2001 (first entry)  
 XX  
 XX Human brain expressed single exon probe SEQ ID NO: 16814.  
 DE  
 XX

KW Human; brain expressed exon; gene expression analysis; probe; microarray;  
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157275-A2.  
 XX

XX 09-AUG-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US000667.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR

PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX

XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-483446/52.  
 XX

XX Single exon nucleic acid probes for analyzing gene expression in human  
 XX brains.  
 PT  
 XX Example 4; SEQ ID NO 16814; 650pp + Sequence Listing; English.  
 PS

XX The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is one of the probes of the  
 CC invention  
 XX

SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 4; Length 1218;  
 Best Local Similarity 85.7%; Pred. No. 6.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 AAAGGCTTTCGGGGTGCTC 22  
 ||| ||||| ||||| |||||  
 Db 139 AAATGCTTTGGGAGTGCTC 119

RESULT 50  
 ABS42209/c  
 ID ABS42209 standard; DNA; 1218 BP.  
 XX  
 AC ABS42209;  
 XX

XX 25-FEB-2003 (first entry)  
 DT  
 XX Human liver single exon probe, SEQ ID NO 17199.  
 DE

XX Human; single exon nucleic acid probe; liver; cirrhosis;  
 KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;  
 KW coronary heart disease; ss.  
 XX

OS Homo sapiens.  
 XX  
 PN WO200157273-A2.  
 XX  
 PD 09-AUG-2001.  
 XX

XX 30-JAN-2001; 2001WO-US000664.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 PR 26-MAY-2000; 2000US-0207456P.  
 PR 30-JUN-2000; 2000US-00608408.  
 PR 03-AUG-2000; 2000US-00632366.  
 PR 21-SEP-2000; 2000US-0234687P.  
 PR 27-SEP-2000; 2000US-0236359P.  
 PR 04-OCT-2000; 2000GB-00024263.  
 XX

XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX WPI; 2001-488998/53.  
 XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
 XX gene expression in human adult liver.  
 PT

XX Claim 4; SEQ ID NO 17199; 658pp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

XX measuring human gene expression in a sample derived from human adult

XX liver, comprising one of 13109 defined nucleotide sequences given in the

XX specification (or complements/ fragments). The probe hybridises at high

XX stringency to a nucleic acid molecule expressed in the human adult liver.

XX (I) may be used for predicting, measuring and displaying gene expression

XX in samples derived from human adult liver. The genes identified may be

XX involved in genetic liver diseases such as cirrhosis,

XX hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

XX associated with coronary heart disease. ABS25011-ABS51005 represent human

XX liver single exon nucleic acid probes of the invention. Note: The

XX sequence information for this patent does not appear in the printed

XX specification but was obtained in electronic format directly from WIPO at

XX ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1218;

Best Local Similarity 85.7%; Pred. No. 6.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCGCTTCGGGGGTGCTC 22

DB 139 AAATGCGCTTGGGGAGTGCTC 119

RESULT 51

AA108981/c

ID AA108981 standard; DNA; 1218 BP.

XX AA108981;

XX

XX

DT 09-OCT-2001 (first entry)

XX

XX Probe #8972 used to measure gene expression in human breast sample.

XX Probe; human; breast disease; breast cancer; development disorder; ss;

XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.

XX Homo sapiens.

XX

XX WO200157270-A2.

XX

XX

XX 09-AUG-2001.

XX

XX 29-JAN-2001; 2001WO-US0000661.

XX

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2001-476286/51.

XX

XX Novel single exon nucleic acid probe used to measuring gene expression in

XX a human breast.

XX

XX Claim 25; SEQ ID NO 8972; 322pp; English.

XX

XX The present invention relates to novel single exon nucleic acid probes.

XX The present sequence is one such probe. The probes are useful for

XX measuring human gene expression in a human breast sample, where the probe

XX hybridises at high stringency to a nucleic acid expressed in the human

CC breast. The probes are useful for predicting, diagnosing, grading,

CC staging, monitoring and prognosing diseases of the human breast,

CC particularly those diseases with polygenic aetiology. The diseases

CC include: breast cancer, disorders of development, inflammatory diseases

CC of the breast, fibrocystic changes, proliferative breast disease and non-

CC carcinoma tumours. Note: The sequence data for this patent did not form

CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 5; Length 1218;

Best Local Similarity 85.7%; Pred. No. 6.6e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCGCTTCGGGGGTGCTC 22

DB 139 AAATGCGCTTGGGGAGTGCTC 119

RESULT 52

ABS16646/c

ID ABS16646 standard; DNA; 1218 BP.

XX ABS16646;

XX

XX

DT 19-AUG-2002 (first entry)

XX

XX Human genome-derived single exon probe ORF from lung SEQ ID NO 16637.

XX

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

XX chronic obstructive pulmonary disease; interstitial lung disease;

XX familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

XX pulmonary histiocytosis; lymphangiomyomatosis; Karagener syndrome;

XX pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;

XX primary ciliary dyskinesia; pulmonary hypertension;

XX hyaline membrane disease; open reading frame; ORF.

XX

XX Homo sapiens.

XX

XX WO200186003-A2.

XX

XX

XX 15-NOV-2001.

XX

XX 30-JAN-2001; 2001WO-US0000665.

XX

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX

XX WPI; 2002-114183/15.

XX

XX Spatially-addressable set of single exon nucleic acid probes, used to

XX measure gene expression in human lung samples.

XX

XX Claim 4; SEQ ID NO 16637; 634pp; English.

XX

XX The invention relates to a spatially-addressable set of single exon

XX nucleic acid probes for measuring gene expression in a sample derived

XX from human lung comprising single exon nucleic acid probes having one of

XX 12614 nucleic acid sequences mentioned in the specification, or their

XX complements or the 12387 open reading frames derived from the 12614

XX probes. Also included are a microarray comprising the novel set of probes

CC ; the novel set of probes which hybridise at high stringency to a nucleic  
CC acid expressed in the human lung; measuring gene expression in a sample  
CC derived from human lung, comprising (a) contacting the array with a  
CC collection of detectably labeled nucleic acids derived from human lung  
CC mRNA, and (b) measuring the label detectably bound to each probe of the  
CC array; identifying exons in a eukaryotic genome, comprising (a)  
CC algorithmically predicting at least one exon from genomic sequences of  
CC the eukaryote; and (b) detecting specific hybridisation of detectably  
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
CC having a fragment identical to the predicted exon, the probe is included  
CC in the above mentioned microarray; assigning exons to a single gene,  
CC comprising (a) identifying exons from genomic sequence by the method  
CC above and (b) measuring the expression of each of the exons in several  
CC tissues and/or cell types using hybridisation to a single exon  
CC microarrays having a probe with the exon, where a common pattern of  
CC expression of the exons in the tissues and/or cell types indicates that  
CC the exons should be assigned to a single gene; a peptide comprising one  
CC of 12011 sequences, mentioned in the specification, or encoded by the  
CC probes/open reading frames (ORF). The probes are used for gene expression  
CC analysis, and for identifying exons in a gene, particularly using human  
CC lung derived mRNA, and for the study of lung diseases such as asthma, lung  
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
CC Karagenar syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
CC present sequence is a single exon probe open reading frame of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 1218 BP; 256 A; 339 C; 273 G; 350 T; 0 U; 0 Other;  
Query Match 73.6%; Score 16.2; DB 6; Length 1218;  
Best Local Similarity 85.7%; Pred. No. 6.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAGGCGCTTCGGGGTGCTC 22  
DB 139 AAATGCGCTTGGGAGTGCTC 119  
|||||

RESULT 53  
ABD02999  
ID ABD02999 standard; DNA; 1239 BP.  
XX AC ABD02999;  
XX DT 29-JUL-2004 (first entry)  
XX DE Pseudomonas aeruginosa polynucleotide #1603.  
XX KW Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;  
XX KW antibacterial.  
XX OS Pseudomonas aeruginosa.  
XX XX US6551795-B1.  
XX PN 22-APR-2003.  
XX PF 18-FEB-1999; 99US-00252991.  
XX PR 18-FEB-1998; 98US-0074788P.  
XX PR 27-JUL-1998; 98US-0094190P.  
XX XX (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.

DR P-PSDB; ABO69428.  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX PS Disclosure; SEQ ID NO 1603; 455pp; English.  
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biotech technology. Sequences ABD01397-  
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
CC the sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html  
XX SQ Sequence 1239 BP; 203 A; 422 C; 410 G; 204 T; 0 U; 0 Other;  
Query Match 73.6%; Score 16.2; DB 11; Length 1239;  
Best Local Similarity 85.7%; Pred. No. 6.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GAAAGCGCTTCGGGGTGCT 21  
DB 1155 GAAGGCGCTTCGGGGTGCT 1175  
|||||

RESULT 54  
ACA38376  
ID ACA38376 standard; DNA; 1377 BP.  
XX AC ACA38376;  
XX DT 19-JUN-2003 (first entry)  
XX DE Prokaryotic essential gene #20033.  
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
XX KW drug design; gene.  
XX OS Mycobacterium bovis.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR P-PSDB; ABU34506.  
XX PR New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to



PT isolate candidate molecules for rational drug discovery programs.  
PS Claim 14; SEQ ID NO 26246; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the  
XX proliferation of an organism. The antisense nucleic acids are useful for  
XX identifying proteins or screening for homologous nucleic acids required  
XX for cellular proliferation to isolate candidate molecules for rational  
XX drug discovery programs, or for screening homologous nucleic acids  
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
XX prokaryotic essential genes. Note: The sequence data for this patent did  
XX not form part of the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 1377 BP; 257 A; 452 C; 465 G; 203 T; 0 U; 0 Other;  
XX  
XX Query Match 73.6%; Score 16.2; DB 8; Length 1377;  
XX Best Local Similarity 85.7%; Pred. No. 6.7e+02;  
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX QY 2 AAAGGCTTTCGGGGTGCTC 22  
XX ||||| |||||  
XX Db 538 AAAGCGCGTTCGGGGTGCTC 558  
XX  
XX RESULT 55  
XX ACA40722  
XX ID ACA40722 standard; DNA; 1380 BP.  
XX AC ACA40722;  
XX XX  
XX DT 19-JUN-2003 (first entry)  
XX XX  
XX DE Prokaryotic essential gene #22379.  
XX XX  
XX KW Antisense; da; prokaryotic essential gene; cell proliferation;  
XX KW drug design; gene.  
XX OS Mycobacterium tuberculosis.  
XX PN W0200277183-A2.  
XX XX  
XX PD 03-OCT-2002.  
XX XX  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX XX  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX DR WPI; 2003-0299926/02.  
XX P-PSDB; ABU36852.  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 14; SEQ ID NO 28592; 1766pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the  
XX proliferation of an organism. The antisense nucleic acids are useful for  
XX identifying proteins or screening for homologous nucleic acids required  
XX for cellular proliferation to isolate candidate molecules for rational  
XX drug discovery programs, or for screening homologous nucleic acids  
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target  
XX prokaryotic essential genes. Note: The sequence data for this patent did  
XX not form part of the printed specification, but was obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 1380 BP; 258 A; 452 C; 466 G; 204 T; 0 U; 0 Other;  
XX  
XX Query Match 73.6%; Score 16.2; DB 8; Length 1380;  
XX Best Local Similarity 85.7%; Pred. No. 6.7e+02;  
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX QY 2 AAAGGCTTTCGGGGTGCTC 22  
XX ||||| |||||  
XX Db 538 AAAGCGCGTTCGGGGTGCTC 558  
XX  
XX RESULT 56  
XX AAS94778/C  
XX ID AAS94778 standard; DNA; 1704 BP.  
XX AC AAS94778;  
XX XX  
XX DT 14-FEB-2002 (first entry)  
XX XX  
XX DE Human DNA sequence #33 expressed during foam cell differentiation.  
XX KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;  
XX KW cardiovascular disorder; coronary artery disease; gene therapy; da.  
XX OS Homo sapiens.  
XX XX

PN WO200177389-A2.  
 XX 18-OCT-2001.  
 XX 04-APR-2001; 2001WO-US011128.  
 XX 05-APR-2000; 2000US-0195106P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Shiffman D, Somogyi R, Lawn R, Seilhamer JU, Porter GJ, Mikita T;  
 PI Tai J;  
 XX WPI; 2002-010925/01.  
 XX Composition useful for diagnosis of conditions, disorders or diseases  
 PT associated with atherosclerosis, comprises several polynucleotides that  
 PT are differentially expressed in foam cell development.  
 XX PS Claim 1; Page 90; 315pp; English.  
 XX The present invention relates to the isolation of human polynucleotide  
 CC sequences that are differentially expressed during foam cell  
 CC differentiation. The polynucleotide sequences of the invention or a  
 CC composition comprising these polynucleotides are useful as a high  
 CC throughput method for detecting altered expression of one or more  
 CC polynucleotides in a sample. The polynucleotides can be used in the  
 CC diagnosis of disorders associated with foam cell development such as  
 CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as  
 CC coronary artery disease. The polynucleotide sequences can also be used as  
 CC PCR primers and probes. The polynucleotides of the invention are also  
 CC useful in gene therapy. AAS94746-AAS95021 represent the human  
 CC polynucleotide sequences of the invention which are differentially  
 CC expressed during foam cell differentiation  
 XX SQ Sequence 1704 BP; 382 A; 354 C; 326 G; 422 T; 0 U; 220 Other;  
 Query Match 73.6%; Score 16.2; DB 6; Length 1704;  
 Best Local Similarity 85.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCGCTTCGGGGTGCT 21  
 Db |||||  
 41 GAAAGGCGCTTCGAGATGCT 21  
 RESULT 57  
 AAC85094/c  
 ID AAC85094 standard; DNA; 1740 BP.  
 XX AAC85094;  
 XX 08-MAY-2001 (first entry)  
 XX Homo sapiens.  
 DE Atherosclerosis-associated gene seq ID No. 30.  
 XX Atherosclerosis-associated gene; stroke; myocardial infarction; human;  
 KW ischemia; coronary artery disease; angina pectoris; hypertension;  
 KW peripheral vascular disease; renal artery stenosis; atherosclerotic;  
 KW cerebroprotective; cardiac; gene therapy; hypotensive; vasotropic;  
 KW antianginal; ds.  
 XX OS  
 XX Homo sapiens.  
 XX WO200104264-A2.  
 XX 18-JAN-2001.  
 XX 28-JUN-2000; 2000WO-US017887.  
 XX 07-JUL-1999; 99US-00349015.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PI Jones KA, Volkmut W, Walker MG, Murry LE;  
 XX WPI; 2003-617118/58.  
 XX New combination of atherosclerosis-associated genes, useful for the  
 PT differential diagnosis of e.g. myocardial infarction, hypertension,  
 PT ischemia or stroke, or for staging or treating atherosclerosis-associated  
 PT disorders.

XX Jones KA, Volkmut W, Walker MG;  
 XX WPI; 2001-138330/14.  
 XX Composition comprising atherosclerosis-associated polynucleotide useful  
 PT in diagnosis, prognosis, treatment, and prevention of atherosclerosis and  
 PT stroke, myocardial infarction, or hypertension.  
 XX PS Claim 1; Page 54; 58pp; English.  
 XX The invention provides novel atherosclerosis-associated polynucleotides  
 CC and polypeptides encoded by the genes. Expression vectors and host cells  
 CC for producing the polypeptides are disclosed and methods for screening or  
 CC purifying ligands which specifically bind to the polypeptides are also  
 CC provided. The polynucleotides are useful for treating diseases associated  
 CC with the altered expression of a gene that is coexpressed with one or  
 CC more known atherosclerosis-associated genes in a subject. They are useful  
 CC in diagnosis, prognosis, treatment, prevention, selection and evaluation  
 CC of therapies for atherosclerosis including stroke, myocardial infarction,  
 CC transient cerebral ischemia, mesenteric ischemia, coronary artery  
 CC disease, angina pectoris, peripheral vascular disease, renal artery  
 CC stenosis, and hypertension. Sequences AAC85065-85098 represent  
 CC atherosclerosis-associated genes of the invention  
 XX SQ Sequence 1740 BP; 394 A; 362 C; 333 G; 432 T; 0 U; 219 Other;  
 Query Match 73.6%; Score 16.2; DB 4; Length 1740;  
 Best Local Similarity 85.7%; Pred. No. 6.8e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCGCTTCGGGGTGCT 21  
 Db |||||  
 41 GAAAGGCGCTTCGAGATGCT 21  
 RESULT 58  
 ADM29578/c  
 ID ADM29578 standard; cDNA; 1740 BP.  
 XX ADM29578;  
 XX 20-MAY-2004 (first entry)  
 XX Human atherosclerosis associated cDNA #22.  
 DE Human; ss; gene; atherosclerosis; angina pectoris;  
 KW coronary artery disease; myocardial infarction; hypertension;  
 KW transient cerebral ischemia; mesenteric ischemia;  
 KW peripheral vascular disease; renal artery stenosis; diabetes mellitus;  
 KW obesity; polycystic ovarian syndrome; stroke; diabetes mellitus; obesity;  
 KW polycystic ovarian syndrome; cancer.  
 XX OS  
 XX Homo sapiens.  
 OS US2003129176-A1.  
 PN 10-JUL-2003.  
 PD 14-AUG-2002; 2002US-00219664.  
 XX 07-JUL-1999; 99US-00349015.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA Jones KA, Volkmut W, Walker MG, Murry LE;  
 PI WPI; 2003-617118/58.  
 XX New combination of atherosclerosis-associated genes, useful for the  
 PT differential diagnosis of e.g. myocardial infarction, hypertension,  
 PT ischemia or stroke, or for staging or treating atherosclerosis-associated  
 PT disorders.

XX Claim 1; SEQ ID NO 22; 60pp; English.

XX The invention relates to a combination of several cDNAs, which are co-

CC expressed with one or more known human atherosclerosis-associated genes,

CC is new. The cDNAs comprise any of 25 sequences appearing as ADM29557-

CC ADM29581or the complements of any of these sequences. Also included are

CC detecting differential expression of one or more cDNAs in a sample

CC containing nucleic acids, using cDNAs to screen a sample and identify a

CC ligand that specifically binds a cDNA, a vector containing the cDNA, a

CC host cell containing the vector, producing a protein, an atherosclerosis-

CC associated protein appearing as ADM29582, using a protein to screen

CC several molecules or compounds (and identify at least one ligand that

CC specifically binds the protein), using a protein to produce an antibody,

CC an antibody produced by the method, and using an antibody to detect gene

CC expression in a sample. The cDNAs are useful for detecting differential

CC expression of one or more cDNAs in a sample containing nucleic acids.

CC This differential expression is diagnostic of angina pectoris, coronary

CC artery disease, myocardial infarction, hypertension, transient cerebral

CC ischaemia, mesenteric ischaemia, peripheral vascular disease, renal

CC artery stenosis, diabetes mellitus, obesity, polycystic ovarian syndrome,

CC or stroke. The cDNAs or proteins are useful for screening a sample and

CC identifying a ligand, which specifically binds a cDNA or protein,

CC respectively. The protein is also useful for producing an antibody for

CC detecting gene expression in a sample. The combination of cDNAs is also

CC useful for staging, treating, or monitoring the progression of, disorders

CC associated with atherosclerosis, such as diabetes mellitus, obesity,

CC polycystic ovarian syndrome, and cancers. The present sequence is a human

CC atherosclerosis-associated cDNA of the invention.

XX

XX Sequence 1740 BP; 394 A; 362 C; 333 G; 432 T; 0 U; 219 Other;

Query Match 73.6%; Score 16.2; DB 11; Length 1740;

Best Local Similarity 85.7%; Pred. No. 6.8e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAGGCGCTTTCGGGGTGCT 21

Db 41 GAAGGCGCTTTCGGGGTGCT 21

RESULT 59

AAI14134/c

ID AAI14134 standard; DNA; 1954 BP.

AC AAI14134;

DT 12-OCT-2001 (first entry)

XX Probe #4067 for gene expression analysis in human cervical cell sample.

DE Probe; human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer; ss.

KW Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000670.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

PI WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 4165; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human fetal liver. The

XX WPI; 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human cervical epithelial cells.

XX Claim 25; SEQ ID NO 4067; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes

CC (SENPs). The present sequence is one such probe. The SENPs are derived

CC from human HeLa cells. The SENPs can be used to produce a single exon

CC microarray, which can be used for measuring human gene expression in a

CC sample derived from human cervical epithelial cells. By measuring gene

CC expression, the probes are therefore useful in grading and/or staging of

CC diseases of the cervix, notably cervical cancer. Note: The sequence data

CC for this patent did not form part of the printed specification, but was

CC obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 1954;

Best Local Similarity 85.7%; Pred. No. 6.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCGCTTTCGGGGTGCT 22

Db 394 AAATGCGCTTTCGGGGTGCT 374

RESULT 60

ABA55860/c

ID ABA55860 standard; DNA; 1954 BP.

XX ABA55860;

XX 01-FEB-2002 (first entry)

XX Human foetal liver single exon nucleic acid probe #4165.

XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US0000669.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-483447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 1; SEQ ID NO 4165; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring

CC human gene expression in a sample derived from human foetal liver. The

CC single exon nucleic acid probes may be used for predicting, measuring and

CC displaying gene expression in samples derived from human fetal liver. The



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ID ABA25535 standard; DNA; 1954 BP.
XX AC ABA25535;
XX DT 23-JAN-2002 (first entry)
XX DE Probe #4001 for gene expression analysis in human heart cell sample.
XX KW Human; gene expression; heart; microarray; vascular system; probe;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease; ss.
XX OS Homo sapiens.
XX PN WO200157274-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000666.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488899/53.
XX PT Single exon nucleic acid probes for analyzing gene expression in human
XX PT hearts.
XX SQ Claim 1; SEQ ID NO 4001; 530pp; English.
XX PS The present invention relates to single exon nucleic acid probes for
XX CC measuring human gene expression in a sample derived from human heart. The
XX CC present sequence is one such probe. The probes may be used for
XX CC predicting, measuring and displaying gene expression in samples derived
XX CC from the human heart via microarrays. By measuring gene expression, the
XX CC probes are useful for predicting, diagnosing, grading, staging,
XX CC monitoring and prognosing diseases of the human heart and vascular system
XX CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
XX CC congenital heart disease. Note: The sequence data for this patent did not
XX CC form part of the printed specification, but was obtained in electronic
XX CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX AC AAK29561;
XX DT 06-NOV-2001 (first entry)
XX DE Human bone marrow expressed single exon probe SEQ ID NO: 4118.
XX KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX OS Homo sapiens.
XX PN WO200157276-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000668.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-488900/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human bone marrow.
XX PS Example 4; SEQ ID NO 4118; 658pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
XX CC probes which are derived from genomic sequences expressed in the human
XX CC bone marrow. They can be used to measure gene expression in bone marrow
XX CC samples, which may enable the improved diagnosis and treatment of cancers
XX CC such as lymphoma, leukaemia and myeloma. The present sequence is one of
XX CC the probes of the invention.
XX SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1954;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGGCCTTTGGGGGTGCTC 22
DB 394 AAATGCTTTGGGGAGTGCTC 374
RESULT 65
AAK04079/c
ID AAK04079 standard; DNA; 1954 BP.
XX AC AAK04079;
XX DT 05-NOV-2001 (first entry)
XX DE Human brain expressed single exon probe SEQ ID NO: 4070.
XX KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KW ss.
XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000667.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
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PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
PT
XX
XX Example 4; SEQ ID NO 4070; 650pp + Sequence Listing; English.
PS
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention
XX
SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1954;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
Db 394 AAATGCCTTTGGGAGTGCTC 374
|||||
RESULT 66
ABS29189/c
ID ABS29189 standard; DNA; 1954 BP.
XX
AC ABS29189;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver single exon probe, SEQ ID No 4179.
XX
DE Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
OS Homo sapiens.
XX
XX WO200157273-A2.
XX
XX 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000664.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
PT
XX
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PS Claim 1; SEQ ID NO 4179; 658pp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (I) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABS25011-ABS51005 represent human
CC liver single exon nucleic acid probes of the invention. Note: The
CC sequence information for this patent does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 4; Length 1954;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22
Db 394 AAATGCCTTTGGGAGTGCTC 374
|||||
RESULT 67
AAI03983/c
ID AAI03983 standard; DNA; 1954 BP.
XX
AC AAI03983;
XX
DT 09-OCT-2001 (first entry)
XX
DE Probe #3974 used to measure gene expression in human breast sample.
XX
DE Probe; human; breast disease; breast cancer; development disorder; ss;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
XX WO200157270-A2.
XX
XX 09-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-US000661.
XX
XX 04-FEB-2000; 2000US-0180312P.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX
XX 30-JUN-2000; 2000US-00608408.
XX
XX 03-AUG-2000; 2000US-00632366.
XX
XX 21-SEP-2000; 2000US-0234687P.
XX
XX 27-SEP-2000; 2000US-0236359P.
XX
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression in
PT a human breast.
PT
XX
XX Claim 25; SEQ ID NO 3974; 322pp; English.
XX
XX The present invention relates to novel single exon nucleic acid probes.
CC The present sequence is one such probe. The probes are useful for
CC measuring human gene expression in a human breast sample, where the probe
CC hybridises at high stringency to a nucleic acid expressed in the human
CC breast. The probes are useful for predicting, diagnosing, grading,
```

CC staging, monitoring and prognosing diseases of the human breast,  
 CC particularly those diseases with polygenic aetiology. The diseases  
 CC include: breast cancer, disorders of development, inflammatory diseases  
 CC of the breast, fibrocystic changes, proliferative breast disease and non-  
 CC carcinoma tumours. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 5; Length 1954;  
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 AAAGGCTTTGGGGTGCTC 22  
 DB 394 AAATGCTTTGGGGAGTGCTC 374  
 RESULT 68  
 ID ABS04116/c  
 AC ABS04116;  
 XX  
 XX 19-AUG-2002 (first entry)  
 DT  
 DE Human genome-derived single exon probe from lung SEQ ID No 4107.  
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;  
 KW chronic obstructive pulmonary disease; interstitial lung disease;  
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;  
 KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;  
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;  
 KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;  
 KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;  
 KW primary ciliary dyskinesia; pulmonary hypertension;  
 KW hyaline membrane disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200186003-A2.  
 XX  
 XX 15-NOV-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US000665.  
 XX  
 XX 04-FEB-2000; 2000US-0180312P.  
 XX 26-MAY-2000; 2000US-0207456P.  
 XX 30-JUN-2000; 2000US-00608408.  
 XX 03-AUG-2000; 2000US-00632366.  
 XX 21-SEP-2000; 2000US-0234687P.  
 XX 27-SEP-2000; 2000US-0236359P.  
 XX 04-OCT-2000; 2000GB-00024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 XX  
 XX Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI; 2002-114183/15.  
 XX  
 XX Spatially-addressable set of single exon nucleic acid probes, used to  
 XX measure gene expression in human lung samples.  
 XX  
 XX Claim 1; SEQ ID NO 4107; 634pp; English.  
 XX  
 XX The invention relates to a spatially-addressable set of single exon  
 XX nucleic acid probes for measuring gene expression in a sample derived  
 XX from human lung comprising single exon nucleic acid probes having one of  
 XX 12614 nucleic acid sequences mentioned in the specification, or their  
 XX complements or the 12387 open reading frames derived from the 12614  
 XX probes. Also included are a microarray comprising the novel set of probes  
 XX ; the novel set of probes which hybridise at high stringency to a nucleic

CC acid expressed in the human lung; measuring gene expression in a sample  
 CC derived from human lung, comprising (a) contacting the array with a  
 CC collection of detectably labeled nucleic acids derived from human lung  
 CC mRNA, and (b) measuring the label detectably bound to each probe of the  
 CC array; identifying exons in a eukaryotic genome, comprising (a)  
 CC algorithmically predicting at least one exon from genomic sequences of  
 CC the eukaryote; and (b) detecting specific hybridisation of detectably  
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,  
 CC having a fragment identical to the predicted exon, the probe is included  
 CC in the above mentioned microarray; assigning exons to a single gene,  
 CC comprising (a) identifying exons from genomic sequence by the method  
 CC above and (b) measuring the expression of each of the exons in several  
 CC tissues and/or cell types using hybridisation to a single exon  
 CC microarrays having a probe with the exon, where a common pattern of  
 CC expression of the exons in the tissues and/or cell types indicates that  
 CC the exons should be assigned to a single gene; a peptide comprising one  
 CC of 12011 sequences, mentioned in the specification, or encoded by the  
 CC probes/open reading frames (ORF). The probes are used for gene expression  
 CC analysis, and for identifying exons in a gene, particularly using human  
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung  
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung  
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,  
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-  
 CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary  
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,  
 CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary  
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The  
 CC present sequence is a single exon probe of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1954 BP; 410 A; 510 C; 444 G; 590 T; 0 U; 0 Other;  
 Query Match 73.6%; Score 16.2; DB 6; Length 1954;  
 Best Local Similarity 85.7%; Pred. No. 6.9e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 AAAGGCTTTGGGGTGCTC 22  
 DB 394 AAATGCTTTGGGGAGTGCTC 374  
 RESULT 69  
 ABQ54935  
 ID ABQ54935 standard; cDNA; 2772 BP.  
 XX  
 AC ABQ54935;  
 XX  
 XX 22-AUG-2002 (first entry)  
 DT  
 DE Human ovarian antigen HFPHF52 cDNA, SEQ ID NO:815.  
 XX  
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;  
 XX ovarian cancer; breast cancer; tumour; reproductive system disorder;  
 XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;  
 XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;  
 XX inflammatory condition; immune disorder; blood disorder;  
 XX cardiovascular disorder; respiratory disorder; neurological disorder;  
 XX gastrointestinal disorder; urinary system disorder; drug screening;  
 XX gene therapy; chromosome mapping; forensic analysis;  
 XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;  
 XX antiinflammatory; gynaecological; reproductive; chromosome 19q13.4; gene;  
 XX ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200200677-A1.  
 XX  
 XX 03-JAN-2002.  
 XX  
 XX 07-JUN-2001; 2001WO-US018569.  
 XX

PR	07-JUN-2000; 2000US-0209467P.	
XX	(HUMA-) HUMAN GENOME SCI INC.	
PA		
XX		
PI	Birse CE, Rosen CA;	
XX		
DR	WPI; 2002-147878/19.	
DR	P-PSDB; ABP41858.	
XX		
XX	Isolated nucleic acid molecules encoding novel ovarian polypeptides,	
PT	useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian	
PT	cancer), immune disorders, cardiovascular disorders and neurological	
PT	diseases.	
XX		
XX	Claim 1; SEQ ID NO 815; 2922pp; English.	
PS		
XX		
XX	The invention relates to 2175 novel human ovarian antigens (ABP41054-	
CC	ABP4328) and to cDNAs encoding them (ABQ54131-ABQ56305), and also	
CC	encompasses polypeptides 90% identical and polynucleotides 95% identical	
CC	to the sequences of the invention. The invention additionally relates to	
CC	recombinant vectors and host cells comprising human ovarian antigen	
CC	polynucleotides, antibodies against human ovarian antigens, and the use	
CC	of ovarian antigen polynucleotides and polypeptides in diagnosing,	
CC	treating, prognosing or preventing various ovary and/or breast-related	
CC	disorders. Such conditions include ovarian cancer and breast cancer, and	
CC	metastatic tumours of ovarian or breast origin, reproductive system	
CC	disorders (e.g., infertility, disorders of pregnancy, anovulation,	
CC	polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine	
CC	disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic	
CC	shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and	
CC	vaginitis), immune disorders (e.g., congenital and acquired	
CC	immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),	
CC	blood-related disorders (e.g., anaemia), cardiovascular disorders,	
CC	respiratory disorders, neurological disorders, gastrointestinal disorders	
CC	and urinary system disorders. Ovarian antigen polypeptides and	
CC	polynucleotides may also be used in screening for compounds which	
CC	modulate ovarian antigen expression or activity. The polynucleotides may	
CC	further be used for gene therapy, chromosome mapping, in the	
CC	identification of individuals and in forensic analysis, and the	
CC	polypeptides may be used as food additives or to prepare antibodies	
CC	useful in disease diagnosis, drug targeting and phenotyping. The present	
CC	sequence represents a cDNA encoding a human ovarian antigen of the	
CC	invention. Note: The sequence data for this patent did not form part of	
CC	the printed specification, but was obtained in electronic format directly	
CC	from WIPO at <a href="http://ftp.wipo.int/pub/published_pct_sequences">ftp.wipo.int/pub/published_pct_sequences</a>	
XX		
SQ	Sequence 2772 BP; 805 A; 590 C; 687 G; 680 T; 0 U; 10 Other;	
	Query Match 73.6%; Score 16.2; DB 6; Length 2772;	
	Best Local Similarity 85.7%; Pred. No. 7.1e+02;	
	Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 AAAGGCCTTTCGGGGTGCTC 22	
Db	1526 AAATGCCCTTTGGGGAGTGCTC 1546	
RESULT 70		
ADV35075		
ID	ADV35075 standard; cDNA; 3135 BP.	
XX		
AC	ADV35075;	
XX		
DT	10-FEB-2005 (first entry)	
XX		
DE	Human cDNA differentially expressed in the presence of valproate Seq151.	
XX	human; valproate; ss; multi-parameter high throughput screening; MPHTS;	
KW	disease signature; neuropsychiatric; neurodegenerative; schizophrenia;	
KW	bipolar affective disorder; BAD; autism; Parkinson's;	
KW	Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressant.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003096264-A1.	
XX		
PD	22-MAY-2003.	
XX		
PF	18-JUN-2002; 2002US-00175523.	
XX		
PR	18-JUN-2001; 2001US-0299151P.	
PR	07-SEP-2001; 2001US-0317828P.	
PR	25-SEP-2001; 2001US-0325150P.	
PR	14-NOV-2001; 2001US-033047P.	
PR	18-JAN-2002; 2002US-0349936P.	
PR	04-MAR-2002; 2002US-0361834P.	
XX		
PA	(PSYC-) PSYCHIATRIC GENOMICS INC.	
XX		
PI	Altar CA, Brockman JA, Evans D, Hook D, Klimczak LJ, Laeng P;	
PI	Palfreyman M, Rajan P;	
XX		
DR	WPI; 2004-118903/12.	
XX		
XX	Identifying a compound that can treat disease or disorders, such as, a	
PT	neuropsychiatric disorder e.g., schizophrenia, or autism, comprises	
PT	determining the expression of one or more efficacy genes in a cell	
PT	contacted with the test compound.	
XX		
PS	Claim 13; SEQ ID NO 151; 39pp; English.	
XX		
CC	This invention relates to a novel screening method identified as a multi-	
CC	parameter high throughput screening (MPHTS) assay. Specifically, it	
CC	refers to an assay that utilises the disease signature of a plurality of	
CC	specific genes associated with a particular disease, and identifies	
CC	differential expression between those cells taken from individuals	
CC	affected by that disease and those that are not affected. The present	
CC	invention then describes the screening of candidate pharmaceutical	
CC	compounds to identify those that have a potential therapeutic benefit for	
CC	the treatment of neuropsychiatric and neurodegenerative disorders	
CC	including schizophrenia, bipolar affective disorder (BAD) and autism, as	
CC	well as Parkinson's and Alzheimer's disease. Accordingly, the compounds	
CC	of this invention exhibit various activities including neuroleptic,	
CC	nootropic, antimanic and antidepressant. Furthermore, the screening	
CC	method used in MPHTS will be automated, such that a large number of test	
CC	compounds may be rapidly screened with a minimal amount of labour and	
CC	effort. This polynucleotide is a human cDNA sequence of a gene that is	
CC	differentially expressed in the presence of the therapeutic compound	
CC	valproate, given in an exemplification of the invention.	
XX		
SQ	Sequence 3135 BP; 919 A; 671 C; 730 G; 815 T; 0 U; 0 Other;	
	Query Match 73.6%; Score 16.2; DB 13; Length 3135;	
	Best Local Similarity 85.7%; Pred. No. 7.2e+02;	
	Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY	2 AAAGGCCTTTCGGGGTGCTC 22	
Db	1689 AAATGCCCTTTGGGGAGTGCTC 1709	
RESULT 71		
ADP65658		
ID	ADP65658 standard; DNA; 4258 BP.	
XX		
AC	ADP65658;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Human mitochondrial benzodiazepine receptor (MBR) gene, complete DNA.	
XX		
KW	autoimmune disease; arthritis; gene expression analysis;	
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	
KW	antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;	
KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;	
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	



KW immune; ds; human.  
 XX Homo sapiens.  
 XX WO2003072827-A1.  
 XX 04-SEP-2003.  
 XX 31-OCT-2002; 2002WO-US035433.  
 XX 31-OCT-2001; 2001US-0336220P.  
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.  
 XX Hirsch R, Thorton SL;  
 XX WPI: 2003-712740/67.  
 XX GENBANK; U12421.  
 XX Diagnosing and analyzing autoimmune disease using gene expression  
 PT profiles and microarray technology, useful for diagnosing and treating  
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and  
 PT gout.  
 XX Disclosure; Page; 56pp; English.  
 XX The invention relates to a novel method for diagnosing and analysing  
 CC autoimmune disease or arthritides. The method comprises obtaining a  
 CC patient sample containing mRNA, analysing gene expression using the mRNA  
 CC that results in a gene expression signature of the mRNA, and using that  
 CC gene expression signature to diagnose or analyse the autoimmune disease  
 CC or arthritides in the patient, where gene expression of at least 60% of  
 CC the genes correlates with that of the gene signature. The invention  
 CC further comprises: a treatment of rheumatoid arthritis; identification of  
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal  
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an  
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or  
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the  
 CC efficacy of a candidate drug in vitro for the treatment of collagen-  
 CC induced arthritis; and reducing the symptoms associated with collagen-  
 CC induced arthritis. The compositions of the invention have the following  
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,  
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The  
 CC methods and compositions of the present invention are useful for  
 CC diagnosing and treating autoimmune disease or arthritides, such as  
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,  
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an  
 CC immune disease caused by an infectious agent. This polynucleotide  
 CC represents a DNA sequence relating to the genes used in the analysis and  
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is  
 CC not shown in the specification. It has been supplied in an electronic  
 CC format from WIPO.  
 XX Sequence 4258 BP; 794 A; 1246 C; 1221 G; 997 T; 0 U; 0 Other;  
 SQ Query Match 73.6%; Score 16.2; DB 11; Length 4258;  
 Best Local Similarity 85.7%; Pred. No. 7.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGGCTTTCCGGGGTGCT 21  
 Db 12 GACAGGCTTTCCGGGGTGCT 32  
 RESULT 72  
 AAC77830  
 ID AAC77830 standard; cDNA; 4395 BP.  
 XX AAC77830;  
 AC  
 XX 08-FEB-2001 (first entry)  
 DT Human cancer associated gene sequence SEQ ID NO:224.  
 DE

XX Human; cancer associated gene; cancer antigen; detection; cancer;  
 KW diagnosis; cytostatic; proliferative; vulnery; immunomodulator;  
 KW antidiabetic; antiaesthetic; antirheumatic; antiarthritic; antiviral;  
 KW antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;  
 KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;  
 KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;  
 KW immune disorder; haematopoietic cell disorder; autoimmune disorder;  
 KW allergic reaction; graft versus host disease; organ rejection;  
 KW haemostatic; thrombolytic; cardiovascular disorder; infection;  
 KW neurological disease; drug screening; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200005350-A1.  
 XX 21-SEP-2000.  
 XX 08-MAR-2000; 2000WO-US005882.  
 XX 12-MAR-1999; 99US-0124270P.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM;  
 XX WPI: 2000-587533/55.  
 XX P-PSDB; AAB43621.  
 XX Novel isolated nucleic acids comprising sequences encoding peptides  
 PT useful for treating or diagnosing e.g. cancer.  
 XX Claim 1; Page 795-796; 2352pp; English.  
 XX AAC77607 to AAC78448 encode the human cancer associated proteins given in  
 CC AAB43398 to AAB44339. The proteins can have activities based on the  
 CC tissues and cells the genes are expressed in. Example of activities  
 CC include: cycostatic; proliferative; vulnery; immunomodulator;  
 CC antidiabetic; antiaesthetic; antirheumatic; antiarthritic;  
 CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;  
 CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;  
 CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The  
 CC polynucleotides and polypeptides can be used for preventing, treating or  
 CC ameliorating medical conditions and diagnosing pathological conditions.  
 CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from  
 CC the present invention may be used to treat immune disorders by activating  
 CC or inhibiting the proliferation, differentiation or mobilisation of  
 CC immune cells, to treat disorders of haematopoietic cells, autoimmune  
 CC disorders, allergic reactions, graft versus host disease and organ  
 CC rejection, modulate haemostatic or thrombolytic activity, modulate  
 CC inflammation, cancers, cardiovascular disorders, neurological diseases and  
 CC bacterial or viral infections. The peptides, nucleotides, antibodies,  
 CC agonists and antagonists may be also be used in drug screens. AAC78449 to  
 CC AAC78457 and AAB44240 represent sequences used in the exemplification of  
 CC the present invention  
 XX Sequence 4395 BP; 1364 A; 765 C; 923 G; 1335 T; 0 U; 8 Other;  
 SQ Query Match 73.6%; Score 16.2; DB 3; Length 4395;  
 Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 AAAGGCTTTCCGGGGTGCTC 22  
 Db 603 AAATGCTTTGGGAGTGCTC 623  
 RESULT 73  
 ADL96632/c  
 ID ADL96632 standard; DNA; 4415 BP.  
 XX ADL96632;  
 AC  
 XX

DT	20-MAY-2004	(first entry)
XX		
DE	M. paratuberculosis DNA #23.	
XX		
KW	M. paratuberculosis; gene; ds; milk; faeces; blood;	
KW	M. paratuberculosis infection; Johnes disease; polypeptide purification.	
XX		
OS	Mycobacterium avium subsp. paratuberculosis.	
XX		
PN	US2003175725-A1.	
XX		
PD	18-SEP-2003.	
XX		
PF	30-APR-2002; 2002US-00137113.	
XX		
PR	06-MAR-2002; 2002US-0362396P.	
XX		
PA	(KAPU/) KAPUR V.	
PA	(BANN/) BANNANTINE J P.	
XX		
PI	Kapur V, Bannantine JP;	
XX		
DR	WPI; 2003-863842/80.	
XX		
PT	New isolated nucleic acids and encoded polypeptides useful for detecting	
PT	Mycobacterium paratuberculosis, and as antibacterial vaccines.	
XX		
PS	Claim 39; SEQ ID NO 23; 38pp; English.	
XX		
CC	The invention relates to Mycobacterium avium subsp. paratuberculosis (M.	
CC	paratuberculosis) nucleic acid molecules. A nucleic acid of the invention	
CC	combined with a second nucleic acid will generate an amplification	
CC	product from M. paratuberculosis but not from human, pseudomonas	
CC	aeruginosa, Streptomyces viridochromogenes, mouse, cat or Xanthomonas	
CC	campestris. The nucleic acids and other sequences specific for	
CC	Mycobacterium paratuberculosis are used to detect M. paratuberculosis in	
CC	e.g. milk, faeces or blood. The polypeptides encoded by these sequences	
CC	and antibodies directed against them, are also used to detect M.	
CC	paratuberculosis by immunoassay. The nucleic acids and the polypeptides	
CC	are also used as vaccines to prevent infection (Johnes's disease) by M.	
CC	paratuberculosis. The antibodies are also useful for polypeptide	
CC	purification. This sequence represents an M. paratuberculosis nucleic	
CC	acid of the invention.	
XX		
SQ	Sequence 4415 BP; 682 A; 1431 C; 1507 G; 794 T; 0 U; 1 Other;	
	Query Match 73.6%; Score 16.2; DB 11; Length 4415;	
	Best Local Similarity 85.7%; Pred. No. 7.4e+02;	
	Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0	
QY	2 AAAGGCTTTTCGGGGTGCTC 22	
Db	625 AAAGACTGTCGGGGTGCCC 605	
RESULT 74		
AEA20710		
ID	AEA20710 standard; cDNA; 4670 BP.	
XX		
AC	AEA20710;	
XX		
DT	11-AUG-2005 (first entry)	
XX		
DE	Novel human polynucleotide SEQ ID NO 1404.	
XX		
KW	vulnary; CNS-gen.; gene therapy; diagnostic; forensic; mapping;	
KW	DNA purification; protein purification; osteoarthritis; antiarthritic;	
KW	osteopathic; musculoskeletal disease; osteoporosis; endocrine disease;	
KW	periodontal disease; antiinflammatory; mouth disease; burns; injury;	
KW	peripheral neuropathy; Alzheimers disease; neuroprotective; neurologic disease;	
KW	degeneration; parkinsons disease; antiparkinsonian; neurological disease;	
KW	cerebrovascular ischemia; cerebroprotective; vasotropic;	
KW	cardiovascular disease; autoimmune disease; immunosuppressive;	

```

ID ADY91665 standard; DNA; 4738 BP.
XX
AC ADY91665;
XX
XX
DT 16-JUN-2005 (first entry)
XX
DE Human prostatic cancer marker, PEG3 Kruppel-type zinc finger DNA.
XX
XX tumor marker; cytostatic; prostate tumor; andrology;
KW genitourinary disease; neoplasm; immunotherapy; ds; gene; PEG3.
XX
XX Homo sapiens.
XX
XX JP2005080524-A.
XX
XX 31-MAR-2005.
XX
XX 05-SEP-2003; 2003JP-00313565.
XX
XX 05-SEP-2003; 2003JP-00313565.
XX
XX (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
XX
XX WPI; 2005-266555/28.
XX
XX P-PSDB; ADY91630.
XX
XX Novel prostatic-cancer marker polypeptide, useful for diagnosing
XX prostatic-cancer or androgen independent prostatic-cancer.
XX
XX Claim 23; SEQ ID NO 64; 43pp; Japanese.
XX
XX The invention relates to a novel prostatic cancer marker polypeptide
XX comprising any one of 35 fully defined amino acid sequences (SEQ ID NOS:1
XX -35) as given in specification. Prostate-specific antigen (PSA) is
XX currently widely used as a prostatic tumor marker. Certain problems are
XX associated with diagnosis using PSA, however, such as false positives and
XX ambiguity between benign and malignant results. The polypeptides of the
XX invention demonstrate cytostatic activity and may be useful for
XX diagnosing and treating prostatic cancer or androgen-independent
XX prostatic cancer. The polypeptides may be utilized for immunotherapy. The
XX current sequence is that of the human prostatic cancer marker, PEG3
XX Kruppel-type zinc finger DNA of the invention.
XX
XX Sequence 4738 BP; 1405 A; 1055 C; 1269 G; 1009 T; 0 U; 0 Other;
XX
XX Query Match 73.6%; Score 16.2; DB 14; Length 4738;
XX Best Local Similarity 85.7%; Pred. No. 7.4e+02;
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 AAAGGCCTTTGGGGGTGCTC 22
XX ||| ||||| ||| |||||
XX 4582 AAATGCCTTTGGGGAGTGCTC 4602
XX
XX RESULT 76
XX ABX93240
XX ID ABX93240 standard; cDNA; 4758 BP.
XX
XX AC ABX93240;
XX
XX 30-MAY-2003 (first entry)
XX
XX Full-length cDNA encoding human zinc finger protein, PEG3.
XX
XX Human; paternally expressed gene 3; PEG3; zinc finger protein;
XX transcription factor; gene expression; body weight; obesity; behaviour;
XX thermoregulation; thermoregulatory disorder; cell death; degeneration;
XX Alzheimer's disease; anorectic; gene therapy; gene; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX 5'UTR 1..363
XX
```

```

FT CDS /*tag= a
FT FT 364..4758
FT FT /*tag= b
XX /*product= "PEG3"
XX
XX US2002182668-A1.
XX
XX 05-DEC-2002.
XX
XX 27-APR-2001; 2001US-00842777.
XX
XX 27-APR-2001; 2001US-00842777.
XX
XX (SURA/) SURANI A.
XX (SZET/) SZETO Y Y.
XX
XX Surani A, Szeto YY;
XX
XX WPI; 2003-340975/32.
XX P-PSDB; ABU08353.
XX
XX New cDNAs of the paternally expressed gene 3 (PEG3), useful in gene
XX therapy to increase or decrease the expression of PEG3 in cells of a
XX patient, particularly for modifying or controlling body weight or
XX behavior, or for thermoregulation.
XX
XX Claim 3; Page 13-15; 39pp; English.
XX
XX The present invention relates to the isolation of cDNA fragments and the
XX full-length cDNA sequence encoding human paternally expressed gene 3
XX (PEG3). PEG3 is a zinc finger protein thought to act as a transcription
XX factor. The polynucleotide sequences encoding PEG3 are useful in gene
XX therapy to increase or decrease (using the antisense form of the nucleic
XX acid) the expression of PEG3 in cells of a human patient, particularly
XX for modifying or controlling body weight (to treat obesity) or behaviour,
XX or for thermoregulation. The PEG3 polynucleotide sequence is also useful
XX in diagnostic assays, e.g. for testing an individual's susceptibility to
XX obesity or a thermoregulatory disorder, or for diagnosing and staging
XX diseases involving cell death and degeneration (e.g. Alzheimer's
XX disease). The PEG3 polypeptide is useful for prophylactic and/or
XX therapeutic treatment. The present sequence encodes human PEG3
XX
XX Sequence 4758 BP; 1410 A; 1055 C; 1281 G; 1012 T; 0 U; 0 Other;
XX
XX Query Match 73.6%; Score 16.2; DB 10; Length 4758;
XX Best Local Similarity 85.7%; Pred. No. 7.4e+02;
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 AAAGGCCTTTGGGGGTGCTC 22
XX ||| ||||| ||| |||||
XX 4599 AAATGCCTTTGGGGAGTGCTC 4619
XX
XX RESULT 77
XX ADK41009
XX ID ADK41009 standard; DNA; 4831 BP.
XX
XX AC ADK41009;
XX
XX 06-MAY-2004 (first entry)
XX
XX Novel human kinase gene #29.
XX
XX Cytostatic; immunomodulator; cardiant; neuroprotective; nootropic;
XX antiparkinsonian; virucide; antibacterial; fungicide; ophthalmological;
XX analgesic; hypotensive; immunosuppressive; kinase inhibitor; kinase;
XX cancer; peripheral nervous system; central nervous system;
XX Alzheimer's disease; Parkinson's disease; multiple sclerosis;
XX amyotrophic lateral sclerosis; viral infection; prion infection;
XX ocular disease; migraine; pain; sexual dysfunction; mood disorder;
XX attention disorder; cognition disorder; hypotension; hypertension;
XX psychotic disorder; neurological disorder; dyskinesia;
XX metabolic disorder; organ transplant rejection; enzyme; gene; ds.
XX
```

XX	OS	Homo sapiens.	Immune-related disease; cardiovascular disease; neuronal-associated disease; metabolic disorder; gene; ds.
XX	PN	W02003057841-A2.	
XX	PD	17-JUL-2003.	
XX	PF	31-DEC-2002; 2002WO-US041687.	
XX	PR	31-DEC-2001; 2001US-0343169P.	
XX	PA	(GRIG/) GRIGORIEV I V.	
XX	PA	(SUDA/) SUDARSANAM S.	
XX	PI	Grigoriev IV, Sudarsanam S;	
XX	DR	WPI; 2003-587115/55.	
XX	PT	New isolated, enriched or purified nucleic acid molecule encoding a kinase polypeptide, useful for treating cancer, immune-related diseases, cardiovascular disease, brain or neuronal-associated diseases and metabolic disorders.	
XX	PS	Claim 33; SEQ ID NO 116; 491pp; English.	
XX	CC	The invention relates to novel isolated, enriched or purified nucleic acid molecules encoding a kinase polypeptide. The nucleic acid molecule comprises a sequence that: (a) encodes a kinase polypeptide; (b) is a complement of (a); (c) hybridizes under stringent conditions to (a) and encodes a naturally occurring kinase polypeptide; (d) encodes the polypeptide in (a), except that it lacks one or more, but not all, of an N-terminal domain, C-terminal catalytic domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a spacer region and a C-terminal tail; or (e) is a complement of (d). The nucleic acid molecules, polypeptides, methods and substance are useful for treating cancers, immune-related diseases or disorders, cardiovascular disease, brain or neuronal-associated diseases, and metabolic disorders. The disorders are preferably cancers of the tissues or of hematopoietic origin, diseases of the central or peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, infections caused by bacteria, infections caused by fungi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders and organ transplant rejection. This sequence corresponds to the DNA encoding one of the kinase polypeptides of the invention.	
XX	SQ	Sequence 4831 BP; 1425 A; 1073 C; 1290 G; 1043 T; 0 U; 0 Other;	
		Query Match 73.6%; Score 16.2; DB 10; Length 4831;	
		Best Local Similarity 85.7%; Pred. No. 7.4e+02;	
		Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
QY		2 AAAGCGCTTTGGGGGTGCTC 22	
Db		4672 AAATGCTTTGGGAGTGCTC 4692	
		RESULT 78	
		ADRI5723	
ID		ADRI5723 standard; DNA; 4831 BP.	
XX	AC	ADR15723;	
XX	XX		
XX	DT	04-NOV-2004 (first entry)	
XX	DE	Kinase 691401 hCTI686651 1 coding sequence, SEQ ID 116.	
XX	XX		
KW	XX	Cytostatic; Cardiovascular; Neuroprotective; Nootropic; Antiparkinsonian; Virucide; Cerebroprotective; Antibacterial; Fungicide; Ophthalmological; Antimigraine; Analgesic; Endocrine; Tranquillizer; Hypotensive; Immunosuppressive; Gene Therapy; Kinase; enzyme; cancer;	

KW	XX	Immune-related disease; cardiovascular disease; neuronal-associated disease; metabolic disorder; gene; ds.
XX	OS	Homo sapiens.
XX	XX	
XX	XX	Key Location/Qualifiers
FT	FT	122..4831
FT	FT	/*tag= a
FT	FT	/product= "Kinase 691401 hCTI686651 1"
XX	PN	W02004069154-A2.
XX	XX	19-AUG-2004.
XX	XX	28-JAN-2003; 2003WO-US002234.
XX	XX	28-JAN-2003; 2003WO-US002234.
PA	PA	(GRIG/) GRIGORIEV I V.
PA	PA	(SUDA/) SUDARSANAM S.
XX	PI	Grigoriev IV, Sudarsanam S;
XX	XX	
DR	DR	WPI; 2004-604329/58.
DR	DR	P-PSDB; ADR15679.
XX	XX	New isolated, enriched, or purified kinase nucleic acids and polypeptides, useful for diagnosing or treating kinase-related diseases and conditions, e.g. cardiovascular disease, brain or neuronal-associated diseases, or metabolic disorders.
XX	PS	Claim 33; Fig 4; 496pp; English.
XX	CC	The present invention relates to a method for detecting remote polypeptide homologues, comprising analysis of conserved secondary structure pattern in a protein family, and conserved active site amino acid residues. The analyses are used to identify conserved residues embedded into the secondary structure pattern (CRISP), which are used to detect remote homologues of the referent protein family, wherein said referent protein family is the protein kinase family. The present sequence is the coding sequence for a kinase, used to illustrate the method of the invention. The kinases are useful for diagnosing or treating various kinase-related diseases and conditions. Diseases or disorders include cancers, immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases, or metabolic disorders. Preferably, the diseases or disorders are cancers of tissues, cancers of hematopoietic origin, diseases of the central nervous system, diseases of the peripheral nervous system, Alzheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, viral infections, infections caused by prions, infections caused by bacteria, infections caused by fungi, or ocular diseases. The disease or disorder is also migraines, pain, sexual dysfunction, mood disorders, attention disorders, cognition disorders, hypertension, psychotic disorders, neurological disorders, dyskinesias, metabolic disorders, or organ transplant rejection.
XX	SQ	Sequence 4831 BP; 1425 A; 1073 C; 1290 G; 1043 T; 0 U; 0 Other;
		Query Match 73.6%; Score 16.2; DB 13; Length 4831;
		Best Local Similarity 85.7%; Pred. No. 7.4e+02;
		Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY		2 AAAGCGCTTTGGGGGTGCTC 22
Db		4672 AAATGCTTTGGGAGTGCTC 4692
		RESULT 79
		AAAX26546
ID		AAAX26546 standard; cDNA to mRNA; 5970 BP.
XX	XX	
AC	XX	AAAX26546;
XX	XX	

```

DT 14-JUN-1999 (first entry)
XX Nucleic acid encoding a carcinogenesis-inhibiting protein.
DE
XX Carcinogenesis-inhibiting activity; genetic treatment; cerebral tumour;
XX ds.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX FH 344..4732
XX CDS /*tag= a
XX FT
XX JPI1075844-A.
XX PN
XX XX
XX PD 23-MAR-1999.
XX PF 01-SEP-1997; 97JP-00236208.
XX PR 01-SEP-1997; 97JP-00236208.
XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX DR WPI; 1999-257694/22.
XX DR P-PSDB; AAY01519.
XX XX
XX A carcinogenesis-inhibiting gene - useful for genetic treatment of
XX cerebral tumors.
XX PS Claim 3; Page 9-15; 21pp; Japanese.
XX CC The present sequence encodes a protein with carcinogenesis-inhibiting
XX activity. The gene is useful for the genetic treatment of cerebral
XX tumours.
XX SQ Sequence 5970 BP; 1745 A; 1297 C; 1502 G; 1426 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 2; Length 5970;
Best Local Similarity 85.7%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGGCCTTTGGGGGTGCTC 22
DB 4573 AAATGCCTTTGGGGAGTGCTC 4593
RESULT 80
ADB80558
ID ADB80558 standard; DNA; 5994 BP.
XX AC
XX ADB80558;
XX DT 04-DEC-2003 (first entry)
XX DE Ovarian cancer-associated transcript #62.
XX cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
XX post-operative chemotherapy; radiation therapy; tumour prognosis;
XX pre-cancerous lesion detection; ds; gene.
XX OS Homo sapiens.
XX XX
XX Key Location/Qualifiers
XX FH 356..4750
XX CDS /*tag= a
XX FT
XX WO2002102235-A2.
XX PN
XX PD 27-DEC-2002.
XX PF 18-JUN-2002; 2002WO-US019297.
XX PR 18-JUN-2001; 2001US-0299234P.
PR 27-AUG-2001; 2001US-0315287P.
PR 05-SEP-2001; 2001US-0317544P.
PR 13-NOV-2001; 2001US-0350666P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Mack DH, Gish KC;
XX WPI; 2003-167431/16.
XX P-PSDB; ADB80559.
XX
XX Detecting an ovarian cancer-associated transcript in a cell from a
XX patient, comprises contacting a biological sample from the patient with a
XX polynucleotide that hybridizes to an ovarian cancer gene.
XX Claim 10; Page 316-317; 332pp; English.
XX
XX The invention relates to a method of detecting an ovarian cancer-
XX associated transcript in a cell from a patient, by contacting a
XX biological sample from the patient with a polynucleotide that selectively
XX hybridizes to a sequence at least 80% identical to any of one of 80
XX nucleic acid sequences given in the specification. The method is useful
XX in diagnosing ovarian cancer and in identifying and using agents and/or
XX targets that inhibit ovarian cancer. The nucleic acid molecule,
XX polypeptide and the antibody may also be used in detecting ovarian
XX cancers, monitoring and early detection of relapse following treatment,
XX monitoring response to therapy, selecting patients for post-operative
XX chemotherapy or radiation therapy, in selecting mode of therapy,
XX determining tumour prognosis, early detection of pre-cancerous lesions,
XX and as vaccines. This sequence corresponds to one of the nucleic acids
XX used for the detection method of the invention.
XX SQ Sequence 5994 BP; 1760 A; 1298 C; 1504 G; 1432 T; 0 U; 0 Other;
Query Match 73.6%; Score 16.2; DB 10; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGGCCTTTGGGGGTGCTC 22
DB 4591 AAATGCCTTTGGGGAGTGCTC 4611
RESULT 81
ADB79896
ID ADB79896 standard; DNA; 5994 BP.
XX AC
XX ADB79896;
XX DT 04-DEC-2003 (first entry)
XX DE Human putative KIAA0287 coding sequence, SEQ ID 136.
XX Analgesic; pain; streptozocin-induced diabetes; human; gene; ds.
XX OS Homo sapiens.
XX EP12979744-A2.
XX PN
XX PD 29-JAN-2003.
XX PF 26-JUL-2002; 2002EP-00255249.
XX PR 27-JUL-2001; 2001GB-00018354.
XX PR 07-FEB-2002; 2002GB-00002910.
XX (WARN ) WARNER LAMBERT CO.
XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
XX WPI; 2003-395407/38.
XX P-PSDB; ADB79895.

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CC carrier; an antibody directed against the polypeptide of (3); a method  
 CC for detecting (1) in a sample; a method for detecting the polypeptide of  
 CC (3) in a sample; a method for identifying a compound that binds to the  
 CC polypeptide of (3); a method for producing the polypeptide of (3); and a  
 CC collection of polynucleotides, where the collection comprising of at  
 CC least one of SEQ ID NOS: 1-567. (1) is a polynucleotide comprising any of  
 CC the sequences of SEQ ID NOS: 1-567 encoding a polypeptide with biological  
 CC activity, which comprises any of the amino acid sequence of SEQ ID NOS:  
 CC 568-1134. All sequences are fully defined in the specification. The  
 CC sequences and methods are useful in diagnostics, forensic, and gene  
 CC mapping, in identifying of mutations responsible for genetic disorders or  
 CC other traits, in assessing biodiversity, and for producing many other  
 CC types of data and products dependent on DNA and amino acid sequences. The  
 CC composition and method are useful for treating a disease or disorder,  
 CC e.g. osteoporosis, osteoarthritis, periodontal disease, burns, CNS and  
 CC peripheral disease, Alzheimer's disease, Parkinson's disease, stroke,  
 CC autoimmune disorders, viral infection, or cancer. This sequence encodes a  
 CC novel polypeptide of the invention.

XX  
 SQ Sequence 6315 BP; 1852 A; 1366 C; 1573 G; 1524 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 14; Length 6315;  
 Best Local Similarity 85.7%; Pred. No. 7.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTGGGGGTGCTC 22

Db 4899 AAATGCTTTGGGGGTGCTC 4919

RESULT 84

ABA09565

ID ABA09565 standard; cDNA; 6332 BP.

XX ABA09565;

DT 11-JAN-2002 (first entry)

DE Human carcinogenesis inhibitor homologue-encoding cDNA, SEQ ID NO:1341.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;  
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;  
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;  
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;  
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;  
 KW chronic inflammatory condition; proliferative retinopathy;  
 KW atherosclerosis; coronary heart disease; arterial ischaemia;  
 KW bone disorder; osteoporosis; vascular growth disorder;  
 KW tissue regeneration; wound healing; infection; immune disorder;  
 KW cell culture; drug screening; gene therapy; antiinflammatory;  
 KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;  
 KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;  
 KW antifungal; vulnery; antiulcer; ss.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457740/49.

XX P-PSDB; ABB12321.

XX Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis  
 PT and cancer.

PS Claim 1; Page 1002-1004; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and  
 CC sequences ABA09225-ABA09574 represent nucleic acids encoding them. The  
 CC invention also relates to vectors and recombinant host cells comprising a  
 CC nucleotide of the invention, methods of producing the novel polypeptides,  
 CC antibodies against the polypeptides, methods of detecting the nucleotides,  
 CC or polypeptides in a sample, and methods of identifying compounds which  
 CC bind to polypeptides of the invention. Although novel, many of the  
 CC polypeptides of the invention have homology to known proteins, and thereby  
 CC giving an insight into their probable biological activities, and hence  
 CC potential therapeutic applications. The polypeptides of the invention may  
 CC have various activities, including cytokine, cell proliferation or cell  
 CC differentiation activities; stem cell growth factor activity;  
 CC haematopoiesis regulatory activity; tissue growth activity;  
 CC immunomodulatory activity; activin- or inhibin-related activities;  
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or  
 CC thrombolytic activities; receptor or ligand activities; or may be  
 CC involved in oncogenesis; cancer cell proliferation or metastasis.  
 CC Depending on their biological activities, polypeptides and nucleotides of  
 CC the invention are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g., by protein or gene therapy. Such conditions include  
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell  
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),  
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,  
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal  
 CC vascular growth. Polypeptides involved with tissue regeneration and  
 CC repair (or nucleic acids encoding them) may be used to promote wound  
 CC healing (e.g., of burns, incisions and ulcers), while those with  
 CC immunomodulatory activities may be used in the treatment of viral,  
 CC bacterial and fungal infections in addition to immune disorders.  
 CC Polypeptides with growth factor activity may be used in cell cultures to  
 CC promote cell growth. For example, such polypeptides may be used to  
 CC manipulate stem cells in culture to give rise to neuroepithelial cells  
 CC that can be used to augment or replace cells damaged by illness,  
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides  
 CC may also be used in the diagnosis of the above conditions, and in drug  
 CC screening techniques. The present sequence represents a cDNA encoding a  
 CC novel human polypeptide of the invention

XX Sequence 6332 BP; 1860 A; 1378 C; 1582 G; 1512 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 6332;  
 Best Local Similarity 85.7%; Pred. No. 7.6e+02;  
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTGGGGGTGCTC 22

Db 4899 AAATGCTTTGGGGGTGCTC 4919

RESULT 85

ADL12831

ID ADL12831 standard; cDNA; 8411 BP.

XX ADL12831;

XX 06-MAY-2004 (first entry)

XX Human steroid-induced C3A liver cell cDNA #560.

XX ss; gene; Hepatotropic; Gene therapy; Wilson disease; liver disorder;  
 KW steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.

XX Homo sapiens.

XX US6673549-B1.

XX 06-JAN-2004.

XX

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PF 12-OCT-2001; 2001US-00976594.
XX
PR 12-OCT-2000; 2000US-0240409P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Furness LM, Buchbinder JL;
PI WPI; 2004-068610/07.
XX
XX Combination useful for preparing a composition for treating liver
PT disorders associated with steroid therapy, e.g., cirrhosis or hepatitis,
PT comprises cDNAs that are differentially expressed in response to steroid
PT treatment.
XX
XX Claim 1; SEQ ID NO 560; 141pp; English.
PS
XX The invention relates to a combination comprising cDNAs that are
CC differentially expressed in response to steroid treatment. Also included
CC are the following: a high throughput method for using a cDNA to detect
CC differential expression of nucleic acids in a sample; and a high
CC throughput method of screening molecules or compounds to identify a
CC ligand that specifically binds a cDNA. The sample is from a subject with
CC Wilson disease and comparison of a standard defines a stage of that
CC disease. The high throughput method of screening molecules or compounds
CC to identify a ligand that specifically binds a cDNA comprises: combining
CC the combination with molecules or compounds under conditions to allow
CC specific binding; and detecting specific binding between each cDNA and at
CC least one molecule or compound. The molecules or compounds are regulatory
CC proteins. The combination is useful for preparing a composition for
CC treating liver disorders associated with steroid therapy, e.g., cirrhosis
CC or hepatitis. The present sequence represents a human cDNA which is
CC differentially expressed in steroid-induced C3A liver cells. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 8411 BP; 2578 A; 1646 C; 1970 G; 2210 T; 0 U; 7 Other;
Query Match 73.6%; Score 16.2; DB 12; Length 8411;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGGCGCTTTGGGGGTGCTC 22
Db 4595 AAATGCTTTGGGAGTGCTC 4615
RESULT 86
ADE77058
ID ADE77058 standard; cDNA; 8412 BP.
XX
AC ADE77058;
XX
XX 29-JAN-2004 (first entry)
DT
DE Human cDNA differentially expressed in a liver disorder #163.
XX
KW human; ss; gene; liver disorder; hyperlipidaemia; hypertension;
KW type II diabetes; tumour; liver; inflammatory disorder;
KW immune response disorder; high-throughput screening;
KW differential gene expression; gene therapy.
XX
OS Homo sapiens.
XX
XX US2003108871-A1.
PN
XX 12-JUN-2003.
PD
XX 30-JUL-2001; 2001US-00919039.
PF
XX 28-JUL-2000; 2000US-0222113P.
PR
XX
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PA (KASE/) KASER M R.
XX
PI Kaser MR;
XX
XX WPI; 2004-031227/03.
XX
XX Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
XX Claim 1; SEQ ID NO 223; 41pp; English.
PS
XX The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents a cDNA
CC differentially expressed in a liver disorder.
XX
SQ Sequence 8412 BP; 2559 A; 1636 C; 1954 G; 2209 T; 0 U; 54 Other;
Query Match 73.6%; Score 16.2; DB 12; Length 8412;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 AAAGGCGCTTTGGGGGTGCTC 22
Db 4595 AAATGCTTTGGGAGTGCTC 4615
RESULT 87
AAK82933
ID AAK82933 standard; DNA; 14063 BP.
XX
AC AAK82933;
XX
XX 07-NOV-2001 (first entry)
DT
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37745.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
XX WO200157182-A2.
PN
XX 09-AUG-2001.
PD
XX 17-JAN-2001; 2001WO-US001354.
PF
XX 31-JAN-2000; 2000US-0179065P.
PR
XX 04-FEB-2000; 2000US-0180628P.
PR
XX 24-FEB-2000; 2000US-0184664P.
PR
XX 02-MAR-2000; 2000US-0186350P.
PR
XX 16-MAR-2000; 2000US-0189874P.
PR
XX 17-MAR-2000; 2000US-0190076P.
PR
XX 18-APR-2000; 2000US-0198123P.
PR
XX 19-MAY-2000; 2000US-0205515P.
PR
XX 07-JUN-2000; 2000US-0209467P.
PR
XX 28-JUN-2000; 2000US-0214886P.
PR
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PR 30-JUN-2000; 2000US-0215135P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0225213P.  
 PR 14-AUG-2000; 2000US-0225214P.  
 PR 14-AUG-2000; 2000US-0225266P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 14-AUG-2000; 2000US-0225759P.  
 PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-0226686P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227099P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 03-SEP-2000; 2000US-0229509P.  
 PR 03-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232337P.  
 PR 14-SEP-2000; 2000US-0232338P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
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 PR 26-SEP-2000; 2000US-0235484P.  
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 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
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 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241212P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0246474P.  
 PR 08-NOV-2000; 2000US-0246475P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-0246523P.  
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 PR 08-NOV-2000; 2000US-0246525P.  
 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
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 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249246P.  
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 PR 01-DEC-2000; 2000US-0250160P.  
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 PR 05-DEC-2000; 2000US-0251030P.  
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 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
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 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 37745; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to

CC supplement the patients own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/haematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/haematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention  
XX  
SQ Sequence 14063 BP; 4698 A; 2703 C; 2660 G; 4002 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 4; Length 14063;  
Best Local Similarity 85.7%; Pred. No. 8.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GAAAGGCTTTCGGGGTGCT 21  
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Db 10020 GAAAGGCTTTCGAGATGCT 10040

## RESULT 88

AAK82934

ID AAK82934 standard; DNA; 14063 BP.

XX

AC AAK82934;

XX

DT 07-NOV-2001 (first entry)

XX

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37746.

XX

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX

OS Homo sapiens.

XX

PN WO200157182-A2.

XX

PD 09-AUG-2001.

XX

PF 17-JAN-2001; 2001WO-US0001354.

XX

XX 31-JAN-2000; 2000US-0179065P.

PR

PR 04-FEB-2000; 2000US-0180628P.

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PR 24-FEB-2000; 2000US-0184664P.

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PR 02-MAR-2000; 2000US-0186350P.

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PR 16-MAR-2000; 2000US-0189874P.

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PR 18-APR-2000; 2000US-0198123P.

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PR 07-JUN-2000; 2000US-0209467P.

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PR 28-JUN-2000; 2000US-0214886P.

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PR 07-JUL-2000; 2000US-0216647P.

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PR 18-AUG-2000; 2000US-0226279P.

PR

PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
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PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
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PR 02-OCT-2000; 2000US-0236802P.  
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PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
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PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249219P.  
PR 17-NOV-2000; 2000US-0249220P.  
PR 17-NOV-2000; 2000US-0249221P.  
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PR 17-NOV-2000; 2000US-0249230P.  
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PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
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PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and metastasis.  
XX  
XX Disclosure; SEQ ID NO 37746; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
XX activity, and can be used in gene therapy and vaccine production. (I)  
XX proteins and polynucleotides may be used in the prevention, diagnosis and  
XX treatment of diseases associated with inappropriate (I) expression. For  
XX example, they may be used to treat disorders associated with decreased  
XX expression by rectifying mutations or deletions in a patient's genome  
XX that affect the activity of (I) by expressing inactive proteins or to  
XX supplement the patients own production of (I). Additionally, (I)  
XX polynucleotides may be used to produce the secreted (I), by inserting the  
XX nucleic acids into a host cell and culturing the cell to express the  
XX protein. (I) proteins and polynucleotides may be used to prevent,  
XX diagnose and treat immune/hematopoietic-related diseases, especially  
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
XX to AAK87694 represent human immune/hematopoietic antigen genomic  
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
XX represent sequences used in the exemplification of the present invention  
XX  
XX Sequence 14063 BP; 4696 A; 2705 C; 2660 G; 4002 T; 0 U; 0 Other;  
XX  
XX Query Match 73.6%; Score 16.2; DB 4; Length 14063;  
XX Best Local Similarity 85.7%; Pred. No. 8.1e+02;  
XX Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
XX  
XX 1 GAAAGGCTTTTCGGGGGTGCT 21  
XX 10018 GAAAGGCTTTTCGATGCT 10038

RESULT 89  
ADW22177  
ID ADW22177 standard; cDNA; 25759 BP.  
XX  
XX AC ADW22177;  
XX  
XX 10-MAR-2005 (first entry)  
XX  
XX Rat hepatotoxicity marker gene, SEQ:556.  
XX  
XX Toxicology screening; drug screening; gene expression;  
XX expression profile; hepatotoxicity; drug-induced; hepatitis;  
XX liver disease; gastrointestinal disease; gene; ss.  
XX  
XX Rattus norvegicus.  
XX  
XX EP1344834-A2.  
XX  
XX 17-SEP-2003.  
XX  
XX 04-MAR-2003; 2003EP-00004810.  
XX  
XX 14-MAR-2002; 2002EP-00005336.  
XX  
XX 17-JUL-2002; 2002EP-00015657.  
XX  
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
XX  
XX Boess F, Suter-Dick L, Wolf D;  
XX  
XX WPI; 2003-723475/69.  
XX  
XX EMBL; X04267.  
XX  
XX Predicting toxicity of compounds, useful in development of safe drugs, by  
XX measuring the differential expression of specific genes in cells exposed  
XX to test compounds.  
XX  
XX Claim 2; SEQ ID NO 556; 895pp; English.  
XX  
XX The invention relates to methods of predicting at least one toxic effect  
XX (or toxicity progression or the mechanism of toxicity) of a compound. The  
XX methods involve detecting the level of expression of at least one of a  
XX set of 80 genes ADW21622-ADW22301 or at least one of a set of 17 genes  
XX (including ADW22362, ADW22414 and ADW22481-ADW22483) in a tissue or cell  
XX exposed to the compound, and determining whether the gene is  
XX differentially expressed compared with a control tissue or cell.  
XX  
XX Differential expression of the gene in the presence of the compound is  
XX indicative of a toxic effect, of toxicity progression or of a specific  
XX mechanism of toxicity. The toxic effect is especially hepatotoxicity,  
XX particularly hepatitis, liver necrosis, protein adduct formation or fatty  
XX liver. The invention also relates to sets of primers and probes specific  
XX for at least two genes selected from ADW21622-ADW22301; solid supports  
XX (e.g., DNA chips) and kits containing the probes; and a database  
XX containing DNA sequence information and expression information for at  
XX least two of the 80 genes from hepatotoxin-exposed tissues. The  
XX invention is based on the determination of global changes in gene  
XX expression in tissues or cells exposed to known toxins, particularly  
XX hepatotoxins, and the identification of individual genes (toxicity  
XX markers) that are differentially expressed on toxin exposure. The changes  
XX in gene expression can be characteristic of different mechanisms of  
XX hepatotoxicity mediated by various classes of compounds. Such compounds  
XX include: direct acting compounds which cause damage to macromolecules,  
XX especially proteins and lipids by directly interacting with them;  
XX steatotic compounds which cause an accumulation of fat in the liver; and  
XX cholestatic compounds which impair bile flow or bile acid transport,  
XX resulting in jaundice. The methods of the invention are useful in  
XX toxicology screening for predicting the toxic effects (especially  
XX hepatotoxic effects) of compounds for the development of safer drugs.  
XX Sequences ADW21622-ADW22301 represent specifically claimed hepatotoxicity  
XX marker genes of rat origin whose expression is altered on exposure to  
XX hepatotoxins.  
XX  
XX Sequence 25759 BP; 6768 A; 5975 C; 6783 G; 6229 T; 0 U; 4 Other;

Query Match 73.6%; Score 16.2; DB 11; Length 25759;  
Best Local Similarity 85.7%; Pred. No. 8.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21  
Db 21445 GAAAGGCATTAGTGGTGCT 21465

RESULT 90  
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ID AEB96542 standard; DNA; 104932 BP.  
XX AC  
XX AEB96542;  
DT 06-OCT-2005 (first entry)  
XX  
DE Human STAT5A gene, SEQ ID 26.  
KW hepatitis C virus infection; antiinflammatory; hepatotropic; virucide;  
KW liver cirrhosis; fibrosis; hepatoma; SNP detection; STAT5A, ds.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT variation  
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FT 4414  
FT variation  
FT /tag= c  
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FT 4481  
FT variation  
FT /tag= d  
FT /standard\_name= "Single nucleotide polymorphism"  
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FT /tag= e  
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Query Match      73.6%; Score 16.2; DB 14; Length 104932;  
Best Local Similarity 85.7%; Pred. No. 9.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      1 GAAAGGCGCTTTCGGGGTGCT 21  
Db      89760 GGAAGGCGCTTTCGGGGAGCT 89780
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## RESULT 91

ADV35021/c

ID ADV35021 standard; cDNA; 106664 BP.

XX ADV35021;

XX ADV35021;  
DT 10-FEB-2005 (first entry)

DE Murine cDNA differentially expressed in the presence of valproate Seq97.  
XX murine; mouse; valproate; ss; multi-parameter high throughput screening;  
XX MPHTS; disease signature; neuropsychiatric; neurodegenerative;  
XX schizophrenia; bipolar affective disorder; BAD; autism; Parkinson's;  
XX Alzheimer's disease; neuroleptic; nootropic; antimanic; antidepressa.

OS Mus musculus.

XX US2003096264-A1.

XX 22-MAY-2003.

XX 18-JUN-2002; 2002US-00175523.

XX 18-JUN-2001; 2001US-0299151P.

PR 07-SEP-2001; 2001US-0317828P.

PR 25-SEP-2001; 2001US-0325150P.

PR 14-NOV-2001; 2001US-0333047P.

PR 18-JAN-2002; 2002US-0349936P.

PR 04-MAR-2002; 2002US-0361834P.

XX (PSYC-) PSYCHIATRIC GENOMICS INC.

XX Altar CA, Brockman JA, Evans D, Hook D, Klimczak LJ, Laeng P;

PI Palfreyman M, Rajan P;

XX WPI; 2004-118903/12.

XX

PT Identifying a compound that can treat disease or disorders, such as, a  
PT neuropsychiatric disorder e.g., schizophrenia, or autism, comprises  
PT determining the expression of one or more efficacy genes in a cell  
PT contacted with the test compound.

PS Claim 9; SEQ ID NO 97; 39pp; English.

XX This invention relates to a novel screening method identified as a multi-  
XX parameter high throughput screening (MPHTS) assay. Specifically, it  
XX refers to an assay that utilizes the disease signature of a plurality of  
XX specific genes associated with a particular disease, and identifies  
XX differential expression between those cells taken from individuals  
XX affected by that disease and those that are not affected. The present  
XX invention then describes the screening of candidate pharmaceutical  
XX compounds to identify those that have a potential therapeutic benefit for  
XX the treatment of neuropsychiatric and neurodegenerative disorders  
XX including schizophrenia, bipolar affective disorder (BAD) and autism, as  
XX well as Parkinson's and Alzheimer's disease. Accordingly, the compounds  
XX of this invention exhibit various activities including neuroleptic,  
XX nootropic, antimanic and antidepressant. Furthermore, the screening  
XX method used in MPHTS will be automated, such that a large number of test  
XX compounds may be rapidly screened with a minimal amount of labour and  
XX effort. This polynucleotide is the cDNA sequence of a gene that is  
XX differentially expressed in mice in the presence of the therapeutic  
XX compound valproate, given in an exemplification of the invention.

SQ Sequence 106664 BP; 30364 A; 21834 C; 21417 G; 33049 T; 0 U; 0 Other;

Query Match 73.6%; Score 16.2; DB 13; Length 106664;

Best Local Similarity 85.7%; Pred. No. 9.4e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTTCGGGGTGCT 21

||| ||||| ||||| ||||| |||||

Db	37462	GATATGCCTTTCGGGTGCT	37442	
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Continuation (31 of 45) of AAI99682 from base 3000001 (Mycobacterium tuberculosis strain				
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682				
WP	Fragment Name	Begin	End	
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WP	AAI99682_01	100001	210000	
WP	AAI99682_02	200001	310000	
WP	AAI99682_03	300001	410000	
WP	AAI99682_04	400001	510000	
WP	AAI99682_05	500001	610000	
WP	AAI99682_06	600001	710000	
WP	AAI99682_07	700001	810000	
WP	AAI99682_08	800001	910000	
WP	AAI99682_09	900001	1010000	
WP	AAI99682_10	1000001	1110000	
WP	AAI99682_11	1100001	1210000	
WP	AAI99682_12	1200001	1310000	
WP	AAI99682_13	1300001	1410000	
WP	AAI99682_14	1400001	1510000	
WP	AAI99682_15	1500001	1610000	
WP	AAI99682_16	1600001	1710000	
WP	AAI99682_17	1700001	1810000	
WP	AAI99682_18	1800001	1910000	
WP	AAI99682_19	1900001	2010000	
WP	AAI99682_20	2000001	2110000	
WP	AAI99682_21	2100001	2210000	
WP	AAI99682_22	2200001	2310000	
WP	AAI99682_23	2300001	2410000	
WP	AAI99682_24	2400001	2510000	
WP	AAI99682_25	2500001	2610000	
WP	AAI99682_26	2600001	2710000	
WP	AAI99682_27	2700001	2810000	
WP	AAI99682_28	2800001	2910000	
WP	AAI99682_29	2900001	3010000	
WP	AAI99682_30	3000001	3110000	
WP	AAI99682_31	3100001	3210000	
WP	AAI99682_32	3200001	3310000	
WP	AAI99682_33	3300001	3410000	
WP	AAI99682_34	3400001	3510000	
WP	AAI99682_35	3500001	3610000	
WP	AAI99682_36	3600001	3710000	
WP	AAI99682_37	3700001	3810000	
WP	AAI99682_38	3800001	3910000	
WP	AAI99682_39	3900001	4010000	
WP	AAI99682_40	4000001	4110000	
WP	AAI99682_41	4100001	4210000	
WP	AAI99682_42	4200001	4310000	
WP	AAI99682_43	4300001	4410000	
WP	AAI99682_44	4400001	4411529	
Query Match 73.6%; Score 16.2; DB 4; Length 110000;				
Best Local Similarity 85.7%; Pred. No. 9.4e+02;				
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
OY	2 AAAGCCCTTTCGGGGTGCTC 22			
Db	101041 AAAGCCGTTCGGGGTGCTC 101021			
RESULT 93				
AAI99682_31/c				
Continuation (32 of 45) of AAI99682 from base 3100001 (Mycobacterium tuberculosis strain				
WP Sequence split into 45 fragments LOCUS AAI99682 Accession Aai99682				
WP	Fragment Name	Begin	End	
WP	AAI99682_00	1	110000	
WP	AAI99682_01	100001	210000	
WP	AAI99682_02	200001	310000	
WP	AAI99682_03	300001	410000	
WP	AAI99682_04	400001	510000	

WP	AAI99682_05	500001	610000	
WP	AAI99682_06	600001	710000	
WP	AAI99682_07	700001	810000	
WP	AAI99682_08	800001	910000	
WP	AAI99682_09	900001	1010000	
WP	AAI99682_10	1000001	1110000	
WP	AAI99682_11	1100001	1210000	
WP	AAI99682_12	1200001	1310000	
WP	AAI99682_13	1300001	1410000	
WP	AAI99682_14	1400001	1510000	
WP	AAI99682_15	1500001	1610000	
WP	AAI99682_16	1600001	1710000	
WP	AAI99682_17	1700001	1810000	
WP	AAI99682_18	1800001	1910000	
WP	AAI99682_19	1900001	2010000	
WP	AAI99682_20	2000001	2110000	
WP	AAI99682_21	2100001	2210000	
WP	AAI99682_22	2200001	2310000	
WP	AAI99682_23	2300001	2410000	
WP	AAI99682_24	2400001	2510000	
WP	AAI99682_25	2500001	2610000	
WP	AAI99682_26	2600001	2710000	
WP	AAI99682_27	2700001	2810000	
WP	AAI99682_28	2800001	2910000	
WP	AAI99682_29	2900001	3010000	
WP	AAI99682_30	3000001	3110000	
WP	AAI99682_31	3100001	3210000	
WP	AAI99682_32	3200001	3310000	
WP	AAI99682_33	3300001	3410000	
WP	AAI99682_34	3400001	3510000	
WP	AAI99682_35	3500001	3610000	
WP	AAI99682_36	3600001	3710000	
WP	AAI99682_37	3700001	3810000	
WP	AAI99682_38	3800001	3910000	
WP	AAI99682_39	3900001	4010000	
WP	AAI99682_40	4000001	4110000	
WP	AAI99682_41	4100001	4210000	
WP	AAI99682_42	4200001	4310000	
WP	AAI99682_43	4300001	4410000	
WP	AAI99682_44	4400001	4411529	

Query Match 73.6%; Score 16.2; DB 4; Length 110000;  
Best Local Similarity 85.7%; Pred. No. 9.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY2 AAAGCCCTTCGGGGTGCTC 22  
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 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WP AA199683_18 1800001 1910000
WP AA199683_19 1900001 2010000
WP AA199683_20 2000001 2110000
WP AA199683_21 2100001 2210000
WP AA199683_22 2200001 2310000
WP AA199683_23 2300001 2410000
WP AA199683_24 2400001 2510000
WP AA199683_25 2500001 2610000
WP AA199683_26 2600001 2710000
WP AA199683_27 2700001 2810000
WP AA199683_28 2800001 2910000
WP AA199683_29 2900001 3010000
WP AA199683_30 3000001 3110000
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WP AA199683_32 3200001 3310000
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WP AA199683_35 3500001 3610000
WP AA199683_36 3600001 3710000
WP AA199683_37 3700001 3810000
WP AA199683_38 3800001 3910000
WP AA199683_39 3900001 4010000
WP AA199683_40 4000001 4110000
WP AA199683_41 4100001 4210000
WP AA199683_42 4200001 4310000
WP AA199683_43 4300001 4403765

Query Match 73.6%; Score 16.2; DB 4; Length 110000;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCGCTTCGGGGTGCTC 22
Db 95717 AAAGGCGCTTCGGGGTGCTC 95697

RESULT 95
ID ADB82110/c
AC ADB82110;
XX
XX
DT 04-DEC-2003 (first entry)
XX
XX Human cDNA sequence useful for the treatment of cancer (SeqID 422).
XX human; prostate; cancer; cytostatic; gene therapy; vaccine;
XX immune response; gene; ss.
XX Homo sapiens.
XX WO2003050236-A2.
XX
XX 19-JUN-2003.
XX
XX 04-SEP-2002; 2002WO-US028214.
XX
XX 07-DEC-2001; 2001US-00012697.
XX
XX (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
XX Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
XX Garcia V, Jones LW, Stache-Crain B, Scott EM;
XX WPI; 2003-513972/48.
XX
XX New polynucleotides derived from human prostate, useful for modulating
XX immune response to prevent or treat cancer.
XX
XX Claim 1; SEQ ID NO 422; 188pp; English.
XX
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CC This invention relates to novel isolated polynucleotides of human origin,
CC particularly isolated from the human prostate. Specifically, it refers to
CC the diagnostics and therapeutics comprising these novel human
CC polynucleotides, and includes the derived probes, antisense
CC oligonucleotides and antibodies thereof. The identification of these
CC human prostate genes that can inhibit tumour growth is useful for
CC understanding the progression and nature of complex diseases such as
CC cancer, and hence they are important in the drug discovery process. The
CC present invention describes these polynucleotides and encoded
CC polypeptides as exhibiting cytostatic activity, and through gene therapy
CC and/or vaccines they can be used to modulate the immune response for the
CC prevention or treatment of cancers, particularly of the prostate, but
CC also for breast, lung and colon cancer. This polynucleotide sequence is a
CC human cDNA sequence useful for the treatment of cancer, used in an
CC exemplification of the invention. NOTE: These sequences are not given in
CC the specification but are provided on the WIPO website.
XX
SQ Sequence 297 BP; 56 A; 72 C; 76 G; 72 T; 0 U; 21 Other;

Query Match 72.7%; Score 16; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTCGGGG 16
Db 74 GAAAGGCGCTTCGGGG 59

RESULT 96
ABQ89167/c
ID ABQ89167 standard; cDNA; 331 BP.
XX
XX AC ABQ89167;
XX
XX DT 27-SEP-2002 (first entry)
XX
XX DE Human prostate expressed polynucleotide SEQ ID NO 423.
XX
XX KW Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;
XX KW ss.
XX OS Homo sapiens.
XX
XX PN WO200255700-A2.
XX
XX PD 18-JUL-2002.
XX
XX PF 07-DEC-2001; 2001WO-US047349.
XX
XX PR 07-DEC-2000; 2000US-0254648P.
XX
XX PR 13-MAR-2001; 2001US-0275688P.
XX
XX PA (CHIR ) CHIRON CORP.
XX (HYSE-) HYSEQ INC.
XX
XX XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;
XX PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;
XX PI Garcia V, Jones WL, Stache-Crain B, Scott EM;
XX
XX DR WPI; 2002-557824/59.
XX
XX New genes and gene products isolated from human prostate, useful for
XX treating or diagnosing tumor or cancer (e.g. prostate cancer or breast
XX cancer), or as vaccines for treating or preventing these diseases.
XX
XX PS Claim 1; SEQ ID NO 423; 186pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide comprising any of
XX 1477 sequences or its fragment, degenerate variant, antisense or
XX complement. The polynucleotides and gene products are useful for treating
XX or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung
XX cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats,
XX rabbits, horse or human). The polynucleotides and polypeptides are also
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CC useful as vaccines for treating or preventing these diseases. The  
CC polynucleotides are useful for gene therapy. The present sequence is that  
CC of one of a group of polynucleotides (ABQ8745-ABQ90015) disclosed  
CC electronically as sequences of the invention. However only 1271  
CC polynucleotide sequences are given, whereas 1477 polynucleotides and 91  
CC proteins are claimed. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 331 BP; 74 A; 77 C; 85 G; 74 T; 0 U; 21 Other;  
  
Query Match 72.7%; Score 16; DB 6; Length 331;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAAAGGCTTTCGGG 16  
Db 99 GAAAGGCTTTCGGG 84  
|||||  
  
RESULT 97  
ABX64840  
ID ABX64840 standard; cDNA; 132 BP.  
XX AC  
AC ABX64840;  
DT  
DT 03-MAR-2003 (first entry)  
XX  
DE Human gene trapped sequence (GTS) cDNA SEQ ID NO 447.  
XX  
KW Human; gene trapped sequence; GTS; gene discovery; forensic; mapping;  
KW gene therapy; antisense therapy; prenatal analysis; autoimmune disease;  
KW developmental disorder; aging; cancer; Crohn's disease; schizophrenia;  
KW multiple sclerosis; skin disorder; rheumatoid arthritis; skeletal system;  
KW atherosclerosis; cardiovascular disease; degenerative disease; neural;  
KW Alzheimer's disease; osteoporosis; asthma; infection; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2002110809-A1.  
XX  
PD 15-AUG-2002.  
PF 28-APR-2000; 2000US-00560863.  
XX  
PR 30-APR-1999; 99US-0132408P.  
XX  
PA (NEHL/) NEHLS M C.  
PA (ZAMB/) ZAMEROWICZ B.  
PA (SAND/) SANDS A T.  
XX  
PI Nehls MC, Zambrowicz B, Sands AT;  
XX  
DR WPI; 2003-090170/08.  
XX  
PT Novel human polynucleotides that correspond to human gene trapped  
PT sequences useful for gene discovery, gene therapy, as markers for gene  
PT expression analysis, forensic analysis and determining genetic basis of  
PT diseases.  
XX  
PS Claim 1; SEQ ID NO 447; 36pp; English.  
XX  
CC This invention describes isolated or purified polynucleotides  
CC corresponding to human gene trapped sequence (GTS) comprising a sense or  
CC antisense sequence chosen from 1000 sequences or its fragment of 8  
CC contiguous nucleotides. GTSs are useful for gene discovery and as markers  
CC for gene expression analysis, identifying and mapping the coding regions  
CC of the mammalian and particularly human, genome, forensic analysis, for  
CC cross species hybridisation analysis, genetic manipulation, antisense  
CC inhibition, gene targeting, identification or generation of full-length  
CC cDNA, mapping the human genome, gene or antisense therapy, gene delivery  
CC and determining the genetic basis of human disease. Portion of the GTS  
CC sequences are useful as a hybridisation probe or for chromosome mapping,  
CC

CC and can be incorporated into phage display system that can be used to  
CC screen for proteins, or other ligands, that are capable of binding an  
CC amino acid sequence encoded by the GTS sequences. The GTS sequences are  
CC also useful to regulate gene expression, as a part of ribozyme and/or  
CC triple helix sequences that can be used to regulate gene expression, as  
CC components of diagnostic methods, for analysing single nucleotide  
CC polymorphisms, and also as genetic markers for prenatal analysis of  
CC congenital traits or defects. The polynucleotides of the invention are  
CC useful for diagnosis, prognosis of disorders involving developmental and  
CC differentiation processes and for the identification of subjects having a  
CC predisposition to such disorders. Diseases or natural processes that can  
CC be correlated with the expression of mutant or normal, variants of GTSs  
CC include, aging, cancer, autoimmune disease, Crohn's disease, multiple  
CC sclerosis, immune disorders, schizophrenia, skin disorders, rheumatoid  
CC arthritis, atherosclerosis, cardiovascular disease, degenerative diseases  
CC of the neural or skeletal systems, Alzheimer's disease, osteoporosis,  
CC asthma, and infections. GTSs can also be used to identify the specific  
CC locations of exon splice junctions, which are important in the study of  
CC disease and cancer. Modulating the level of expression of one or more  
CC genes and/or regulating activity of one or more peptides or proteins is  
CC useful for modifying development and cell differentiation and treating  
CC development and cell differentiation disorders. ABX64402-ABX65401  
CC represent the human gene trapped cDNA sequences described in the  
CC disclosure of the invention. NOTE: The sequence data for this patent did  
CC not form part of the printed specification but was obtained in electronic  
CC format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20020110809  
XX  
SQ Sequence 132 BP; 41 A; 24 C; 33 G; 34 T; 0 U; 0 Other;  
  
Query Match 71.8%; Score 15.8; DB 8; Length 132;  
Best Local Similarity 89.5%; Pred. No. 8.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 GAAAGGCTTTCGGGGTG 19  
Db 21 GGAAGGCTTTCGGGGTG 39  
|||||  
  
RESULT 98  
ADQ50381/c  
ID ADQ50381 standard; DNA; 362 BP.  
XX AC  
AC ADQ50381;  
DT 21-OCT-2004 (first entry)  
XX  
DE Novel canine microarray-related DNA sequence SeqID1683.  
XX  
KW canine microarray; drug screening; toxicity assay;  
KW environmental pollutant; cellular response; gene expression profile;  
KW toxic response; liver necrosis; fatty liver disease;  
KW protein adduct formation; hepatitis; dog; ds.  
XX  
OS Canis familiaris.  
XX  
PN WO2004063324-A2.  
XX  
PD 29-JUL-2004.  
XX  
PF 05-MAY-2003; 2003WO-US013853.  
PR 03-MAY-2002; 2002US-0377240P.  
XX  
PA (GENE-) GENE LOGIC INC.  
PA (PFIZ) PFIZER PROD INC.  
XX  
PI Diggins JC, Porter M, Wei T;  
XX WPI; 2004-561890/54.  
DR  
XX New isolated nucleic acid molecule, useful for drug screening and  
PT toxicity assays or for assessing the impact, including toxicity, of a



PT compound, pharmaceutical agent or environmental pollutant on a cell or  
XX living organism.  
PS Claim 1; SEQ ID NO 1683; 41pp; English.  
XX  
XX This invention is related to a novel isolated canine nucleic acid  
CC sequences and the construction of canine microarrays containing a  
CC significant portion of the canine genome. The isolated canine nucleic  
CC acid sequences of the invention may be useful for drug screening and  
CC toxicity assays. The invention is therefore useful for assessing the  
CC impact, including toxicity, of a compound, pharmaceutical agent or  
CC environmental pollutant on a cell or living organism. The methods are  
CC useful for detecting genes that are up- or down-regulated in canines in a  
CC disease state. The sequences are useful as diagnostic agents or markers  
CC to detect a cellular response in a sample individually or as part of a  
CC gene expression profile. It is also useful as a target for agents that  
CC modulate gene expression or activity. The database is useful for  
CC producing electronic Northern blots that allow the user to determine the cell  
CC type or tissue in which a given gene is expressed and to allow  
CC determination of the abundance or expression level of a given gene in a  
CC particular tissue or cell. The methods are useful for determining the  
CC similarity of a toxic response to one or more individual compounds. The  
CC methods are useful for predicting at least one toxic response or the  
CC likelihood that a compound or test agent will induce various specific  
CC pathologies such as those of the liver (liver necrosis, fatty liver  
CC disease, protein adduct formation or hepatitis), those of the kidney,  
CC heart, brain or testes, or other pathologies associated with at least one  
CC of the toxins. The methods are also useful for predicting or elucidating  
CC the potential cellular pathways influenced, induced or modulated by the  
CC compound or test agent due to the similarity of the expression profile  
CC compared to the profile induced by a known toxin. The present sequence is  
CC that of a canine DNA sequence which was claimed for use during the  
XX production of a canine microarray of the invention.  
XX  
SQ Sequence 362 BP; 76 A; 99 C; 92 G; 71 T; 0 U; 24 Other;

Query Match 71.8%; Score 15.8; DB 13; Length 362;  
Best Local Similarity 89.5%; Pred. No. 9.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGCCCTTCGGGGTGCT 21  
|||||  
Db 271 AAGCCCTTCGGGGTGCT 253  
|||||

RESULT 99  
ADA28874  
ID ADA28874 standard; DNA; 579 BP.  
XX  
XX ADA28874;  
XX  
XX 20-NOV-2003 (first entry)  
XX  
XX DNA encoding Acinetobacter baumannii protein #161.  
DE  
XX ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;  
XX vaccine; plant biocontrol agent.  
XX  
XX Acinetobacter baumannii.  
XX  
XX US6562958-B1.  
XX  
XX 13-MAY-2003.  
XX  
XX 04-JUN-1999; 99US-00328352.  
XX  
XX 09-JUN-1998; 98US-0088701P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Breton G, Bush D;  
XX  
XX WPI; 2003-576092/54.

DR P-PSDB; ADA33000.  
XX  
XX New Acinetobacter baumannii proteins and nucleic acids, useful as reagents  
PT for diagnosing a bacterial disease, as components of antibacterial  
PT vaccines, as targets for antibacterial drugs, or as biocontrol agents for  
PT plants.  
XX  
XX Example; SEQ ID NO 161; 328pp; English.  
XX  
XX The invention relates to isolated Acinetobacter baumannii nucleic acids.  
CC The A. baumannii nucleic acids and polypeptides are useful as reagents  
CC for diagnosing a bacterial disease, as components of antibacterial  
CC vaccines, as targets for antibacterial drugs, to detect the presence of  
CC A. baumannii and other Acinetobacter species in a sample, in screening  
CC compounds for the ability to interfere with the A. baumannii life cycle  
CC or to inhibit A. baumannii infection, and as biocontrol agents for  
CC plants. The present sequence represents DNA encoding an A. baumannii  
CC protein.  
XX  
SQ Sequence 579 BP; 137 A; 99 C; 132 G; 211 T; 0 U; 0 Other;

Query Match 71.8%; Score 15.8; DB 9; Length 579;  
Best Local Similarity 89.5%; Pred. No. 9.8e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGGCCTTCGGGGTGCTC 22  
|||||  
Db 327 AGGCCTTCGGGGTGCTC 345  
|||||

RESULT 100  
ABZ54797  
ID ABZ54797 standard; cDNA; 665 BP.  
XX  
XX AC ABZ54797;  
XX  
XX 28-MAR-2003 (first entry)  
DT  
XX Aspergillus oryzae polynucleotide SEQ ID NO 3910.  
DE  
XX Aspergillus oryzae; fermentation; fungus; industrial; EST;  
XX expressed sequence tag; gene; ss.  
XX  
XX Aspergillus oryzae.  
OS  
XX WO200279476-A1.  
XX  
XX 10-OCT-2002.  
PD  
XX  
XX 22-MAR-2002; 2002WO-1B000890.  
XX  
XX 30-MAR-2001; 2001JP-00098371.  
XX  
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA  
XX (NARE-) NAT RES INST BREWING.  
PA  
XX (NORQ) NAT FOOD RES INST MIN AGRIC.  
XX  
XX Machida M, Akita O, Kashiwagi Y, Kitamoto K, Horiuchi H;  
PI Takeuchi M, Kobayashi T, Kitamoto N, Gomi K, Abe K;  
XX  
XX WPI; 2003-046817/04.  
DR  
XX  
XX Detection of expression of specific Aspergillus genes for monitoring the  
PT fermentation and growth conditions of the fungus, using DNA probes.  
XX  
XX Claim 1; SEQ ID NO 3910; 48pp + Sequence Listing; Japanese.  
XX  
XX The invention relates to a polynucleotide having any of 6006 specific  
CC sequences (ABZ50888-ABZ56893), which are expressed by a fungus under  
CC specific culture conditions including one or more of eutrophic,  
CC oligotrophic, solid, early germination, alkaline, high temperature, low  
CC temperature or maltose culture or polynucleotides stringently hybridising  
CC to these sequences. The polynucleotides are useful for monitoring the

CC progress of fermentation and the growth conditions of a fungus,  
 CC especially of Aspergillus oryzae which is widely used in industrial  
 CC fermentation. Also monitoring for fungal contamination. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 665 BP; 143 A; 196 C; 154 G; 172 T; 0 U; 0 Other;

Query Match 71.8%; Score 15.8; DB 8; Length 665;  
 Best Local Similarity 89.5%; Pred. No. 1e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTTTCGGGGTG 19  
 |||||  
 Db 640 GAAAGCCCTTTTCGGGGTG 658

Search completed: May 19, 2006, 04:19:21  
 Job time : 271.361 secs

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1471.35 Seconds  
(without alignments)  
836.120 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22  
Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST.\*

1: gb\_estl1.\*

2: gb\_est3.\*

3: gb\_est4.\*

4: gb\_est5.\*

5: gb\_est6.\*

6: gb\_est7.\*

7: gb\_est8.\*

8: gb\_est9.\*

9: gb\_est10.\*

10: gb\_est11.\*

11: gb\_est12.\*

12: gb\_est13.\*

13: gb\_est14.\*

14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19.4	88.2	369	12	CC794955
C 2	19.4	88.2	741	7	BB660584
C 3	19.4	88.2	1266	6	AK052580
C 4	19.4	88.2	3468	6	AK036537
C 5	18.8	85.5	514	9	DR082998
C 6	18.8	85.5	583	2	BM344289
C 7	18.8	85.5	927	14	CNS06Q72
C 8	18.8	85.5	1078	14	CNS06Q72
C 9	18.8	85.5	794	5	CJ485936
C 10	17.8	80.9	221	10	DV692385
C 11	17.8	80.9	236	8	CQ308813
C 12	17.8	80.9	267	5	CF045077
C 13	17.8	80.9	288	5	CF044432
C 14	17.8	80.9	510	8	CO711127
C 15	17.8	80.9	536	5	CD277478
C 16	17.8	80.9	598	4	CB754809
C 17	17.8	80.9	658	2	BT215331
C 18	17.8	80.9	664	5	CK133302
C 19	17.8	80.9	683	11	BH385770

BB634710	BB634710	687	7	BB634710
BI104420	602890015	753	2	BI104420
CX343351	JGI_XZT22	847	9	CX343351
CK425517	AUF_Ipfes	950	5	CK425517
BF162561	601770203	977	7	BF162561
BM907310	AGENCOURT	994	3	BM907310
CF376920	AGENCOURT	1016	5	CF376920
DM665607	CNB332-C1	1045	10	DM665607
DT956623	CFW146-D1	1371	10	DT956623
DR985203	JGI_AOKG4	373	10	DR985203
T56721	va71a03_s2	408	10	T56721
BB157276	BB157276	658	7	BB157276
EX26884	EX26884	694	4	EX26884
AG43060	Mus_muscu	765	14	AG43060
AQ746955	HS_5538_A	843	11	AQ746955
BQ689861	AGENCOURT	893	3	BQ689861
DT995647	CNB179-H0	1413	10	DT995647
CD377892	PTMM03061	270	5	CD377892
AW854955	E0289B09-	353	8	AW854955
CD383045	PTMM08215	371	5	CD383045
CG548494	OST150127	378	12	CG548494
AW854998	PM3-CT026	386	7	AW854998
CG548510	OST150188	390	12	CG548510
CG545039	OST142970	394	12	CG545039
AA555150	nl07g10.8	405	1	AA555150
CG548505	OST150171	413	12	CG548505
CG662443	OST46019	417	12	CG662443
DT596565	wmi03-11m	432	10	DT596565
CG505758	OST54874	434	12	CG505758
BF392844	UI-R-CA0-	436	7	BF392844
CJ145102	CJ145102	442	5	CJ145102
DT598769	wmi03-12m	444	10	DT598769
BY370180	BY370180	462	4	BY370180
CB426198	601354_MA	525	4	CB426198
CB426543	601738_MA	525	4	CB426543
CA886724	B0131G09-	549	4	CA886724
CN695093	E0360A01-	553	8	CN695093
CB462716	723046_MA	555	4	CB462716
CB464162	725350_MA	555	4	CB464162
DY385738	CL_Ea000	556	10	DY385738
BG804845	0273-08_M	562	2	BG804845
CA888697	B0147H08-	566	4	CA888697
DN591849	a4907cc.r	591	9	DN591849
AI663484	uk33d10.Y	594	1	AI663484
BE534580	601233510	597	7	BE534580
BG804780	0272-28_M	600	2	BG804780
CV562959	UI-M-FC0-	603	8	CV562959
CA163213	SCRUR2311	608	4	CA163213
CK975625	4106617_B	609	8	CK975625
LBAP055F03	LBAP055F03	614	14	LBAP055F03
CL864502	TM1-GSS00	622	13	CL864502
CE758231	t1gr-q88-	632	12	CE758231
CF902767	A0345F09-	638	5	CF902767
BB614371	BB614371	638	9	BB614371
CX768159	UI-M-HU0-	638	9	CX768159
BH091738	RPCI-24-2	644	11	BH091738
CD406831	Gm_Ck3178	652	5	CD406831
CK976084	4107001_B	659	8	CK976084
BB619260	BB619260	673	7	BB619260
CO426515	UI-M-HU0-	674	5	CO426515
CJ252013	CJ252013	674	5	CJ252013
CJ093902	CJ093902	674	5	CJ093902
DR749476	NG010008B	674	10	DR749476
BU654491	1112113H1	682	3	BU654491
AM029523	AM029523	692	1	AM029523
CE717742	t1gr-q88-	692	12	CE717742
DT891101	1472214_M	700	10	DT891101
AM030124	AM030124	745	1	AM030124
BX326765	BX326765	749	4	BX326765
DT889744	1470678_M	749	10	DT889744
BF766344	BP766344	756	3	BF766344
DN542745	1391525_M	773	9	DN542745

93	17.2	78.2	777	9	DN541686	166	16.8	76.4	658	9	CX480436
C 94	17.2	78.2	780	9	CX887509 JGI_CAA01	C 167	16.8	76.4	674	13	CW323036
95	17.2	78.2	785	9	CX887508 JGI_CAA01	C 168	16.8	76.4	678	13	BF452053
96	17.2	78.2	800	9	DN524756	C 169	16.8	76.4	682	1	AL697364
97	17.2	78.2	806	4	CA315865	C 170	16.8	76.4	682	1	CW057016
C 98	17.2	78.2	829	3	BP434131	C 171	16.8	76.4	683	14	CT186330
C 99	17.2	78.2	848	12	BZ654405	C 172	16.8	76.4	689	1	AM044576
C 100	17.2	78.2	849	8	CV069365	C 173	16.8	76.4	692	8	CO203656
C 101	17.2	78.2	855	3	BO885105	C 174	16.8	76.4	707	4	EX609637
C 102	17.2	78.2	874	3	BO953912	C 175	16.8	76.4	713	8	CO201435
C 103	17.2	78.2	874	13	CZ228082	C 176	16.8	76.4	720	13	CW451938
C 104	17.2	78.2	891	10	DV918769	C 177	16.8	76.4	727	13	CW405695
C 105	17.2	78.2	903	3	BQ931621	C 178	16.8	76.4	737	1	AM022377
C 106	17.2	78.2	915	3	BQ730676	C 179	16.8	76.4	744	8	CO369073
C 107	17.2	78.2	916	13	CW702244	C 180	16.8	76.4	756	1	AM046636
C 108	17.2	78.2	921	14	AG894822	C 181	16.8	76.4	763	10	DR469521
C 109	17.2	78.2	923	13	CL238970	C 182	16.8	76.4	767	8	CR531122
C 110	17.2	78.2	930	13	CZ519583	C 183	16.8	76.4	775	13	CW413553
C 111	17.2	78.2	933	3	BU512781	C 184	16.8	76.4	776	3	BU178253
C 112	17.2	78.2	933	3	BU511985	C 185	16.8	76.4	784	12	CG275138
C 113	17.2	78.2	940	3	BO963681	C 186	16.8	76.4	789	11	BU733665
C 114	17.2	78.2	941	12	CC727409	C 187	16.8	76.4	798	12	CG702034
C 115	17.2	78.2	948	12	CC836602	C 188	16.8	76.4	803	10	DV133910
C 116	17.2	78.2	963	12	CC374402	C 189	16.8	76.4	822	8	CV036037
C 117	17.2	78.2	988	3	BU520184	C 190	16.8	76.4	826	3	BU532058
C 118	17.2	78.2	1008	12	CC733494	C 191	16.8	76.4	832	4	EX625372
C 119	17.2	78.2	1048	14	CNS06R0E	C 192	16.8	76.4	832	12	CG179864
C 120	17.2	78.2	1074	3	BU179665	C 193	16.8	76.4	837	10	DT629302
C 121	17.2	78.2	1113	3	BQ230435	C 194	16.8	76.4	861	12	BZ656570
C 122	17.2	78.2	1114	7	BB897150	C 195	16.8	76.4	864	14	CT286132
C 123	17.2	78.2	1179	12	CC280442	C 196	16.8	76.4	881	3	BQ917467
C 124	17.2	78.2	1256	1	AJ924334	C 197	16.8	76.4	881	14	CNS01016
C 125	17.2	78.2	1313	9	DM667985	C 198	16.8	76.4	882	4	CA979418
C 126	17.2	78.2	2345	6	AK159080	C 199	16.8	76.4	902	8	CN162201
C 127	17.2	78.2	3040	6	AK132703	C 200	16.8	76.4	932	12	CG322551
C 128	17	77.3	610	1	AA042746	C 201	16.8	76.4	943	3	BU538391
C 129	17	77.3	850	9	AA042746	C 202	16.8	76.4	955	10	DR472833
C 130	16.8	76.4	154	10	R58318	C 203	16.8	76.4	961	13	CL499651
C 131	16.8	76.4	196	10	DV894214	C 204	16.8	76.4	994	12	CG462884
C 132	16.8	76.4	205	7	AW010105	C 205	16.8	76.4	1050	5	CK231117
C 133	16.8	76.4	246	4	EX613093	C 206	16.8	76.4	1055	2	BM475890
C 134	16.8	76.4	286	4	EX610825	C 207	16.8	76.4	1182	12	CC280354
C 135	16.8	76.4	302	7	AW010059	C 208	16.8	76.4	1217	13	CL495019
C 136	16.8	76.4	366	12	CE086808	C 209	16.8	76.4	1368	10	DT949410
C 137	16.8	76.4	405	11	BE180803	C 210	16.8	76.4	1381	9	DN716077
C 138	16.8	76.4	437	4	CH790538	C 211	16.8	76.4	1423	9	DN693573
C 139	16.8	76.4	437	9	DR180795	C 212	16.4	74.5	277	7	BE906962
C 140	16.8	76.4	493	11	AZ503760	C 213	16.4	74.5	329	11	BH788475
C 141	16.8	76.4	515	4	EX610657	C 214	16.4	74.5	347	12	CC607962
C 142	16.8	76.4	543	10	DR467635	C 215	16.4	74.5	360	4	C39785
C 143	16.8	76.4	552	8	CV628596	C 216	16.4	74.5	360	4	C39832
C 144	16.8	76.4	564	9	DN628521	C 217	16.4	74.5	427	11	BZ246325
C 145	16.8	76.4	564	9	DN632287	C 218	16.4	74.5	435	11	BZ244283
C 146	16.8	76.4	565	9	DN630032	C 219	16.4	74.5	437	10	H37136
C 147	16.8	76.4	570	9	DN632166	C 220	16.4	74.5	500	2	BI775641
C 148	16.8	76.4	571	9	DN632042	C 221	16.4	74.5	534	2	BI346258
C 149	16.8	76.4	582	3	BU775076	C 222	16.4	74.5	579	7	BE284320
C 150	16.8	76.4	588	3	BQ831172	C 223	16.4	74.5	631	4	EX6666423
C 151	16.8	76.4	591	11	AZ856127	C 224	16.4	74.5	658	12	CG992786
C 152	16.8	76.4	600	12	BZ895496	C 225	16.4	74.5	661	5	CD215304
C 153	16.8	76.4	608	8	CO665914	C 226	16.4	74.5	667	7	BD066580
C 154	16.8	76.4	609	8	CR394054	C 227	16.4	74.5	687	12	CC432179
C 155	16.8	76.4	614	13	CW398950	C 228	16.4	74.5	699	2	BI247626
C 156	16.8	76.4	631	5	CF448920	C 229	16.4	74.5	735	12	CC160643
C 157	16.8	76.4	633	8	CO476243	C 230	16.4	74.5	745	5	CD511623
C 158	16.8	76.4	638	10	DV994366	C 231	16.4	74.5	771	14	CR485289
C 159	16.8	76.4	638	10	DR742857	C 232	16.4	74.5	796	3	BU749503
C 160	16.8	76.4	638	10	DY368013	C 233	16.4	74.5	800	8	CN167783
C 161	16.8	76.4	641	4	CB944804	C 234	16.4	74.5	818	12	CG844554
C 162	16.8	76.4	642	1	AM048474	C 235	16.4	74.5	824	3	BU190398
C 163	16.8	76.4	642	13	CW172666	C 236	16.4	74.5	835	11	AZ681554
C 164	16.8	76.4	643	7	BE660337	C 237	16.4	74.5	843	4	CA791265
C 165	16.8	76.4	647	8	CR531123	C 238	16.4	74.5	845	5	CF552602

```

239 16.4 74.5 846 3 B0860887
240 16.4 74.5 882 3 CF265958
241 16.4 74.5 885 14 AG860886
242 16.4 74.5 914 3 BU166542
243 16.4 74.5 919 7 BE972811
244 16.4 74.5 922 12 CL087178
245 16.4 74.5 923 3 BQ717617
246 16.4 74.5 954 3 BQ435924
247 16.4 74.5 954 3 BX350688
248 16.4 74.5 963 5 CF553765
249 16.4 74.5 984 2 BG165618
250 16.4 74.5 1001 3 BQ647974
251 16.4 74.5 1017 3 BQ055928
252 16.4 74.5 1031 2 B1251933
253 16.4 74.5 1067 3 BQ052172
254 16.4 74.5 1070 12 CC191172
255 16.4 74.5 1092 3 BQ887016
256 16.4 74.5 1093 9 DR154835
257 16.4 74.5 1129 6 CNS0FY24
258 16.4 74.5 1130 2 BG328715
259 16.4 74.5 1134 6 CNS0FSES
260 16.4 74.5 1163 2 BM456058
261 16.4 74.5 1199 12 BZ575326
262 16.4 74.5 1203 9 DN689440
263 16.4 74.5 1297 10 DT976137
264 16.4 74.5 1304 1 AM096213
265 16.4 74.5 1304 1 DN721015
266 16.2 73.6 158 3 BQ906009
267 16.2 73.6 174 11 BH193159
268 16.2 73.6 199 2 BF956085
269 16.2 73.6 201 3 BP590460
270 16.2 73.6 208 12 CE711502
271 16.2 73.6 230 1 AV284162
272 16.2 73.6 233 10 DT380778
273 16.2 73.6 236 1 AV333228
274 16.2 73.6 244 7 BB277305
275 16.2 73.6 268 5 CF043572
276 16.2 73.6 274 12 CC780726
277 16.2 73.6 275 7 BE151351
278 16.2 73.6 279 10 N92694
279 16.2 73.6 289 5 CF041004
280 16.2 73.6 306 7 BB042561
281 16.2 73.6 313 5 CD952536
282 16.2 73.6 316 5 CF041228
283 16.2 73.6 318 10 DR889432
284 16.2 73.6 321 5 CD986461
285 16.2 73.6 323 5 CF045499
286 16.2 73.6 328 14 AG200967
287 16.2 73.6 331 5 CD952561
288 16.2 73.6 338 7 AW078706
289 16.2 73.6 350 5 CF053807
290 16.2 73.6 350 7 AW541641
291 16.2 73.6 364 4 CA725948
292 16.2 73.6 371 8 CO000303
293 16.2 73.6 379 1 AA652906
294 16.2 73.6 384 5 CJ089485
295 16.2 73.6 384 7 AW172975
296 16.2 73.6 385 10 DV631930
297 16.2 73.6 404 8 CO749044
298 16.2 73.6 406 4 CA726259
299 16.2 73.6 407 9 D44704
300 16.2 73.6 409 5 CD799263

ALIGNMENTS
369 bp DNA linear GSS 01-JUL-2003
CC794955 SALK_059534.25.55.x Arabidopsis thaliana TDNA insertion lines
LOCUS Arabidopsis thaliana genomic clone SALK_059534.25.55.x, genomic
DEFINITION survey sequence.

B0860887 AGENCOURT
B0860886 Oryza sat
BU166542 AGENCOURT
BE972811 601652044
CL087178 ISB1-8M12
BQ717617 AGENCOURT
BQ435924 AGENCOURT
BX350688 BX350688
CF553765 AGENCOURT
BG165618 602343790
BQ647974 AGENCOURT
BQ055928 AGENCOURT
B1251933 602952554
BQ052172 AGENCOURT
CC191172 CH261-182
BQ887016 AGENCOURT
DR154835 49241661
CR694692 Tetraodon
BG328715 602427990
CR686184 Tetraodon
BM456058 AGENCOURT
BZ575326 msh2_441.
DN689440 CGK64-E11
AM096213 AM096213
DN721015 CNB137-A0
BQ906009 L007E03 O
BH193159 TC3-62E19
BF956085 MKO-NN116
BP590460 BP590460
CE711502 tigr-gss-
AV284162 AV284162
DT380778 HTE000092
AV333228 AV333228
BB277305 BB277305
CF043572 QC019C05.
BE151351 CM2-HT028
N92694 za19h11.r1
CF041004 QCI20605.
BB042561 BB042561
CD952536 SBC_67 Ge
CF041228 QCI23411.
DR889432 JGI XZG44
CD986461 QAN22b04.
CF045499 QCK14B03.
AG200967 Fan trogl
CD952561 SBC_96 Ge
AW078706 x532f05.x
CF053807 QCN21a01.
AW541641 C0147F07.
CA725948 wet18.pk0
CO000303 UMC-bend_
AA652906 ns68a07.s
CJ089485 CJ089485
AW172975 xj23e10.x
DV631930 EST110052
CO749044 SNESTbaa5
CA726259 wet18.pk0
D44704 HUMSUPY112
CD799263 EST 12924

ACCESSION CC794955
VERSION GI:32390178
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 369)
REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@alk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At3g21150.
Class: TDNA tagged.
FEATURES
Location/Qualifiers
source
1..369
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="SALK_059534.25.55.x"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
ORIGIN
Query Match 88.2%; Score 19.4; DB 12; Length 369;
Best Local Similarity 95.2%; Pred. No. 2.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAAGCCCTTTTCGGGGTGCT 21
Db 70 GAAAGCCCTTTTCGGGGTGCT 90
RESULT 2
LOCUS BB660584 741 bp mRNA linear EST 26-OCT-2001
DEFINITION BB660584 RIKEN full-length enriched, 13 days embryo stomach Mus
musculus cDNA clone D53003C13 5', mRNA sequence.
BB660584
ACCESSION BB660584.1 GI:16494381
VERSION BB660584.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 741)
REFERENCE Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Soga,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
Unpublished (2001)
TITLE
JOURNAL

```



Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

**COMMENT**  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

# **FEATURES**

## **source**

1. 1266

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM,DB:D530039C13"

/db\_xref="taxon:10090"

/clones="D530039C13"

/tissue\_type="stomach"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="13 days embryo"

## **misc\_feature**

1. 1266

/note="putative

similar to BOMAPIN (PROTEASE INHIBITOR 10) (SERPIN B10)

[Homo sapiens] (SWISSPROT|P48595, evidence: FASTY,

74.3%ID, 86.1%length, match=1026)"

# **ORIGIN**

## **Query Match**

Best Local Similarity 88.2%; Score 19.4; DB 6; Length 1266;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 GAAAGGCTTCGGGGTGCT 21

|||||

**Db** 543 GAAAGGCTTCGGGTGCT 523

# **RESULT 4**

## **AK036537/c**

**LOCUS** AK036537 3468 bp mRNA linear HTC 02-SEP-2005

**DEFINITION** Mus musculus adult male bone cDNA, RIKEN full-length enriched

library, clone:9830131G07 product:similar to BOMAPIN (PROTEASE

INHIBITOR 10) (SERPIN B10) [Homo sapiens], full insert sequence.

**AK036537**

**ACCESSION** AK036537.1 GI:26085290

**VERSION** HTC; CAP trapper.

**KEYWORDS** Mus musculus (house mouse)

# **SOURCE**

**ORGANISM** Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

# **REFERENCE**

## **AUTHORS**

1 Carninci,P. and Hayashizaki,Y.

**TITLE** High-efficiency full-length cDNA cloning

**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)

**PUBMED** 10349636

# **AUTHORS**

2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

**TITLE** Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

**Genome Res.** 10 (10), 1617-1630 (2000)

# **REFERENCE**

## **AUTHORS**

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,

Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,

Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,

Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,

Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,

Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
**Genome Res.** 10 (11), 1757-1771 (2000)  
11076861

# **REFERENCE**

## **AUTHORS**

4 The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

**TITLE** Functional annotation of a full-length mouse cDNA collection

**Nature** 409, 685-690 (2001)

# **REFERENCE**

## **AUTHORS**

5 The FANTOM Consortium, the RIKEN Genome Exploration Research Group

Phase I and II Team.

**TITLE** Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

**Nature** 420, 563-573 (2002)

# **REFERENCE**

## **AUTHORS**

6 RIKEN Genome Exploration Research Group, Genome Science Group

(Genome Network Core Team) and the FANTOM Consortium.

**TITLE** Antisense transcription in the Mammalian Transcriptome

**Science** 309, 1564-1566 (2005)

# **REFERENCE**

## **AUTHORS**

7 The FANTOM Consortium, Riken Genome Exploration Research Group and

Genome Science Group (Genome Network Project Core Group).

**TITLE** The Transcriptional Landscape of the Mammalian Genome

**Science** 309, 1559-1563 (2005)

# **REFERENCE**

## **AUTHORS**

8 (bases 1 to 3468)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,

Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,

Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,

Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,

Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,

Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,

Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,

Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yaeunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

**TITLE** Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,

URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,

Fax: 81-45-503-9216)

**COMMENT** cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

# **FEATURES**

## **source**

1. 3468

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM,DB:9830131G07"

/db\_xref="taxon:10090"

/clone="9830131G07"

/sex="male"

/tissue\_type="bone"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

## **misc\_feature**

1. 3468

/note="putative

similar to BOMAPIN (PROTEASE INHIBITOR 10) (SERPIN B10)

[Homo sapiens] (SWISSPROT|P48595, evidence: FASTY,

74.8%ID, 100%length, match=1191)"

# **ORIGIN**

Query Match 88.2%; Score 19.4; DB 6; Length 3468;  
 Best Local Similarity 95.28; Pred. No. 2.9e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21  
 |||||  
 Db 696 GAAAGGCTTTCGGGTGCT 676

RESULT 5  
 DR082998  
 LOCUS PMU51-020CE07.y1\_#634.1 DIAS\_PMUS Sus scrofa cDNA 5', mRNA linear EST 09-JUN-2005  
 DEFINITION sequence.

ACCESSION DR082998  
 VERSION DR082998.1 GI:67206801  
 KEYWORDS EST.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.

REFERENCE 1 (bases 1 to 514)  
 AUTHORS Panitz,F. and Bendixen,C.  
 TITLE Unpublished (Panitz,F., Bendixen,C.)  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Bendixen C

Molecular Genetics and Systems Biology, Department Genetics and  
 Biotechnology  
 Danish Institute of Agricultural Sciences  
 P.O.Box 50, DK 8830-Tjele, Denmark  
 Tel: +45 8999 1351  
 Fax: +45 8999 1300  
 Email: Christian.Bendixen@agrsci.dk.

FEATURES  
 source Location/Qualifiers

1..514  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /tissue\_type="muscle"  
 /clone\_lib="DIAS PMUS"  
 /note="Vector: pT7T3D-Paci; Site 1: EcoRI; Site 2: NotI;  
 Normalised cDNA library, adult muscle (longissimus dors).  
 Single pass sequencing."

## ORIGIN

Query Match 85.5%; Score 18.8; DB 9; Length 514;  
 Best Local Similarity 90.9%; Pred. No. 5e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 171 GAAAGGCTTTCGGGGTGCTC 192

RESULT 6  
 BM344289/c  
 LOCUS rr49b02.y1 Globodera rostochiensis J2 pCDNAII Smant v1 Globodera  
 DEFINITION rostochiensis cDNA 5', similar to TR:Q21420 Q21420 K10D6.1 PROTEIN.  
 [1] ;, mRNA sequence.

ACCESSION BM344289  
 VERSION BM344289.1 GI:18081204  
 KEYWORDS EST.  
 SOURCE Globodera rostochiensis  
 ORGANISM Globodera rostochiensis

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
 Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

REFERENCE 1 (bases 1 to 583)  
 AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,

Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterson,R. and Wilson,R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@wustl.edu  
 The library was contributed by Dr. Geert Smant of the Laboratory of  
 Nematology at Wageningen University, Wageningen,  
 Netherlands (Geert.smant@nema.dpw.wau.nl). DNA Sequencing by:  
 Washington University Genome Sequencing Center  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 421.

## FEATURES

source Location/Qualifiers

1..583  
 /organism="Globodera rostochiensis"  
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 /dev\_stage="J2"  
 /lab\_host="DH10B"  
 /clone\_lib="Globodera rostochiensis J2 pCDNAII Smant v1"  
 /note="Vector: pCDNAII (Invitrogen); Site 1: BstXI;  
 Site 2: EcoRI; The library was donated for sequencing by  
 Geert Smant from Wageningen University, Laboratory of  
 Nematology, The Netherlands."

## ORIGIN

Query Match 85.5%; Score 18.8; DB 2; Length 583;  
 Best Local Similarity 90.9%; Pred. No. 5.1e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 192 GAAAGGCTTTCGGGGTGCTC 171

## RESULT 7

## CNS06SS6/c

LOCUS T7 end of clone AW0AA026A05 of library AW0AA from strain CLIB 89 of  
 DEFINITION Yarrowia lipolytica, genomic survey sequence.

ACCESSION AL413644  
 VERSION AL413644.1 GI:12185773  
 KEYWORDS GSS.

SOURCE Yarrowia lipolytica  
 ORGANISM Yarrowia lipolytica

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomycetales; Dipodascaceae; Yarrowia.

REFERENCE 1 (bases 1 to 927)

AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,

Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Wincker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of  
 yeast species for molecular evolution studies

FEBS Lett. 487 (1), 3-12 (2000)

JOURNAL 11152876

PUBMED 2 (bases 1 to 927)

AUTHORS Casaregola,S., Neuveglise,C., Lepingle,A., Bon,E., Feynrol,C.,

Artiguenave,F., Wincker,P. and Gaillardin,C.

Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia

lipolytica

FEBS Lett. 487 (1), 95-100 (2000)

JOURNAL 11152892

PUBMED 3 (bases 1 to 927)





sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method."

## ORIGIN

Query Match 81.8%; Score 18; DB 5; Length 794;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGT 18

Db 767 GAAAGGCTTTCGGGGT 784

## RESULT 10

DV692385/c 221 bp mRNA linear EST 16-NOV-2005  
LOCUS CGN-36297 Leaf Coffea canephora cDNA clone cccl12b3 5', mRNA  
DEFINITION sequence.

ACCESSION DV692385

VERSION DV692385.1 GI:82472213

KEYWORDS EST.

SOURCE Coffea canephora

## ORGANISM

Coffea canephora  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons;  
asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeae;  
Coffea.

1 (bases 1 to 221)

Lin, C., Mueller, L.A., McCarthy, J., Crouzillat, D., Petiard, V. and Tankley, S.D.

Coffee and Tomato Share Common Gene Repertoires as Revealed by Deep Sequencing of Seed and Cherry Transcripts

Theoretical and Applied Genetics (2005) In press

Contact: Steven D. Tanksley

Department of Plant Breeding

Cornell University

248 Emerson Hall, Ithaca, NY 14853

Tel: 607 255 1673

Fax: 607 255 6683

Email: sdt@cornell.edu

The sequence provided is trimmed of vector and low quality regions. Full sequence and original trace file are available from the Sol

Genome Network website (<http://www.sgn.cornell.edu>)

Plate: 12 row: b column: 3

Seq primer: M13r

High quality sequence stop: 221.

## FEATURES

source

1. .221  
Location/Qualifiers  
/organism="Coffea canephora"  
/mol\_type="mRNA"  
/db\_xref="taxon:49390"  
/clone="cccl12b3"  
/tissue\_type="leaf"  
/dev\_stage="young"  
/clone\_lib="Leaf"  
/note="Vector: pBSSK-; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 80.9%; Score 17.8; DB 10; Length 221;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22

Db 61 AAAAGGCTTTCGAGGGTGCTC 41

## RESULT 11

CO308813/c 236 bp mRNA linear EST 25-JUN-2004  
LOCUS EK259430.5prime Exelixis Flytag CK01 pCDNA-SK+ Drosophila  
DEFINITION melanogaster cDNA clone EK259430 5', mRNA sequence.

## ACCESSION

CO308813

VERSION

CO308813.1 GI:49230691

KEYWORDS

SOURCE EST.

ORGANISM

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 236)

Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,

Peterson, E. and Swimmer, C.

Exelixis Flytag EST Project CK01 Library

Unpublished (2004)

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)

Based upon one or more reads of this clone where vector sequence

was present at both ends, this clone has been determined to contain

contain a cDNA insert on the order of 600-1000 bases.

Plate: EK.2594 row: C column: 6

High quality sequence stop: 157.

Location/Qualifiers

1. .236

/organism="Drosophila melanogaster"

/mol\_type="mRNA"

/db\_xref="taxon:7227"

/clone="EK259430"

/clone\_lib="Exelixis Flytag CK01 pCDNA-SK+"

/note="Organ: mixed stage embryos, imaginal disks, and

adult heads; Vector: pCDNA-SK+; Site\_1: NotI; Site\_2:

XhoI; Random primed, normalized library from mixed stage

embryos, imaginal disks, and adult heads."

Query Match 80.9%; Score 17.8; DB 8; Length 236;

Best Local Similarity 90.5%; Pred. No. 1.4e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22

Db 109 ACAGGCTTTCGGTGCTC 89

## RESULT 12

CF045077

LOCUS

DEFINITION

ACCESSION

CF045077

VERSION

CF045077.1 GI:32940258

KEYWORDS

SOURCE

ORGANISM

EST.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 267)

Genoplante.

Genoplante, a major partnership french program in plant genomics

Unpublished (2003)

JOURNAL

COMMENT

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (<http://www.genoplante.com>

and <http://genoplante-info.infobiogen.fr>).

Location/Qualifiers

1. .267

/organism="Zea mays"

```
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ8a11"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 267;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGTGCT 21
    |||||
Db 193 GAAAGGCTTCGGGGTGCT 213

RESULT 13
CF044432
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 288)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
Location/Qualifiers
1..288
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ29g07"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 288;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGTGCT 21
    |||||
Db 214 GAAAGGCTTCGGGGTGCT 234

RESULT 14
CO711127
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ8a11"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 267;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGTGCT 21
    |||||
Db 193 GAAAGGCTTCGGGGTGCT 213

RESULT 13
CF044432
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 288)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).

FEATURES
source
Location/Qualifiers
1..288
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ29g07"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 288;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGTGCT 21
    |||||
Db 214 GAAAGGCTTCGGGGTGCT 234

RESULT 14
CO711127
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.

/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QCJ8a11"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      80.9%; Score 17.8; DB 8; Length 510;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCTTTCGGGGTGCTC 22
    |||||
Db 471 AAAGGCTTTCGGGGTGCTC 491

RESULT 15
CD277478/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Betula pendula (European white birch)
Betula pendula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fagales; Betulaceae; Betula.
1 (bases 1 to 536)
Johansson, T., Le Quere, A., Ahren, D., Soderstrom, B., Erlandsson, R.,
Lundeberg, J., Uhlen, M. and Funlid, A.
Transcriptional responses of Paxillus involutus and Betula pendula
during formation of ectomycorrhizal root tissue
Mol. Plant Microbe Interact. 17 (2), 202-215 (2004)
14964534
Contact: Johansson, T.
Fungal-Host Interaction Group (FHIG)
Microbial Ecology, Institution of Ecology
Ecology Building, Lund University, SE-223 62 Lund, Sweden
Tel: +46 46 222 45 49
Fax: +46 46 222 41 58
Email: tomas.johansson@bioekol.lu.se
PCR Primers
FORWARD: P104 (5'-GGGAAGCGCGCCATTGTGTT-3')
BACKWARD: P105 (5'-AGTGAGCTCGAATTGGGCGC-3')
Seq primer: P104
High quality sequence stop: 536.
Location/Qualifiers
1..536
/organism="Betula pendula"
/mol_type="mRNA"
/strain="Skuleskogen, Skogsforsk, Sweden"
/db_xref="taxon:3505"
/tissue_type="Root tissue"
/dev_stage="25 days of growth after transfer"

REFERENCE
AUTHORS
Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,
Henrich, J. and Loeber, R.
Dog arrayTAG cDNA clone collection
Unpublished (2004)
Contact: Thomas Schlueter
LION Bioscience AG
Walhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.

FEATURES
source
Location/Qualifiers
1..510
/organism="Canis familiaris"
/mol_type="mRNA"
/strain="Beagle"
/db_xref="taxon:9615"
/tissue_type="muscle"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="DG14-muscle"
/notes="Organ: muscle; Vector: Dog pBluescript LION"
```

```
/lab_host="Escherichia coli BM25.8"
/clone_lib="(FHIG:C) Axenic plate culture"
/notes=Vector: pTriplex2; Site_1: SfiI; Site_2: SfiI; This
EST clone is originating from one of three cDNA libraries,
constructed for transcript profiling of the mycorrhizal
interaction between the basidiomycete Paxillus involutus
and Betula pendula (birch). One library represents the
developed and functional mycorrhizal root tissue
('FHIG:A) Ectomycorrhiza plate culture'), a second
library represents axenically grown fungus ('FHIG:B)
Axenic plate culture') and a third library represents
axenically grown plants ('FHIG:C) Axenic plate culture').
Libraries were analyzed in parallel and 3555 (FHIG:A),
3964 (FHIG:B), and 2532 (FHIG:C) high-quality (PHRED 20)
ESTs of >99bp have been deposited. The cDNA libraries were
constructed from total RNA using the SMART cDNA library
construction kit (HK1051-1, Clontech, Palo Alto, CA, USA)
according to the manufacturer's instructions. Full-length
cDNAs were trimmed by SfiI, fractionated and directionally
ligated into (lambda)Triplex2 arms. The lambda library was
converted to a plasmid library via site-specific
recombination at loxP sites in a Cre+ strain (E. coli
BM25.8). Plasmid clones were randomly collected and
analysed by DNA sequencing using a plasmid-specific
forward primer (P104)."
```

ORIGIN

```
Query Match      80.9%; Score 17.8; DB 5; Length 536;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AAAGGCGCTTTCGGGGTGCTC 22
        ||||| ||||| ||||| |||||
DB      151 AAAGGCGCTTTCGGGGTGCTC 131
```

RESULT 16

```
CB754809
LOCUS      CB754809
DEFINITION TgESTy111c07.y1 TgME49 3 day invitro bradyzoite Toxoplasma gondii
CNA clone
CB754809
VERSION    CB754809.1 GI:29822101
KEYWORDS   Toxoplasma gondii
SOURCE     Toxoplasma gondii
ORGANISM   Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Sarcocystidae; Toxoplasma.
```

REFERENCE

```
AUTHORS      Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioke,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
Ritter,E., Bennett,J., Franklin,C., Teagarden,R., Ronko,I.,
Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
Toxoplasma EST Project
Unpublished (2001)
Contact: Clifton, S.
```

TITLE

```
JOURNAL      Toxoplasma EST Project
COMMENT       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@wustl.wustl.edu
Contact David Sibley (toxoe@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40RP from Gibco.
```

FEATURES

```
source
1. .598
   /organism="Toxoplasma gondii"
   /mol_type="mRNA"
   /db_xref="taxon:5811"
   /clone="TgESTy111c07.y1"
   /dev_stage="3 day"
```

ORIGIN

```
Query Match      80.9%; Score 17.8; DB 4; Length 598;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AAAGGCGCTTTCGGGGTGCTC 22
        ||||| ||||| ||||| |||||
DB      371 AAAGGCGCTTTCGGGGTGCTC 391
```

RESULT 17

```
BI215331/c
LOCUS      BI215331
DEFINITION Drosophila melanogaster cDNA clone RE21703 5, mRNA sequence.
```

ACCESSION

```
VERSION      BI215331
KEYWORDS     1 (bases 1 to 658)
SOURCE       Drosophila melanogaster (fruit fly)
ORGANISM     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
```

REFERENCE

```
AUTHORS      Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B.,
Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E.,
George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G.,
Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and
Rubin,G.M.
BDGP/HMMI RE Drosophila EST Project
Unpublished (2001)
Other ESTs: RE21703.3prime
Contact: Stapleton, M.
```

TITLE

```
JOURNAL      BDGP
COMMENT       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003172: arm:U [6931003,6963876] estimated-cyto?:
04/12/2001
Plate: RE.217 row: A column: 3
High quality sequence stop: 600.
Location/Qualifiers
1. .658
   /organism="Drosophila melanogaster"
   /mol_type="mRNA"
   /db_xref="taxon:7227"
   /clone="RE21703"
   /sex="male and female"
   /dev_stage="0-24 hours mixed stage embryonic"
   /lab_host="DHS-alpha Tona"
   /clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
   /note="Organ: embryo; Vector: pFlc1, Site_1: XhoI, Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
```

FEATURES

```
source
1. .658
   /organism="Drosophila melanogaster"
   /mol_type="mRNA"
   /db_xref="taxon:7227"
   /clone="RE21703"
   /sex="male and female"
   /dev_stage="0-24 hours mixed stage embryonic"
   /lab_host="DHS-alpha Tona"
   /clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
   /note="Organ: embryo; Vector: pFlc1, Site_1: XhoI, Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
```

## Cre recombinase. Plasmid cDNA library."

```

ORIGIN
Query Match      80.9%; Score 17.8; DB 2; Length 658;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  AAAGCGCTTCGGGGGTGCTC 22
    | ||||| ||||| |||||
Db   330 ACAGGCTTCGGTGGTGGCTC 310

RESULT 18
CK133302
LOCUS
DEFINITION
Drosophila melanogaster cDNA clone RE21703 3, mRNA sequence.
ACCESSION
CK133302
VERSION
CK133302.1 GI:38625238
KEYWORDS
EST.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 664)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E.,
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
Miera, S., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
Rubin, G.M.
BDGP/HHMI RE Drosophila EST Project
Unpublished (2001)
Other ESTs: RE21703.5prime
Contact: Stapleton, M.
BDGP

Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Based upon the presence of a XhoI site followed by a run of 14 or
more T residues at the beginning of the sequence, this clone was
polyadenylated. The resulting Poly-T sequence has been removed. hit
genomic AE003172: arm:U [6931003,6963876] estimated-cyto:?:
02/05/2002
Plate: RE.217 row: A column: 3
High quality sequence stop: 592.
Location/Qualifiers
1..664
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="RE21703"
/sex="male and female"
/dev_stage="0-24 hours mixed stage embryonic"
/lab_host="DH5-alpha Tona"
/clone_lib="RE Drosophila melanogaster normalized Embryo
pFlc-1"
/notes="Organ: embryo; Vector: pFlc1; Site 1: XhoI; Site 2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
Cre recombinase. Plasmid cDNA library."

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 664;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  AAAGCGCTTCGGGGGTGCTC 22
    | ||||| ||||| |||||
Db   337 ACAGGCTTCGGTGGTGGCTC 357

RESULT 19
BH385770/c
LOCUS
DEFINITION
AG-ND-173E6.TF ND-TAM Anopheles gambiae genomic clone AG-ND-173E6,
genomic survey sequence.
ACCESSION
BH385770
VERSION
BH385770.1 GI:17331912
KEYWORDS
GSS.
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Anophelinae; Anopheles.
REFERENCE
1 (bases 1 to 683)
Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,
Ren, C., Huff, E.R., Carlile, J.L., Black, K., Zhang, H.-B.,
Gardner, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end
sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae
Mol. Genet. Genomics 268 (6), 720-728 (2003)
12655398
Other_GSSs: AG-ND-173E6.TR
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@igr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
partial digest.
Seq primer: M13 For
Class: BAC ends.
Location/Qualifiers
1..683
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone_lib="AG-ND-173E6"
/clone_lib="ND-TAM"
/notes="Vector: pECBAC1; Site 1: HindIII"

FEATURES
source
1..683
Query Match      80.9%; Score 17.8; DB 11; Length 683;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GAAAGCGCTTCGGGGGTGCT 21
    | ||||| ||||| |||||
Db   660 GAAAGCGCTTCGGGGGTGCT 640

ORIGIN
Query Match      80.9%; Score 17.8; DB 11; Length 683;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GAAAGCGCTTCGGGGGTGCT 21
    | ||||| ||||| |||||
Db   660 GAAAGCGCTTCGGGGGTGCT 640

RESULT 20
BB634710/c
LOCUS
DEFINITION
BB634710 RIKEN full-length enriched, 0 day neonate thymus Mus
musculus cDNA clone A430041D14 5', mRNA sequence.
ACCESSION
BB634710
VERSION
BB634710.1 GI:16470919
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```



**REFERENCE**  
**AUTHORS** Ictaluridae; Ictalurus.  
 1 (bases 1 to 950)  
 Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L.,  
 Peatman,E., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J.,  
 Dunham,R. and Brady,Y.  
**TITLE** 30,000 new catfish ESTs: new resources for functional analysis of  
 Genes involved in aquaculture performance traits  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Liu ZJ  
 The Fish Molecular Genetics and Biotechnology Laboratory,  
 Department of Fisheries and Allied Aquacultures and Program of Cell  
 and Molecular Biosciences  
 Auburn University  
 203 Swingle Hall, Auburn University, Auburn, AL 36849, USA  
 Tel: 334 844 4054  
 Fax: 334 844 9208  
 Email: zliu@acesag.auburn.edu  
**FEATURES** Seq primer: T7.  
 Location/Qualifiers  
 1..950  
 /organism="Ictalurus punctatus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7998"  
 /clone\_lib="Testis cDNA library"  
 /note="Organ: Testis; Vector: pSport1; Site\_1: NotI;  
 Site\_2: SalI"  
**ORIGIN**  
 Query Match 80.9%; Score 17.8; DB 5; Length 950;  
 Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
 QY 1 GAAAGGCCCTTTCGGGGTGCT 21  
 |||||  
 |||||  
 Db 924 GAAAGGCCCATTCGGGGTTCT 904  
  
**RESULT 24**  
 BF162561/c  
**LOCUS** BF162561  
**DEFINITION** 601770203F1 NCI\_CGAP\_Lu29 Mus musculus cDNA clone IMAGE:3989377 5';  
 mRNA sequence.  
**ACCESSION** BF162561  
**VERSION** BF162561.1 GI:11042781  
**KEYWORDS** EST.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
  
**REFERENCE**  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: cgabp-r@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM9199 row: f column: 02  
 High quality sequence stop: 706.  
 Location/Qualifiers  
 1..977  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="Czech II"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:3989377"  
 /tissue type="spontaneous tumor, metastatic to mammary."

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Stem cell origin."
/lab host="NCI CGAP Lu29"
/clone lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      80.9%; Score 17.8; DB 7; Length 977;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCGGGGTGCT 21
    |||
Db 653 GAAAGCCTTCGGGTGCTT 633

RESULT 25
BM907310
LOCUS
DEFINITION
AGENCOURT_6638575 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5735530
5', mRNA sequence.
ACCESSION
BM907310
VERSION
BM907310.1 GI:19357689
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1 (bases 1 to 994)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12742 row: j column: 11
High quality sequence stop: 652.
Location/Qualifiers
1. .994
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5735530"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match      80.9%; Score 17.8; DB 3; Length 994;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGCCTTCGGGGTGCTC 22
    |||
Db 912 AATGGCCTTCGGGGTGCTC 932

RESULT 26
CF376920
LOCUS
DEFINITION
AGENCOURT_15348767 NICHD_XGC_Swb1N Xenopus tropicalis cDNA clone
IMAGE:7006248 5', mRNA sequence.
CF376920
VERSION
CF376920.1 GI:34314364
KEYWORDS
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14706 row: h column: 22
High quality sequence stop: 565.
Location/Qualifiers
1. .1016
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7006248"
/tissue_type="whole body"
/note="Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the F6 strain. 1st strand cDNA was primed with a Not
I - oligo(dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pExpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cot5 with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHD_XGC_Swb1). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
contamination by worm"

ORIGIN
Query Match      80.9%; Score 17.8; DB 5; Length 1016;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGCCTTCGGGGTGCTC 22
    |||
Db 308 AAAGCCTTCGGGGTGCTC 328

RESULT 27
DW665607/c
LOCUS
DEFINITION
CNB332-C11_xld-t SHGC-CNB2 Gasterosteus aculeatus cDNA clone
CNB332-C11 3', mRNA sequence.
DW665607
VERSION
DW665607.1 GI:85458785
KEYWORDS
SOURCE
Gasterosteus aculeatus (three spined stickleback)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

```



REFERENCE 1 (bases 1 to 1045)  
 AUTHORS Kingsley,D.M., Peichel,C., Knecht,A., Balabhadra,S., Grimwood,J.,  
 Dickson,M., Schmutz,J. and Myers,R.M.  
 TITLE Expressed sequence tags from *Gasterosteus aculeatus* (2004)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@shgc.stanford.edu  
 Plate: 332  
 High quality sequence stop: 821.

FEATURES  
 source  
 Location/Qualifiers  
 1..1045  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CNB332-C11"  
 /sex="mixed male and female"  
 /tissue\_type="brain"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="SHGC-CNE2"  
 /note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna\_library\_construction\_fa.q.php# The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

ORIGIN  
 Query Match 80.9%; Score 17.8; DB 10; Length 1045;  
 Best Local Similarity 90.5%; Pred.No.1.6e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AAAGGCTTTTCGGGGTGCTC 22  
 |||||  
 Db 953 AAAGGCTTTTCGGGTGGTGTC 933  
 |||||

RESULT 28  
 DT956623/c  
 LOCUS CFW146-D12 yld-s SHGC-CFW *Gasterosteus aculeatus* cDNA clone  
 DEFINITION CFW146-D12 5', mRNA sequence.  
 ACCESSION DT956623  
 VERSION DT956623.1 GI:76029447  
 KEYWORDS EST.  
 SOURCE *Gasterosteus aculeatus* (three spined stickleback)  
 ORGANISM *Gasterosteus aculeatus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.  
 REFERENCE 1 (bases 1 to 1371)  
 AUTHORS Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.  
 TITLE Expressed sequence tags from *Gasterosteus aculeatus*

Unpublished (2003)  
 Contact: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@shgc.stanford.edu  
 Plate: 146  
 High quality sequence start: 29  
 High quality sequence stop: 875.

FEATURES  
 source  
 Location/Qualifiers  
 1..1371  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"  
 /strain="Conner Creek sticklebacks, WA USA"  
 /db\_xref="taxon:69293"  
 /clone="CFW146-D12"  
 /sex="mixed male and female"  
 /tissue\_type="gills"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="SHGC-CFW"  
 /note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGCGGCC(T)25-3'). Following second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at: http://www.openbiosystems.com/cdna\_library\_construction\_fa.q.php# The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:  
 http://www.openbiosystems.com/stickleback"

ORIGIN  
 Query Match 80.9%; Score 17.8; DB 10; Length 1371;  
 Best Local Similarity 90.5%; Pred.No.1.6e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AAAGGCTTTTCGGGGTGCTC 22  
 |||||  
 Db 1184 AAAGGCTTTTCGGGGTGCCC 1164  
 |||||

RESULT 29  
 DR985203  
 LOCUS JGI\_AOKG417, rev AOKG Acropora palmata spawned eggs Acropora palmata  
 DEFINITION cDNA clone AOKG417 3', mRNA sequence.  
 ACCESSION DR985203  
 VERSION DR985203.1 GI:71779909  
 KEYWORDS EST.  
 SOURCE Acropora palmata  
 ORGANISM Acropora palmata  
 Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Scleractinia; Asterozoa; Acroporidae; Acropora.  
 REFERENCE 1 (bases 1 to 373)  
 AUTHORS Schwarz,J.A., Brokstein,P., Manohar,C., Coffroth,M.A., Szmant,A. and Medina,M.  
 TITLE Coral-Symbiodinium EST Project  
 JOURNAL Unpublished (2005)  
 COMMENT Other ESTs: JGI\_AOKG417.fwd  
 Contact: Schwarz, JA, Medina, M.

Evolutionary Genomics  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925-296-5823  
Email: jaschwarz@lbl.gov  
CDNA Library Preparation: DOE Joint Genome Institute:  
http://www.jgi.doe.gov  
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix ".rev" indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Poly-T: A run of 14 or more T residues at the beginning of this sequence has been removed.  
Plate: AOKG 0005 row: a column: 9  
High quality sequence stop: 200.  
Location/Qualifiers  
1. .373  
/organism="Acropora palmata"  
/mol\_type="mRNA"  
/db\_xref="taxon:6131"  
/clone="AOKG417"  
/dev\_stage="Freshly spawned eggs"  
/lab\_host="ElectroMAX DH10B"  
/clone\_lib="AOKG Acropora palmata spawned eggs"  
/notes="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; The library was prepared from total RNA using the Creator SMART cDNA library Construction Kit with the LD-PCR method to amplify the cDNA. Amplified cDNA was digested with Sfil, size selected for >1000bp, and ligated into the pDNR-LIB vector."

FEATURES  
source  
Query Match 79.1%; Score 17.4; DB 10; Length 373;  
Best Local Similarity 94.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 AAAGGCTTTCGGGGGTGC 20  
|||||  
DB 9 AAAGGCTTTCGGGGGGC 27  
|||||  
RESULT 30  
T56721  
LOCUS  
DEFINITION  
Y871a03.s2 Stratagene placenta (#937225) Homo sapiens cDNA clone  
IMAGE:67084 3', mRNA sequence.  
T56721  
VERSION  
T56721.1 GI:658582  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 408)  
REFERENCE  
AUTHORS  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,  
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
Trevisan, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.,  
and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
8889549  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 277

Source: IMAGE Consortium, L1NL  
This clone is available royalty-free through L1NL; contact the  
IMAGE Consortium (info@image.l1nl.gov) for further information.  
Seq primer: -21ml3  
High quality sequence stop: 277.  
Location/Qualifiers  
1. .408  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:67084"  
/sex="male"  
/lab\_host="SOLR cells (kanamycin resistant)"  
/clone\_lib="Stratagene placenta (#937225)"  
/note="Organ: placenta; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:  
Oligo dt. Caucasian. Average insert size: 1.2 kb; Uni-ZAP  
XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3'  
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

FEATURES  
source  
Query Match 79.1%; Score 17.4; DB 10; Length 408;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 AAAGGCTTTCGGGGGTGCT 21  
|||||  
DB 367 AAAGGCTTTCGGGGGTGCT 386  
|||||  
RESULT 31  
BB157276/c  
LOCUS  
DEFINITION  
BB157276 RIKEN full-length enriched, 16 days neonate thymus Mus  
musculus cDNA clone Al30035115 3', mRNA sequence.  
BB157276  
VERSION  
BB157276.2 GI:16268376  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 658)  
REFERENCE  
AUTHORS  
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,  
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,  
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,  
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished (2001)  
On Jun 29, 2000 this sequence version replaced gi:8813206.  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,  
Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.  
and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.



Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

## PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. .765

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

/db\_xref="taxon:57486"

/clone="MSMg01-351M07.TJ"

/sex="male"

/tissue types="mixture of kidney and spleen"

/clone\_lib="MSMg01 Mouse Male BAC Library"

## ORIGIN

Query Match

Best Local Similarity 79.1%; Score 17.4; DB 11; Length 843;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTG 19

||||| |||||||

Db 716 GAAAGCCCTTCGGGGTG 734

## RESULT 35

BQ689861/c

LOCUS

DEFINITION

5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LCM2363 row: f column: 02

High quality sequence stop: 714.

## FEATURES

Source

1. .893

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6207361"

/tissue type="ductal carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_110"

/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;

Site:2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match

Best Local Similarity 79.1%; Score 17.4; DB 3; Length 893;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTG 19

||||| |||||||

Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

## PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACe3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

1. .765

/organism="Mus musculus molossinus"

/mol\_type="genomic DNA"

/sub\_species="molossinus"

/db\_xref="taxon:57486"

/clone="MSMg01-351M07.TJ"

/sex="male"

/tissue types="mixture of kidney and spleen"

/clone\_lib="MSMg01 Mouse Male BAC Library"

## ORIGIN

Query Match

Best Local Similarity 79.1%; Score 17.4; DB 14; Length 765;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTG 19

||||| |||||||

Db 723 GAAAGCTCTTCGGGGTG 705

## RESULT 34

AQ746955

LOCUS

DEFINITION

Genomic clone Plate=1114 Col=21 Row=E, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 843)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,

Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and

Hood,L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

10449764

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieterdejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)

or from Research Genetics (Info@resgen.com). BAC end Web Server:

http://www.htsc.washington.edu

Plate: 1114 row: E column: 21

Seq primer: T7

Class: BAC ends

High quality sequence stop: 843.

Location/Qualifiers

1. .843

/organism="Homo sapiens"

Source

```

Db      845 GAAAGGCGCTTCTCGGGTG 827
|||||
RESULT 36
DT995647      1413 bp      mRNA      linear      EST 22-SEP-2005
LOCUS      CNB179-H01.y1d-s SHGC-CNB Gasterosteus aculeatus cDNA clone
DEFINITION      DT995647
ACCESSION      DT995647
VERSION      DT995647
KEYWORDS      EST.
SOURCE      Gasterosteus aculeatus (three spined stickleback)
ORGANISM      Gasterosteus aculeatus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
                Gasterosteidae; Gasterosteus.
REFERENCE      1 (bases 1 to 1413)
AUTHORS      Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
                Schmutz,J. and Myers,R.M.
TITLE      Expressed sequence tags from Gasterosteus aculeatus
JOURNAL      Unpublished (2003)
COMMENT      Contact: Grimwood, Jane
                Stanford Human Genome Center
                Stanford University School of Medicine
                975 S California Ave, Palo Alto, CA 94304, USA
                Tel: 650 320 5917
                Fax: 650 320 5801
                Email: jane@shgc.stanford.edu
                Plate: 179
                High quality sequence start: 20
                High quality sequence stop: 848.

FEATURES             source
    Location/Qualifiers
        1..1413
            /organism="Gasterosteus aculeatus"
            /mol_type="mRNA"
            /strain="Conner Creek sticklebacks, WA USA"
            /db_xref="taxon:69293"
            /clone="CNB179-H01"
            /sex="mixed male and female"
            /tissue_type="brain"
            /dev_stage="adult"
            /lab_host="DH10B (T1 phage resistant)"
            /clone_lib="SHGC-CNB"
            /notes="Vector: Express 1; Total and poly A+ RNA was
                isolated from the indicated stickleback tissue, and a cDNA
                library was constructed in the Express 1 plasmid vector by
                Open Biosystems. First strand cDNA synthesis was primed
                with an 54 bp linker primer containing an oligodt sequence
                preceded by a synthetic NotI site (first strand primer:
                5'-GACTAGTCTAGATCGGCGGCCGCTT)25-3'. Following
                second strand synthesis, cDNAs were made blunt at the end
                corresponding to the original 5 prime end of mRNA, and
                cloned directionally into the NotI and EcoRV sites of
                Express 1. Note that the EcoRV site is typically destroyed
                in the blunt end cloning, leaving a junction of the form
                'xxxATC' (where is ATC is the second half of the EcoRV
                site, and xxx is derived from the cDNA sequence). A map of
                the Express 1 vector is available at:
                http://www.openbiosystems.com/cdna_library_construction_fa
                q.php#8 The primary library was transformed and amplified
                in DH10B (T1 phage resistant) bacteria. Clones available
                from Open Biosystems:
                http://www.openbiosystems.com/stickleback"

ORIGIN
Query Match      79.1%;      Score 17.4;      DB 10;      Length 1413;
Best Local Similarity      94.7%;      Pred. No. 2.5e+03;
Matches 18;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

Qy      1 GAAAGGCGCTTCTCGGGGTG 19
|||||

Db      1230 GAAAGGCGCTTCTAGGGGTG 1248
|||||
RESULT 37
CD377892      270 bp      mRNA      linear      EST 31-MAY-2003
LOCUS      PTM03081 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
DEFINITION      CD377892
ACCESSION      CD377892
VERSION      CD377892.1 GI:31253506
KEYWORDS      EST.
SOURCE      Phaeodactylum tricornutum
ORGANISM      Phaeodactylum tricornutum
                Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
                Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
REFERENCE      1 (bases 1 to 270)
AUTHORS      Scala,S., Carls,N., Falcione,A., Chiuseano,M.L. and Bowler,C.
TITLE      Genome properties of the diatom Phaeodactylum tricornutum
JOURNAL      Plant Physiol. 129 (3), 993-1002 (2002)
COMMENT      PUBMED 12114555
                Contact: Bowler C
                Laboratory of Molecular Plant Biology
                Stazione Zoologica 'Anton Dohrn'
                Villa Comunale, I-80121, Napoli, Italy
                Tel: 39 081 583 3268/3211
                Fax: 39 081 764 1355
                Email: chris@alpha.szn.it
                Diatom EST Database(http://aves.thagen.sznbowler.com)
                Seq primer: T3 backward
                POLYA=No.

FEATURES             Location/Qualifiers
    source      1..270
            /organism="Phaeodactylum tricornutum"
            /mol_type="mRNA"
            /db_xref="taxon:2850"
            /cell_line="CCMP632"
            /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
            /notes="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
                Xho I"

ORIGIN
Query Match      78.2%;      Score 17.2;      DB 5;      Length 270;
Best Local Similarity      86.4%;      Pred. No. 2.8e+03;
Matches 19;      Conservative      0;      Mismatches      3;      Indels      0;      Gaps      0;

Qy      1 GAAAGGCGCTTCTCGGGGTGCTC 22
|||||
Db      59 GAAAGGCGCTTCTCGCAGTGCTC 80
|||||

RESULT 38
CN690130      353 bp      mRNA      linear      EST 17-MAY-2004
LOCUS      E0289B09-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high
DEFINITION      density) cDNA library (Long) Mus musculus cDNA clone NIA:E0289B09
                IMAGE:30857876 5', mRNA sequence.
ACCESSION      CN690130
VERSION      CN690130.1 GI:47456576
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 353)
AUTHORS      Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y.,
                VanBuren,V., Falco,G., Martin,P.R., Staggs,C.A., Basseey,U.C.,
                Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L.,
                Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S.,
                Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L.,
                Schlessinger,D., Keller,J., Klotz,E., Kelsae,G., Umazawa,A.,
                Vescovi,A.L., Rossant,J., Kunath,T., Hogan,B.L., Curci,A.,
                D'Urso,M., Kelsae,J., Hide,W. and Ko,M.S.

```

**TITLE** Transcriptome analysis of mouse stem cells and early embryos  
**JOURNAL** PLOS Biol. 1 (3), 410-419 (2003)  
**COMMENT** Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 Plate: E0289 row: B column: 09  
 Seq primer: M13 Reverse  
 High quality sequence stop: 353  
 POLYA=No.

**FEATURES** Location/Qualifiers  
 source  
 1. .353  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/EvTac"  
 /db\_xref="niaEST:E0289B09-5"  
 /db\_xref="taxon:10090"  
 /clone="NIA:E0289B09 IMAGE:30857876"  
 /sex="Male"  
 /tissue\_type="Embryonic Stem Cell"  
 /cell\_line="129.3 ES cells"  
 /lab\_host="DH108"  
 /clone\_lib="NIA Mouse Embryonic Stem (ES) cell (luf-, 48 h, high density) cDNA library (Long)"  
 /notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES cells were plated at density 3x10<sup>4</sup>/cm<sup>2</sup>, on gelatin-coated plates and cultured for 48 hrs at 37 °C, 5% CO<sub>2</sub>. Culture medium: DMEM supplemented with 15% FBS, 2 mM L-glutamine, 0.1 mM NEAA, 1mM Sodium pyruvate, 0.1 mM beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml streptomycin. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-pGACTAGTTCAGTCGCGCGCGCCCTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4 kb. The library was constructed by Yulan Piao."

**ORIGIN**  
 Query Match 78.2%; Score 17.2; DB 8; Length 353;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 147 GAAAGCCCTTCGGATGAGCTC 168  
 |||||

**RESULT 39**  
 AW854955/c  
 LOCUS AW854955 363 bp mRNA linear EST 19-MAY-2000  
 DEFINITION PM0-CT0263-261099-004-h12 CT0263 Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW854955  
 VERSION AW854955.1 GI:7950648  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

**REFERENCE** AUTHORS  
 1 (bases 1 to 363)  
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
**TITLE** Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
**PUBMED** 10737800  
**COMMENT** Contact: Simpson A.J.G.  
 Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
 Tel: +55-11-2704922  
 Fax: +55-11-2707001  
 Email: asimpson@ludwig.org.br  
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=&t2=PM0-CT0263-261099-004-h12&t3=1999-10-26&t4=1)  
 Seq primer: puc 18 forward  
 High quality sequence start: 3  
 High quality sequence stop: 363.

**FEATURES** Location/Qualifiers  
 source  
 1. .363  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="CT0263"  
 /note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

**ORIGIN**  
 Query Match 78.2%; Score 17.2; DB 7; Length 363;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 300 GACAAGCATTCGGGGTGCTC 279  
 |||||

**RESULT 40**  
 CD383045  
 LOCUS CD383045 371 bp mRNA linear EST 31-MAY-2003  
 DEFINITION PTM08215 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum tricornutum cDNA 5', mRNA sequence.  
 ACCESSION CD383045  
 VERSION CD383045.1 GI:31259659  
 KEYWORDS EST.  
 SOURCE Phaeodactylum tricornutum  
 ORGANISM Phaeodactylum tricornutum  
 Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae; Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.  
 1 (bases 1 to 371)  
**REFERENCE** AUTHORS  
 Scala,S., Carls,N., Falciatore,A., Chiusano,M.L. and Bowler,C.  
**TITLE** Genome properties of the diatom Phaeodactylum tricornutum  
**JOURNAL** Plant Physiol. 129 (3), 993-1002 (2002)  
**PUBMED** 12114555  
**COMMENT** Contact: Bowler C  
 Laboratory of Molecular Plant Biology  
 Stazione Zoologica 'Anton Dohrn'

Villa Comunale, I-80121, Napoli, Italy  
 Tel: 39 081 583 3268/3211  
 Fax: 39 081 764 1355  
 Email: [chriss@alpha.szn.it](mailto:chriss@alpha.szn.it)  
 Dlatom EST Database (<http://avesthagen.sznbowler.com>)  
 Seq primer: T3 backward  
 POLYA=No.

## FEATURES

source Location/Qualifiers

1. .371  
 /organism="Phaeodactylum tricornutum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:2850"  
 /cell\_line="CCMP632"  
 /clone\_lib="Phaeodactylum tricornutum Uni-Zap XR"  
 /note="vector: Uni-Zap XR vector; Site\_1: Eco RI; Site\_2: Xho I"

## ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 371;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 161 GAAAGGCTTTTCGCAGTGCTC 182

## RESULT 41

CG548494 378 bp mRNA linear GSS 01-OCT-2003  
 LOCUS OST150127 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150127,  
 mRNA sequence.

ACCESSION CG548494

VERSION CG548494.1 GI:37335081

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 378)

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,  
 Piggott, J., Beltrandeiro, H., Buxton, E.C., Edwards, J., Finch, R.A.,  
 Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,  
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,  
 Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,  
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,  
 Zhu, O., Person, C. and Sands, A.T.

TITLE Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap  
 screen to identify potential targets for therapeutic intervention  
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

JOURNAL 14610273

PUBMED Contact: Zambrowicz BP

COMMENT OmniBank  
 Lexicon Genetics Incorporated  
 4000 Research Forest Drive, The Woodlands, TX 77381, USA  
 Email: [materials@lexgen.com](mailto:materials@lexgen.com)  
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as  
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)  
 Class: Gene Trap.

## FEATURES

source Location/Qualifiers

1. .378  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129Sv/Ev"  
 /db\_xref="taxon:10090"  
 /clone="OST150127"  
 /cell\_type="embryonic stem cell"  
 /clone\_lib="Mus musculus 129Sv/Ev"

## ORIGIN

Query Match 78.2%; Score 17.2; DB 12; Length 378;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 288 GAAAGGCTTTTCGATCAGCTC 309

## RESULT 42

AW854998

LOCUS

DEFINITION AW854998 386 bp mRNA linear EST 19-MAY-2000

ACCESSION PM3-CT0263-091299-007-c06 CT0263 Homo sapiens cDNA, mRNA sequence.

VERSION AW854998.1 GI:7950691

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primate; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 386)

AUTHORS Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, P.F.,

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL 10737800

PUBMED

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: [asimpson@ludwig.org.br](mailto:asimpson@ludwig.org.br)

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=PM3-CT0263-091>)

299-007-c06et3=1999-12-09et4=1

Seq primer: puc 18 forward

High quality sequence start: 18

High quality sequence stop: 386.

FEATURES

source Location/Qualifiers

1. 386

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/dev\_stage="Adult"

/clone\_lib="CT0263"

/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 386;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22

Db 64 GACAAGCATTTTCGGGGTGCTC 85

## RESULT 43

CG548510

LOCUS

Query Match 78.2%; Score 17.2; DB 12; Length 378;  
 Best Local Similarity 86.4%; Pred. No. 2.9e+03;

DEFINITION	OST150188 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150188, mRNA sequence.	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
ACCESSION	CG548510	PUBMED	14610273
VERSION	CG548510.1	COMMENT	Contact: Zambrowicz BP
KEYWORDS	GSS.		Omnibank
SOURCE	Mus musculus (house mouse)		Lexicon Genetics Incorporated
ORGANISM	Mus musculus		4000 Research Forest Drive, The Woodlands, TX 77381, USA
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.		Email: materials@lexgen.com
AUTHORS	1 (bases 1 to 390)		Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
	Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J., Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A., Friddle,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C., Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D., Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z., Sparks,M.J., Van Slightenhorst,I., Vogel,P., Walke,W., Xu,N., Zhu,Q., Person,C. and Sands,A.T.		Class: Gene Trap.
TITLE	Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)		
PUBMED	14610273		
COMMENT	Contact: Zambrowicz BP		
	Omnibank		
	Lexicon Genetics Incorporated		
	4000 Research Forest Drive, The Woodlands, TX 77381, USA		
	Email: materials@lexgen.com		
	Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)		
	Class: Gene Trap.		
	Class: Gene Trap.		
FEATURES	Location/Qualifiers		
source	1..390		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="129Sv/Ev"		
	/db_xref="taxon:10090"		
	/clone="OST150188"		
	/cell_type="embryonic stem cell"		
	/clone_lib="Mus musculus 129Sv/Ev"		
ORIGIN			
	Query Match 78.2%; Score 17.2; DB 12; Length 390;		
	Best Local Similarity 86.4%; Pred. No. 2.9e+03;		
	Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
QY	1 GAAAGGCTTCGGGGTGCTC 22		
Db	288 GAAAGGCTTCGGATGAGCTC 309		
RESULT 45			
AA555150/c			
LOCUS	AA555150		
DEFINITION	nl07g10.s1 NCI CGAP_Prl1 Homo sapiens cDNA clone IMAGE:1029666 similar to TR:G168081 G168081 UNIDENTIFIED GENE.; mRNA sequence.		
ACCESSION	AA555150		
VERSION	AA555150.1		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 405)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F. Chuqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.		
	cDNA Library Preparation: David B. Krizman, Ph.D.		
	cDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/hbrp/image/image.html		
	Insert length: 910 Std Error: 0.00		
	Seq primer: -40m13 fwd. ET from Amersham		
	High quality sequence stop: 400.		
FEATURES	Location/Qualifiers		
source	1..405		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1029666"		
	/sex="male"		
	/tissue_type="normal prostatic epithelial cells"		
	/lab_host="DH10B"		
	/clone_lib="NCI-CGAP_Prl1"		
	/note="Organ: prostate; Vector: pAMP10; mRNA made from normal prostatic epithelial cells, cDNA made by oligo-dt"		



priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 405;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

||||| ||||| ||||| ||||| |||||

Db 45 GAAAGGCTTCGGGATGTCAC 24

## RESULT 46

CG548505 413 bp mRNA linear GSS 01-OCT-2003  
LOCUS OST150171 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST150171,  
mRNA sequence.

## ACCESSION

CG548505

## VERSION

CG548505.1 GI:37335092

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Mus.

1 (bases 1 to 413)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .413

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST150171"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

78.2%; Score 17.2; DB 12; Length 413;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

||||| ||||| ||||| ||||| |||||

Db 258 GAAAGGCTTCGGATGCTC 279

## RESULT 47

CG562443 417 bp mRNA linear GSS 02-OCT-2003  
LOCUS OST446019 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST446019,  
mRNA sequence.

## ACCESSION

CG562443

## VERSION

CG62443.1

GI:37486292

## KEYWORDS

GSS.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Mus.

1 (bases 1 to 417)

Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhaufl, B., Ma, Z.-Q., Markesich, D.,

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Slightenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, Q., Person, C. and Sands, A.T.

Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap

screen to identify potential targets for therapeutic intervention

Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)

14610273

Contact: Zambrowicz BP

OmniBank

Lexicon Genetics Incorporated

4000 Research Forest Drive, The Woodlands, TX 77381, USA

Email: materials@lexgen.com

Gene trap sequence tag generated by 3' RACE from mouse ES cells as

described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)

Class: Gene Trap.

Location/Qualifiers

1. .417

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129Sv/Ev"

/db\_xref="taxon:10090"

/clone="OST446019"

/cell\_type="embryonic stem cell"

/clone\_lib="Mus musculus 129Sv/Ev"

78.2%; Score 17.2; DB 12; Length 417;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTCGGGGGTGCTC 22

||||| ||||| ||||| ||||| |||||

Db 289 GAAAGGCTTCGGATGCTC 310

## RESULT 48

DT596565

LOCUS

DEFINITION

wmi03-11ms2-a04 Wmi03 Welwitschia mirabilis cDNA clone

wmi03-11ms2-a04 5', mRNA sequence.

DT596565

DT596565.1 GI:74107838

EST.

KEYWORDS

SOURCE

ORGANISM

Welwitschia mirabilis

Welwitschia mirabilis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Gnastophyta; Gnastophyta; Gnastophyta; Gnastophyta;

Welwitschiaceae; Welwitschia.

1 (bases 1 to 432)

Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,

Leebens-Mack, J., McNeal, J., Landherr, L., Ilut, D. and Wall, K.

Generation of ESTs from early flower buds of Welwitschia mirabilis

Unpublished (2003)

Contact: Claude dePamphilis or James Leebens-Mack

Mueller Laboratory

Penn State University

208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn

State University, University Park, PA 16802, USA

Tel: 814 863 6413

Fax: 814 865 9131







Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

## REFERENCE

1 (bases 1 to 525)

## AUTHORS

Smith, T.P.L., Roberts, A.J., Ehternkamp, S.E., Chitko-McKown, C.G.,

Wray, J.E. and Keel, J.W. Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.

## TITLE

A second set of bovine ESTs from pooled-tissue normalized libraries

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@mail.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.

Plate: FQY8029 row: L column: 13

Seq primer: TAGAGGCACATCGAGG.

## FEATURES

source

Location/Qualifiers

1..525

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 6BOV"

/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including liver, lung, hypothalamus, pituitary, and

placenta/endometrium."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 525;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22

||||| ||||| ||||| |||||

Db 426 GAAGGACCTTTCGGGGTGCTC 447

## RESULT 56

CA886724

LOCUS

B0131G09-5N NIA Mouse Neural Stem Cell (Differentiated) cDNA

Library (Long) Mus musculus cDNA clone NIA:B0131G09 IMAGE:30096848

5', mRNA sequence.

CA886724

CA886724.1 GI:27338273

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 549)

Piao, Y., Dudekula, D.B., Qian, Y., Martin, P.R., Alba, K., Vescovi, A.L.

and Ko, M.S.H.

Systematic Analyses of NIA Mouse Neural Stem Cell (Differentiated)

cDNA Library (Long)

Unpublished (2002)

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsum.grc.nia.nih.gov

Plate: B0131 row: G column: 09

Seq primer: -21M13 Reverse

High quality sequence stop: 549

POLYA-No.

Location/Qualifiers

1..549

## FEATURES

source

Location/Qualifiers

1..549

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="CD1"

/db\_xref="niaEST:B0131G09-5N"

/db\_xref="taxon:10090"

/clone="NIA:B0131G09 IMAGE:30096848"

/dev\_stage="Adult"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse Neural Stem Cell (Differentiated)

cDNA Library (Long)"

/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:

NotI; Mouse cDNA project by the Laboratory of Genetics,

National Institute on Aging (NIA), Intramural Research

Program, NIH (http://lgsum.grc.nia.nih.gov/cDNA). This is

a long-transcript enriched cDNA library (Ref. Genome Res.

11: 1553-1558 (2001). [PMID: 11544199]. Total RNAs were

obtained from Dr. Angelo L. Vescovi (Institute for Stem

Cell Research, Italy). Double-stranded cDNAs were

synthesized with an Oligo(dT) primer [Invitrogen:

5'-pGACTAGTTCATGACGCGCGCCCTTTT-3'] from

2.0 Microgram of total RNA, treated with T4 DNA

polymerase, and purified by ethanol-precipitation. The

cDNAs were ligated to lone-linker L1-Sal4, purified by

phenol/chloroform, and separated from free linkers by

Centricon 100. Then, the cDNAs were amplified by

long-range high fidelity PCR using Ex Taq polymerase

(Takara) with a primer Sal4-S. The products were purified

by phenol/chloroform and Centricon 100. The cDNAs were

digested with SalI and NotI enzymes and cloned into

SalI/NotI site of pSPORT1 plasmid vector. The DH10B E.

coli host was transformed with the ligation mixture by the

standard chemical method. The average insert size is about

3.2 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 549;

Best Local Similarity 86.4%; Pred. No. 2.9e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22

||||| ||||| ||||| |||||

Db 526 GAAAGGCTTTCGGATGAGCTC 547

## RESULT 57

CN695093

LOCUS

DEFINITION

musculus cDNA clone NIA:E0360A01 IMAGE:30864672 5', mRNA sequence.

CN695093

VERSION

CN695093.1 GI:47463842

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 553)

Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,

VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, J.C.,

Wang, Y., Carter, M.G., Hamatani, T., Alba, K., Akutsu, H., Sharova, L.,

Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,

Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,

Schlessinger, D., Keller, J., Klotz, E., Kelsae, G., Umezawa, A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,

D'Urso, M., Kelsae, J., Hide, W., and Ko, M.S.

Transcriptome analysis of mouse stem cells and early embryos

PLOS Biol. 1 (3): 410-419 (2003)

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@lgsum.grc.nia.nih.gov

Plate: B0131 row: G column: 09

Seq primer: -21M13 Reverse

High quality sequence stop: 549

POLYA-No.

Location/Qualifiers

1..549

Plate: E0360 row: A column: 01  
Seq primer: M13 Reverse  
High quality sequence stop: 553  
POLYA-No. Location/Qualifiers  
FEATURES  
source  
1. .553  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:E0360A01-5"  
/db\_xref="taxon:10090"  
/clone="NIA:E0360A01 IMAGE:30864672"  
/tissue\_type="whole embryo including extraembryonic  
tissues at 10.5-days postcoitum"  
/dev\_stage="E10.5"  
/lab\_host="DH10B"  
/clone\_lib="NIA Mouse E10.5 whole embryo cDNA library  
(Long)"  
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;  
Site 2: NotI; Mouse cDNA project by the Laboratory of  
Genetics, National Institute on Aging (NIA), Intramural  
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).  
This is a long-transcript enriched cDNA library (Ref.  
Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. Total  
RNAs were extracted from a pool of 8 embryos at 10.5-days  
postcoitum. Double-stranded cDNAs were synthesized with an  
Oligo(dT) primer [Invitrogen].  
5'-PGACTGTTCTAGATCGGCGCGCCCTTTT-3' from  
2ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to Lone-linker LL-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid  
vector. The DH10B E. coli host was transformed with the  
ligation mixture by the standard chemical method. The  
average insert size is about 3.4Kb. The library was  
constructed by Yulan Piao."

Query Match 78.2%; Score 17.2; DB 8; Length 553;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22  
|||||  
Db 515 GAAAGCCCTTCGGATGAGCTC 536

RESULT 58  
CB462716/c  
LOCUS 555 bp mRNA linear EST 26-MAR-2003  
DEFINITION 723046 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION CB462716  
VERSION GI:29269100  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 555)  
Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,  
Wray, J.E. and Keefe, J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross match v0.990329.  
Plate: LAM8002 row: M column: 8  
Seq primer: TAGAAGGCACACTCGAGG.  
FEATURES  
source  
1. .555  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

Query Match 78.2%; Score 17.2; DB 4; Length 555;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22  
|||||  
Db 129 GAAGGACCTTCGGGATGCTC 108

RESULT 59  
CB464162  
LOCUS 555 bp mRNA linear EST 26-MAR-2003  
DEFINITION 725350 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.  
ACCESSION CB464162  
VERSION GI:29270547  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 555)  
Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,  
Wray, J.E. and Keefe, J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross match v0.990329.  
Plate: LAM8002 row: M column: 8  
Seq primer: TAGAAGGCACACTCGAGG.  
FEATURES  
source  
1. .555  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

Query Match 78.2%; Score 17.2; DB 4; Length 555;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22  
|||||  
Db 129 GAAGGACCTTCGGGATGCTC 108

RESULT 59  
CB464162  
LOCUS 555 bp mRNA linear EST 26-MAR-2003  
DEFINITION 725350 MARC 6BOV Bos taurus cDNA 3', mRNA sequence.  
ACCESSION CB464162  
VERSION GI:29270547  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 555)  
Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,  
Wray, J.E. and Keefe, J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross match v0.990329.  
Plate: LAM8002 row: M column: 8  
Seq primer: TAGAAGGCACACTCGAGG.  
FEATURES  
source  
1. .555  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 6BOV"  
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including liver, lung, hypothalamus, pituitary, and  
placenta/endometrium."

Query Match 78.2%; Score 17.2; DB 4; Length 555;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22  
|||||  
Db 129 GAAGGACCTTCGGGATGCTC 108



National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Angelo L. Vescovi (Institute for Stem Cell Research, Italy). Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTTTTT-3'] from 2.0 microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.2 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 566;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22

Db 526 GAAAGCCCTTCGGATGAGCTC 547

## RESULT 63

DN591849/c

LOCUS a4g07cc.r1 Coprinus cinereus fruit body cap cDNAs in meiotic  
DEFINITION prophase (K+6) Coprinopsis cinerea cDNA 3', mRNA sequence.

ACCESSION DN591849

VERSION DN591849.1 GI:61242453

KEYWORDS EST.

SOURCE Coprinopsis cinerea (Coprinus cinereus)

ORGANISM Coprinopsis cinerea  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Agaricales; Psathyrellaceae; Coprinopsis.

REFERENCE 1 (bases 1 to 591)

AUTHORS Zolan,M.E., Roe,B., Kupfer,D., Palmerini,H., Ramesh,M.A., Gathman,A.C., Lilly,W.W. and Pukkila,P.J.

TITLE Expressed sequence tags from Coprinus cinereus (Coprinopsis

JOURNAL cinerea) cDNAs, 2002

COMMENT Unpublished (2002)

Contact: Gathman AC

Biologiy Department

Southeast Missouri State University

1 University Plaza, Cape Girardeau, MO 63701, USA

Tel: 5736512361

Fax: 573 651 2382

Email: agathman@semo.edu

Seq primer: T7.

Location/Qualifiers

1..591

/organism="Coprinopsis cinerea"

/mol\_type="mRNA"

/strain="Dikaryon - strains backcrossed into Okayama7#130

thru 5 gens"

/db\_xref="taxon:5346"

/dev\_stage="Fruit body caps harvested six hours after

karyogamy (nuclear fusion)"

/lab\_host="E. coli DH10B"

/clone\_lib="Coprinus cinereus fruit body cap cDNAs in

meiotic prophase (K+6)"

/note="Vector: pAD-Gal 4-2.1; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 594;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match 78.2%; Score 17.2; DB 9; Length 591;  
Best Local Similarity 86.4%; Pred. No. 2.9e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCTC 22

Db 168 GAAAGACCTTCGTGGTGCTC 147

## RESULT 64

AI663484

LOCUS AI663484

DEFINITION

AI663484 594 bp mRNA linear EST 10-MAY-1999  
IMAGE:1970803 5', similar to gb.X17617 Mouse Zfp-35 mRNA for zinc  
finger protein ZFP-35 (MOUSE);, mRNA sequence.

ACCESSION AI663484

VERSION AI663484.1 GI:4767067

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS

Marta,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,

Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R.,

Ritter,B., Kohn,S., Shin,T., Jackson,f., Cardenas,M., McCann,R.,

Waterston,R. and Wilson.R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Other ESTs: uk33d10.x1

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

MGI:987543

Seq primer: custom primer used

High quality sequence stop: 515.

Location/Qualifiers

1..594

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL"

/db\_xref="taxon:10090"

/clone="IMAGE:1970803"

/sex="female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="Sugano mouse kidney mkia"

/note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII

(CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA

was primed with an oligo(dT) primer

[ATGGGCTTTTCTTTTCTTTTCTTTT]; double-stranded cDNA was

ligated to a DraIII adaptor [TGTGGCTTACTGG], digested

and cloned into distinct DraIII sites of the pME18S-FL3

vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should

be used to isolate the cDNA insert. Size selection was

performed to exclude fragments <1.5kb. Library

constructed by Dr. Sumio Sugano (University of Tokyo

Institute of Medical Science). Custom primers for

sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end

primer CGACCTGCAGTCGAGCACA."

## ORIGIN



```

QY 1 GAAAGGCTTTCGGGGTGCTC 22
    |||||
Db 543 GAAAGGCTTTCGGATGAGCTC 564

RESULT 65
BE534580
LOCUS BE534580 597 bp mRNA linear EST 09-AUG-2000
DEFINITION 601233510F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3597243 5',
mRNA sequence.
ACCESSION BE534580
VERSION BE534580.1 GI:9763134
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 597)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM8776 row: c column: 04
High quality sequence stop: 597.
Location/Qualifiers
FEATURES
source
1..597
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3597243"
/sex="female; virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Salt;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match 78.2%; Score 17.2; DB 7; Length 597;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
    |||||
Db 523 GAAAGGCTTTCGGATGAGCTC 544

RESULT 66
BG804780
LOCUS BG804780 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 0272-28 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
ACCESSION BG804780
VERSION BG804780.1 GI:17951704
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 600)
AUTHORS Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing
and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
PUBMED 11812828
COMMENT Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
Location/Qualifiers
FEATURES
source
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN
Query Match 78.2%; Score 17.2; DB 2; Length 600;
Best Local Similarity 86.4%; Pred. No. 2.9e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
    |||||
Db 515 GAAAGGCTTTCGGATGAGCTC 536

RESULT 67
CV562959
LOCUS CV562959 603 bp mRNA linear EST 22-OCT-2004
DEFINITION UI-M-FC0-ctx-g-16-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6734729 5', mRNA sequence.
ACCESSION CV562959
VERSION CV562959.1 GI:54454174
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 603)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
FEATURES
source
1..603
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_F00"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to

```



```

LOCUS      LBAF055F03      614 bp      DNA      linear      GSS 20-JUN-2003
DEFINITION Leishmania braziliensis GSS, clone LBAF055F03, genomic survey
sequence.
ACCESSION  BX542565
VERSION     BX542565.1   GI:32137791
KEYWORDS    GSS; genomic survey sequence.
SOURCE      Leishmania braziliensis
            Leishmania braziliensis
ORGANISM    Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
            Leishmania; Leishmania braziliensis species complex.
REFERENCE   1
AUTHORS     Laurentino E.C., Ruiz J.C. and Cruz A.K.
TITLE       GSS analysis of the Leishmania braziliensis genome
JOURNAL     Unpublished
REFERENCE   2   (bases 1 to 614)
AUTHORS     Cruz A.K.
TITLE       Direct Submission
JOURNAL     Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
            Department of Molecular and Cell Biology, FMRP, Avenida
            Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
COMMENT     Clone requests: akcruz@fmrp.usp.br.
FEATURES    Location/Qualifiers
            1..614
            /organism="Leishmania braziliensis"
            /mol_type="genomic DNA"
            /strain="MHOM/BR/75/M2904"
            /db_xref="taxon:5660"
            /clone="LBAF055F03"
ORIGIN
Query Match      78.2%; Score 17.2; DB 14; Length 614;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
        |||||
Db      27  GAAAGGCGCTTCGGGGGTGCTC 6

RESULT 71
CL864502
LOCUS      CL864502      622 bp      DNA      linear      GSS 19-AUG-2004
DEFINITION TM1-GSS000422r BAC and BIBAC libraries from upland cotton genetic
standard TM-1 Gossypium hirsutum genomic clone GH-TM1-CBV131B22 5',
genomic survey sequence.
ACCESSION  CL864502
VERSION     CL864502.1   GI:51321232
KEYWORDS    GSS.
SOURCE      Gossypium hirsutum (upland cotton)
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE   1   (bases 1 to 622)
AUTHORS     Xu Z., Kohel R.J., Zhang H.B., Dong J., Covalada L., Lee M., Koo P.,
            and Yu J.Z.
TITLE       Genome-Wide Synteny between Arabidopsis and Cotton
JOURNAL     Unpublished (2004)
COMMENT     Other GSSs: TM1-GSS000422f
            Contact: John Z. Yu
            Cotton Molecular Genetics Laboratory
            USDA-ARS Crop Germplasm Research Unit
            2765 F&B Road, Building 11, College Station, TX 77845. USA
            Tel: 979-260-9237
            Fax: 979-260-9333
            Email: zyu@qutun.tamu.edu
            for more detail, please see
            http://algonon.tamu.edu/htdocs-cotton/cottondb.html
            Seq primer: sp030
            Class: BAC ends
            High quality sequence stop: 622.
FEATURES    Location/Qualifiers
            1..622
source

```

```

/organism="Gossypium hirsutum"
/mol_type="genomic DNA"
/cultivar="TM-1"
/db_xref="taxon:3635"
/clone="GH-TM1-CBV131B22"
/tissue_type="young leaves"
/lab_host="DH10B"
/clone_lib="BAC and BIBAC libraries from upland cotton
genetic standard TM-1"
/notes="Vector: pCL04541; pBelOBAC11; For more details on
library construction, ordering clones and sequence
analysis see
http://algonon.tamu.edu/htdocs-cotton/cottondb.html"
ORIGIN
Query Match      78.2%; Score 17.2; DB 13; Length 622;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
        |||||
Db      25  GAAAGGCGCTTCGGGGGTGCTC 46

RESULT 72
CE758231
LOCUS      CE758231      632 bp      DNA      linear      GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000369688951 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION  CE758231
VERSION     CE758231.1   GI:37098850
KEYWORDS    GSS.
SOURCE      Canis familiaris (dog)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1   (bases 1 to 632)
AUTHORS     Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,
            Rusch D.B., Deicher A.L., Pop M., Wang W., Fraser C.M. and
            Venter J.C.
TITLE       The dog genome: survey sequencing and comparative analysis
JOURNAL     Science 301 (5641), 1898-1903 (2003)
COMMENT     Contact: Kirkness EF
            The Institute for Genomic Research
            Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
            Rockville, MD 20850, USA
            Tel: 301-838-0200
            Fax: 301-838-0208
            Email: ekirknes@tigr.org
            Class: shotgun.
FEATURES    Location/Qualifiers
            1..632
            /organism="Canis familiaris"
            /mol_type="genomic DNA"
            /strain="Standard Poodle"
            /db_xref="taxon:9615"
            /clone_lib="Dog Library"
            /notes="Site 1: BstXI; Libraries were prepared from
            peripheral blood"
ORIGIN
Query Match      78.2%; Score 17.2; DB 12; Length 632;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1  GAAAGGCGCTTCGGGGGTGCTC 22
        |||||
Db      371  GAAAGGCGCTTCGGGGGTGCTC 392

RESULT 73

```

CF902767 638 bp mRNA linear EST 04-NOV-2003  
 LOCUS A0345F09-5 NIA Mouse Trophoblast Stem Cell cDNA Library (long 1)  
 DEFINITION Mus musculus cDNA clone NIA:A0345F09 IMAGE:30737540 5', mRNA sequence.

ACCESSION CF902767  
 VERSION CF902767.1 GI:38169816  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
 1 (bases 1 to 638)  
 AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
 TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
 PUBMED 11544199  
 COMMENT Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgun.grc.nia.nih.gov  
 Plate: A0345 row: F column: 09  
 Seq primer: M13 Reverse  
 High quality sequence stop: 638  
 POLYA=No.

## FEATURES

## source

1. .638 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="B5/EGFP transgenic ICR mice"  
 /db\_xref="taeost:A0345F09-5"  
 /db\_xref="taxon:10090"  
 /clone="NIA:A0345F09 IMAGE:30737540"  
 /dev\_stage="3.5-dpc"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (long 1)"  
 /notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library [Ref. Genome Res. 11: 1553-1558 (2001). PMID: 11544199]. Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo (dT) primer (Invitrogen):  
 5'-pGACTAGTCTAGTCGCGAGCGCGCCCTTTT-3' from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 5; Length 638;  
 Best Local Similarity 86.4%; Pred. No. 3e+03;  
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCTC 22  
 |||||

## Db

516 GAAAGCCTTTCGGATGAGCTC 537

## RESULT 74

BB614371  
 LOCUS BB614371

## DEFINITION

BB614371 RIKEN full-length enriched, adult male testis Mus musculus cDNA clone 4921535F14 5', mRNA sequence.

## ACCESSION

BB614371  
 VERSION BB614371.1 GI:16454813

## KEYWORDS

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
 1 (bases 1 to 638)

## AUTHORS

Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished (2001)

## TITLE

JOURNAL Contact: Yoshihide Hayashizaki  
 COMMENT Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute

## COMMENT

The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yananaka, I., and Hayashizaki, Y.  
 Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
 e mouse tissues.

## FEATURES

## source

1. .638 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="CS7BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="4921535F14"  
 /sex="male"  
 /tissue\_type="testis"  
 /dev\_stage="adult"  
 /lab\_host="SOL3"  
 /clone\_lib="RIKEN full-length enriched, adult male testis"  
 /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',  
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',  
GAGAGAGAGCGCCGCAATTATCTCGAGTTAATAATATCCCGCCCC 3']. cDNA was cloned into the XhoI and BamHI sites."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 638;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GAAAGGCTTCGGGGTGCTC 22  
|||||  
Db 591 GAAAGGCTTCGGATGAGCTC 612

## RESULT 75

CX768159 638 bp mRNA linear EST 25-JAN-2005  
LOCUS UI-M-HUO-crfd-03-0-UI.r1 NIH\_BMAP\_HUO Mus musculus cDNA clone  
DEFINITION IMAGE:30680042 5', mRNA sequence.

ACCESSION CX768159

VERSION 1 GI:58178512

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 638)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1..638  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30680042"  
/tissue\_type="whole eye"  
/dev\_stage="newborn (1, 5, 15 days)"  
/lab\_host="DH10B (TI phage resistant)"  
/clone\_lib="NIH\_BMAP\_HUO"  
/notes="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AATAATTACG. This library was created for the University

## FEATURES

## source

## ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 638;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GAAAGGCTTCGGGGTGCTC 22  
|||||  
Db 52 GAAAGGCTTCGATGAGCTC 73

## RESULT 76

BH091738/c

LOCUS BH091738

DEFINITION RPCI-24-251H6.TV RPCI-24 Mus musculus genomic clone RPCI-24-251H6,  
genomic survey sequence.

ACCESSION BH091738

VERSION BH091738.1 GI:14911643

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 644)

Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,  
Tsengaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregorgis,E.,  
Russell,D., de Jong,P. and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-24

Unpublished (1999)

Other GSSs: RPCI-24-251H6.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: [szhao@tigr.org](mailto:szhao@tigr.org)

Clones are derived from the mouse BAC library RPCI-24. For BAC  
library availability, please contact Pieter de Jong  
([pdejong@mail.cho.org](mailto:pdejong@mail.cho.org)). Clones may be purchased from BACPAC  
Resources (<http://www.choi.org/bacpac/orderingframe.htm>). BAC end  
page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 251 row: H column: 6

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..644  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-24-251H6"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/clone\_lib="RPCI-24"  
/notes="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI;  
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
library was cloned in the pTARBAC1 cloning vector at the  
BamHI sites using MboI partially digested male C57BL/6J  
DNA."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 11; Length 644;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GAAAGGCTTCGGGGTGCTC 22  
|||||  
Db 54 GAAAGGCTTTGTGGTGCTC 33

RESULT 77 CD406831/c LOCUS DEFINITION	CD406831		652 bp	mRNA	linear	EST 07-JUN-2003
	Gm ck3178 Soybean induced by Salicylic Acid		Glycine max cDNA 3', mRNA sequence.			
	CD406831					
	CD406831.1		GI:31464818			
	EST.					
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Glycine max (soybean)					
	Glycine max					
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.					
	1 (bases 1 to 652)					
	Tian,A.G., Wang,J., Cui,P., Han,Y.J., Xu,H., Cong,L.J., Huang,X.G., Wang,X.L., Jiao,Y.Z., Wang,B.J., Wang,Y.J., Zhang,J.S. and Chen,S.Y.					
REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT	Characterization of soybean genomic features by analysis of its expressed sequence tags					
	Theor. Appl. Genet. 108 (5), 903-913 (2004)					
	14624337					
	Contact: Chen S-Y					
	Plant Biotechnology Laboratory Institute of Genetics and Developmental Biology, CAS, China Datun road, Beijing 100101, China Tel: 86-10-64886859 Fax: 86-10-64873428 Email: sychen@genetics.ac.cn Email: sychen@genetics.ac.cn Seq primer: T7 primer.					
FEATURES source	Location/Qualifiers					
	1. .652					
	/organism="Glycine max"					
	/mol_type="mRNA"					
	/cultivar="Kefeng 1"					
ORIGIN	/db_xref="taxon:3847"					
	/tissue_type="Seedlings"					
	/dev_stage="two-week seedlings"					
	/lab_host="XLI-Blue MRF, strain"					
	/clone_lib="Soybean induced by Salicylic Acid"					
ORIGIN	/note="Vector: pBluescript SK+; Site_1: EcoR I; Site_2: Xho I; The cDNA library was constructed by He, C-Y from mRNA isolated from two-week seedlings (cultivar Kefeng 1) treated by spraying 2.0mM salicylic acid for 24, 36, 48 and 72 h. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XLI-Blue MRF, host cells (Stratagene)."					
	78.2%; Score 17.2; DB 5; Length 652;					
	Query Match					
	Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;					
	Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;					
ORIGIN	QY 1 GAAAGGCTTTCGGGGTGCTC 22					
	Db 243 GAAAGGCTTTCGGGTGGTGCTC 222					
RESULT 78 CK976084/c LOCUS DEFINITION	CK976084		659 bp	mRNA	linear	EST 16-MAR-2004
	4107001 BARC 9BOV Bos taurus cDNA clone 9BOV33_C24 5', mRNA sequence.					
	CK976084					
	CK976084					
	CK976084.1		GI:45494058			
REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT						
KEYWORDS SOURCE ORGANISM	EST.					
	Bos taurus (cattle)					
	Bos taurus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.					
	1 (bases 1 to 659)					
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.					
	Production of EST from cDNA libraries derived from immunologically activated bovine gut					
	Unpublished (2004)					
	Contact: Tad S. Sonstegard					
	Bovine Functional Genomics Laboratory Animal and Natural Resources Institute Bd1g. 200 Rm2A BARC-East, Beltsville, MD 20705, USA Tel: 3015048416 Fax: 3015048414 Email: tads@anri.barc.usda.gov					
FEATURES source	Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt " -trim fasta. Vector identified by cross match using options -minmatch 12 -minscore 12 Plate: 33 row: C column: 24 Seq primer: CCCAGTCACGAGCTGTGTAACCG High quality sequence stop: 659.					
	Location/Qualifiers					
	1. .659					
	/organism="Bos taurus"					
	/mol_type="mRNA"					
ORIGIN	/strain="Holstein"					
	/db_xref="taxon:9913"					
	/clone="9BOV33_C24"					
	/sex="Male"					
	/tissue_type="Pooled"					
ORIGIN	/dev_stage="Multiple"					
	/lab_host="DH10B T1 phage resistant"					
	/clone_lib="BARC 9BOV"					
	/note="Organ: Abomasum; Vector: pAgen-1; Site_1: EcoRV; Site_2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasums of 18 and 21 week old steers. Exposure to Ostertagia ostertagi was initiated at 15 weeks of age. fundic and pyloric abomasum"					
	78.2%; Score 17.2; DB 8; Length 659;					
ORIGIN	Query Match					
	Best Local Similarity 86.4%; Pred. NO. 3e+03; Mismatches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;					
	QY 1 GAAAGGCTTTCGGGGTGCTC 22					
	Db 334 GAAGGACCTTTCGGGGATGCTC 313					
ORIGIN						
RESULT 79 BB619260/c LOCUS DEFINITION	BB619260		673 bp	mRNA	linear	EST 07-NOV-2005
	BB619260 RIKEN full-length enriched mouse cDNA library. C57BL/6J 8 days embryo Mus musculus cDNA clone 5730519C19 5', mRNA sequence.					
	BB619260					
	BB619260.1		GI:15396773			
	EST.					
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Mus musculus (house mouse)					
	Mus musculus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.					
	1 (bases 1 to 673)					
	The FANTOM Consortium and RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).					
REFERENCE AUTHORS TITLE JOURNAL PUBMED COMMENT	The transcriptional landscape of the mammalian genome					
	Science 309 (5740), 1559-1563 (2005)					
	16141072					
	Contact: Yoshihide Hayashizaki					

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute.  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>.

## FEATURES

source  
1. .673  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="5730519C19"  
/dev\_stage="8 days embryo"  
/clone\_lib="RIKEN full-length enriched mouse cDNA library,  
C57BL/6J 8 days embryo"

## ORIGIN

Query Match 78.2%; Score 17.2; DB 7; Length 673;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGTGCTC 22

Db 597 GAAAGGCGCTTTCGGGGTGCTC 576

## RESULT 80

CO426515  
LOCUS  
DEFINITION  
UI-M-HU0-crg-i-05-0-UI.r1 NIH BMAP\_HU0 Mus musculus cDNA clone  
IMAGE:30682084 5', mRNA sequence.

ACCESSION  
CO426515

VERSION  
CO426515.1

KEYWORDS  
EST.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 673)

REFERENCE  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This genome was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pyX-5.

Location/Qualifiers

## FEATURES

source  
1. .673  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30682084"  
/tissue\_type="whole eye"  
/dev\_stage="newborn (1, 5, 15 days )"  
/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH BMAP\_HU0"  
/note="Organ: Eye; Vector: pyX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according  
Bonaïdo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pyX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is AATAATTACG. This library was created for the University  
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

## ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 673;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGTGCTC 22

Db 237 GAAAGGCGCTTTCGGATGAGCTC 258

## RESULT 81

CO426515

LOCUS

DEFINITION

CI252013 Oryza sativa (japonica cultivar-group) Panicles mixture of  
one, two, three weeks after flowering and supermix Oryza sativa  
(japonica cultivar-group) cDNA clone 044-M012R-G09 3', mRNA  
sequence.

ACCESSION  
CI252013

VERSION  
CI252013.1

KEYWORDS  
EST.

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP

clade; Ehrhartoideae; Oryzoae; Oryza.

1 (bases 1 to 674)

REFERENCE  
Kikuchi, S.

Collection and mapping of over 30,000 transcription units by the

rice full-length cDNA project from japonica rice

Unpublished (2006)

CONTACT: Shoshi Kikuchi

Department of Molecular Genetics, Head of Laboratory of Gene

Expression

National Institute of Agrobiological Sciences

2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan

Tel: 81-29-838-7007

Fax: 81-29-838-7007

Email: [skikuchi@nias.affrc.go.jp](mailto:skikuchi@nias.affrc.go.jp)

This EST clone is one of 780k ESTs of Rice full length cDNA Project

URL: <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K.,

Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,

Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,

Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,

Yamanoto, M. and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,

Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,

Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center

and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

```
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saichoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
Location/Qualifiers
1..674
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="044-M012R-C09"
/tissue_type="Panicles mixture of one, two, three weeks
after flowering and supermix"
/clone_lib="Oryza sativa (japonica cultivar-group)
Panicles mixture of one, two, three weeks after flowering
and supermix"

ORIGIN
Query Match 78.2%; Score 17.2; DB 5; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
|||||
Db 503 GAAAGGCATCGGGGGTGCTC 524

RESULT 82
CJ093902 674 bp mRNA linear EST 23-SEP-2005
LOCUS
DEFINITION
CJ093902 RIKEN full-length enriched mouse cDNA library, C57BL/6J
kidney 17 days embryo Mus musculus cDNA clone 1920142B03 5', mRNA
sequence.
ACCESSION
CJ093902.1 GI:76194172
VERSION
CJ093902
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 674)
The FANTOM Consortium and RIKEN Genome Exploration Research Group
and Genome Science Group (Genome Network Project Core Group).
The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072
COMMENT
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
Location/Qualifiers
1..674
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I920142B03"

FEATURES
source
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saichoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
/tissue_type="kidney"
/dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched mouse cDNA library,
C57BL/6J kidney 17 days embryo"

ORIGIN
Query Match 78.2%; Score 17.2; DB 5; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
|||||
Db 548 GAAAGGCCTTTCGGATGAGCTC 569

RESULT 83
DR749476 674 bp mRNA linear EST 19-JUL-2005
LOCUS
DEFINITION
DR749476 taurus cDNA clone BP250026B10D12 3', mRNA sequence.
ACCESSION
DR749476.1 GI:71034816
VERSION
DR749476
KEYWORDS
EST.
SOURCE
Bos taurus (cattle)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 674)
Kumar,C.G., Larson,J.H., Band,M.R. and Lewin,H.A.
Unpublished (Kumar,C.G., Larson,J.H., Band,M.R. and Lewin,H.A.)
JOURNAL
Unpublished (2005)
COMMENT
Contact: Lewin HA
Department of Animal Sciences
University of Illinois at Urbana-Champaign
206 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Base Calling/Quality Scores using PHRED from Washington University
Genome Center. Vector Trimming using Cross_match from Washington
University Genome Center PHRAP suite. This sequence is vector-free
and at least 200 bp in length.
PCR Primers
BACKWARD: TCACACAGGAAACAGCTATGAC
Plate: BP250026B10 row: D column: 12
Seq primer: dt(18)N
High quality sequence stop: 674.
Location/Qualifiers
1..674
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="BP250026B10D12"
/dev_stage="near-term"
/clone_lib="NG01 rearrayed Soares normalized bovine
placenta"
/note="Organ: placenta"

ORIGIN
Query Match 78.2%; Score 17.2; DB 10; Length 674;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCTC 22
|||||
Db 393 GAAGGACCTTTCGGGATGCTC 414

RESULT 84
BU654491/c 682 bp mRNA linear EST 30-SEP-2002
LOCUS
```



```

DEFINITION 1112113H11.Y1 C. reinhardtii CC-1690 (mt+), CC-1691 (mt-), Gamete
(normalized), Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA
sequence.
ACCESSION BU654491
VERSION BU654491.1 GI:23366672
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1 (bases 1 to 682)
AUTHORS Grossman,A., Chang,C.-W., Davies,J., Harris,E., Hauser,C.,
Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1112
JOURNAL Unpublished (2002)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
FEATURES
source
1..682
Location/Qualifiers
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="21gr (CC-1690 wild type mt+) & 6145c (CC-1691
wild type mt-)"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690 (mt+), CC-1691 (mt-),
Gamete (normalized), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; Gamete library was constructed by Hui Zhao, Min Lu,
Jeffrey McDermott, William J. Snell and John Davies.
Strain 21gr cells (CC-1690; mating type plus) and strain
6145c cells (CC-1691; mating type minus) that had been
growing on a light-dark cycle (13:11 L/D) in R-medium
(Sager and Granick) were separately transferred into
nitrogen-free medium at 8 hours into the light period.
PolyA mRNA was purified from each sample every 2 hours for
the next 18 hours. The mRNA was pooled and used for cDNA
synthesis. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda Zap clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaldo et al., (1996) Genome
Research 6: 791-806."
ORIGIN
Query Match 78.2%; Score 17.2; DB 3; Length 682;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGGTGCTC 22
|||||
DB 204 GAAAGCCGTAGGGGATGCTC 183

RESULT 85
AM029523/c
LOCUS AM029523 692 bp mRNA linear EST 30-JUN-2005
DEFINITION AM029523 KN-252-lymph, Bos indicus Bos indicus cDNA clone
C0007396117 5', mRNA sequence.
ACCESSION AM029523
VERSION AM029523.1 GI:68428974
KEYWORDS EST.
SOURCE Bos indicus (Bos taurus indicus)
ORGANISM Bos indicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

```

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Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 692)
AUTHORS Anderson,S.I., Taylor,R., Talbot,R., Speed,D., Law,A.S.,
Humphray,S., Hanotte,O., Mwakaya,J. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying host responses
to trypanosome infection in cattle
JOURNAL Unpublished (2005)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM.
FEATURES
source
1..692
Location/Qualifiers
/organism="Bos indicus"
/mol_type="mRNA"
/db_xref="taxon:9915"
/clone="C0007396117"
/tissue_type="lymph node"
/clone_lib="KN-252-lymph, Bos indicus"
/note="breed: Boran"
ORIGIN
Query Match 78.2%; Score 17.2; DB 1; Length 692;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGGTGCTC 22
|||||
DB 275 GAAAGACCTTCGGGGATGCTC 254

RESULT 86
CE717742/c
LOCUS CE717742 692 bp DNA linear GSS 29-SEP-2003
DEFINITION tigr-gss-dog-17000314584495 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE717742
VERSION CE717742.1 GI:37037180
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 692)
AUTHORS Kirkness,E.F., Bafna V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source
1..692
Location/Qualifiers
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
ORIGIN
Query Match 78.2%; Score 17.2; DB 12; Length 692;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
128 GAAAGGCGCTTCGGGGTGCTC 107

RESULT 87  
DT891101/c  
LOCUS 700 bp mRNA linear EST 19-SEP-2005  
DEFINITION 1472214 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION DT891101  
VERSION DT891101.1 GI:75871508  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 700)  
Smith,T.P.L., Roberts,A.J., Ehternkamp,S.E., Chitko-McKown,C.G., Wray,J.B. and Keele,J.W.  
A second set of bovine ESTs from pooled-tissue normalized libraries  
Unpublished (2003)  
JOURNAL Contact: Smith TPL  
COMMENT USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.  
Plate: QOP8030 row: B column: 10  
Seq primer: GTAATACGACTCACTATAGG.  
Location/Qualifiers  
1..700  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 7BOV"  
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

Query Match 78.2%; Score 17.2; DB 10; Length 700;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 509 GAAGGACCTTCGGGGTGCTC 488  
|||||

RESULT 88  
AM030124  
LOCUS 745 bp mRNA linear EST 30-JUN-2005  
DEFINITION AM030124 KN-252-lymph, Bos indicus Bos indicus cDNA clone  
C0007396117 3', mRNA sequence.  
ACCESSION AM030124  
VERSION AM030124.1 GI:68429633  
KEYWORDS EST.  
SOURCE Bos indicus (Bos taurus indicus)  
ORGANISM Bos indicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 745)  
Anderson,S.I., Taylor,R., Talbot,R., Speed,D., Law,A.S., Humphray,S.I., Hanotte,O., Mwakaya,J. and Archibald,A.I.

Query Match 78.2%; Score 17.2; DB 10; Length 745;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 509 GAAGGACCTTCGGGGTGCTC 488  
|||||

RESULT 89  
BX326765/c  
LOCUS 749 bp mRNA linear EST 07-APR-2004  
DEFINITION BX326765 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CSODB004YA15 5-PRIME, mRNA sequence.  
ACCESSION BX326765  
VERSION BX326765.2 GI:46273446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL On May 2, 2003 this sequence version replaced gi:30338575.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10138.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0BAE007ZF01\_AE00583\_2&c=10138.

Query Match 78.2%; Score 17.2; DB 10; Length 749;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 471 GAAGGACCTTCGGGGTGCTC 492  
|||||

RESULT 89  
BX326765/c  
LOCUS 749 bp mRNA linear EST 07-APR-2004  
DEFINITION BX326765 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CSODB004YA15 5-PRIME, mRNA sequence.  
ACCESSION BX326765  
VERSION BX326765.2 GI:46273446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL On May 2, 2003 this sequence version replaced gi:30338575.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10138.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0BAE007ZF01\_AE00583\_2&c=10138.

Query Match 78.2%; Score 17.2; DB 10; Length 749;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 471 GAAGGACCTTCGGGGTGCTC 492  
|||||

RESULT 89  
BX326765/c  
LOCUS 749 bp mRNA linear EST 07-APR-2004  
DEFINITION BX326765 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CSODB004YA15 5-PRIME, mRNA sequence.  
ACCESSION BX326765  
VERSION BX326765.2 GI:46273446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL On May 2, 2003 this sequence version replaced gi:30338575.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10138.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0BAE007ZF01\_AE00583\_2&c=10138.

Query Match 78.2%; Score 17.2; DB 10; Length 749;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 471 GAAGGACCTTCGGGGTGCTC 492  
|||||

RESULT 89  
BX326765/c  
LOCUS 749 bp mRNA linear EST 07-APR-2004  
DEFINITION BX326765 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CSODB004YA15 5-PRIME, mRNA sequence.  
ACCESSION BX326765  
VERSION BX326765.2 GI:46273446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL On May 2, 2003 this sequence version replaced gi:30338575.  
COMMENT Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10138.r  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0BAE007ZF01\_AE00583\_2&c=10138.

Query Match 78.2%; Score 17.2; DB 10; Length 749;  
Best Local Similarity 86.4%; Pred. No. 3e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGTGCTC 22  
|||||  
Db 471 GAAGGACCTTCGGGGTGCTC 492  
|||||

RESULT 89  
BX326765/c  
LOCUS 749 bp mRNA linear EST 07-APR-2004  
DEFINITION BX326765 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens cDNA clone CSODB004YA15 5-PRIME, mRNA sequence.  
ACCESSION BX326765  
VERSION BX326765.2 GI:46273446  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL On May 2, 2003 this sequence version replaced gi:30338575.  
COMMENT Contact: Gen

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Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||
Db 734 GAAAGGACTTTCGGGGGTGCTC 713

RESULT 90
DT889744 749 bp mRNA linear EST 19-SEP-2005
LOCUS 1470678 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DT889744
ACCESSION DT889744
VERSION DT889744.1 GI:75870151
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 749)
AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: QOP8030 row: B column: 10
Seq primer: TAGAAGCAGATCGAGG.
Location/Qualifiers
1..749
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"
/notes="Vector; pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Query Match 78.2%; Score 17.2; DB 10; Length 749;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCGCTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||
Db 386 GAAGGACCTTCGGGGGTGCTC 407

RESULT 91
BP766344 756 bp mRNA linear EST 02-DEC-2004
LOCUS BP766344 mouse (C57BL/6) pancreatic islet library with
DEFINITION BP766344
ACCESSION BP766344.1 GI:50225042
VERSION BP766344
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 756)
AUTHORS Nishimura, M., Yokoi, N., Miki, T., Horikawa, Y., Yoshioka, H.,
Takeda, J., Ohara, O. and Seino, S.
TITLE Construction of a multi-functional cDNA library specific for mouse
pancreatic islets and its application to microarray
JOURNAL DNA Res. 11 (5), 315-323 (2004)
PUBMED 15747579
COMMENT Contact: Susumu Seino
Division of Cellular and Molecular Medicine
Kobe University Graduate School of Medicine
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan
Tel: 81-78-382-5360
Fax: 81-78-382-5370
Email: seino@med.kobe-u.ac.jp.
Location/Qualifiers
1..756
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="mid10071"
/sex="male"
/tissue_type="pancreatic islet"
/dev_stage="adult"
/clone_lib="mouse (C57BL/6) pancreatic islet library with
recombination-based method"

ORIGIN
Query Match 78.2%; Score 17.2; DB 3; Length 756;
Best Local Similarity 86.4%; Pred. No. 3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCGCTTCGGGGGTGCTC 22
||||| ||||| ||||| ||||| |||||
Db 577 GAAAGCGCTTCGGATGAGCTC 598

RESULT 92
DN542745/c 773 bp mRNA linear EST 11-MAR-2005
LOCUS DN542745
DEFINITION 1391525 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION DN542745
VERSION DN542745.1 GI:61001051
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 773)
AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: RLK8071 row: J column: 24
Seq primer: GTAATAGGACTCATTATAGGG.
Location/Qualifiers
1..773
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 7BOV"

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ORIGIN

/notes=Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including ovary, hindbrain, uterus, and day-30 whole  
embryos."

Query Match 78.2%; Score 17.2; DB 9; Length 773;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCTC 22  
||| | ||||| |||||  
Db 550 GAAGGACCTTTCGGGGTGCTC 529

RESULT 93  
DN541686  
LOCUS  
DEFINITION 777 bp mRNA linear EST 11-MAR-2005  
ACCESSION 1390293 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.  
VERSION DN541686  
KEYWORDS DN541686.1 GI:60998800  
SOURCE EST.  
ORGANISM Bos taurus (cattle)

REFERENCE  
AUTHORS Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 777)  
Smith, R.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G.,  
Wray, J.E., and Keele, J.W.  
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries  
JOURNAL Unpublished (2003)  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called with phred v0.020425.c and  
trimmed with the aid of the trim\_alt option. Vector identified with  
cross\_match v0.990329.  
Plate: RLK8071 row: J column: 24  
Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES  
source  
1..777  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 7BOV"  
/notes=Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including ovary, hindbrain, uterus, and day-30 whole  
embryos."

ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 777;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCTC 22  
||| | ||||| |||||  
Db 426 GAAGGACCTTTCGGGGTGCTC 447

RESULT 94  
CX887509/c  
LOCUS  
DEFINITION 780 bp mRNA linear EST 04-FEB-2005  
ACCESSION JGI CAAM1558.fwd NIH XGC tropTe3 Xenopus tropicalis cDNA clone  
IMAGE:7675903 5', mRNA sequence.  
VERSION CX887509.1 GI:58626853

KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

EST.  
Xenopus tropicalis (western clawed frog)  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 780)  
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,  
Brokstein, P., and Lindquist, E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
Other ESTs: JGI CAAM1558.rev  
Contact: Lindquist, E.A., Richardson, P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,  
University of California, Berkeley;  
http://tropicalis.berkeley.edu/home)  
CDNA Library Preparation: DOE Joint Genome Institute:  
http://www.jgi.doe.gov  
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
http://image.llnl.gov  
Naming Conventions: EST name is generated by the concatenation of  
the JGI Clone Id and the direction of sequencing. The suffix '.fwd'  
indicates a forward sequencing read of the insert. It does not  
necessarily reflect the orientation of the insert.  
Plate: CAAM 0017 row: k column: 5  
High quality sequence stop: 777.  
Location/Qualifiers  
1..780  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7675903"  
/sex="male"  
/tissue\_type="Testes"  
/dev\_stage="Adult"  
/lab\_host="NIH XGC tropTe3"  
/clone\_lib="NIH XGC tropTe3"  
/note=Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
This library was made from dt primed cDNA and cloned into  
Invitrogen pCMVSPORT6 vector. The work was done at DOE  
Joint Genome Institute. Poly A RNA were primed with 5'  
GACTAGTCTAGATCGCGAG CGGCCGCCCTTTTCTTTTCTTTT 3'. CDNA  
were ligated to SalI adapter (5' TCGACCCACGCGTCG and  
5'CGGACGCGTGG), digested with NotI, size fractionated in  
1.1% agarose gel electrophoresis and ligated into NotI and  
SalI digested pCMVSPORT6 vector."

FEATURES  
source

1..780  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7675903"  
/sex="male"  
/tissue\_type="Testes"  
/dev\_stage="Adult"  
/lab\_host="NIH XGC tropTe3"  
/clone\_lib="NIH XGC tropTe3"  
/note=Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
This library was made from dt primed cDNA and cloned into  
Invitrogen pCMVSPORT6 vector. The work was done at DOE  
Joint Genome Institute. Poly A RNA were primed with 5'  
GACTAGTCTAGATCGCGAG CGGCCGCCCTTTTCTTTTCTTTT 3'. CDNA  
were ligated to SalI adapter (5' TCGACCCACGCGTCG and  
5'CGGACGCGTGG), digested with NotI, size fractionated in  
1.1% agarose gel electrophoresis and ligated into NotI and  
SalI digested pCMVSPORT6 vector."

ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 780;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCTC 22  
||| | ||||| |||||  
Db 520 GGAAGCCTGTCTGGGGTGCCC 499

RESULT 95  
CX887508  
LOCUS

DEFINITION 785 bp mRNA linear EST 03-AUG-2005  
ACCESSION JGI CAAM1558.rev NIH XGC tropTe3 Xenopus tropicalis cDNA clone  
IMAGE:7675903 3', mRNA sequence.  
VERSION CX887508  
CX887508.2 GI:71788737  
KEYWORDS EST.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.

1 (bases 1 to 785)

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Brokstein, P., and Lindquist, E.A.

DOE Joint Genome Institute Xenopus tropicalis EST project

Unpublished (2004)

On Feb 4, 2005 this sequence version replaced gi:58626852.

Other ESTs: JGI CAAM1558.fwd

Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute

2800 Mitchell Drive, Walnut Creek, CA 94598, USA

Tel: 925 296 5600

Fax: 925 296 5710

Email: cdna@jgi-psf.org

Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley:

http://tropicalis.berkeley.edu/home)

cDNA Library Preparation: DOE Joint Genome Institute:

http://www.jgi.doe.gov

DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.E. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

Plate: CAAM 0017 row: k column: 5

High quality sequence stop: 691

POLYA=Yes.

#### FEATURES

source

1. .785  
Location/Qualifiers  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7675903"  
/sex="male"  
/tissue\_type="Testes"  
/dev\_stage="Adult"  
/lab\_host="ElectroMAX DH10B"  
/clone\_lib="NIH\_XGC\_crypt3"  
/notes="vector: pCMVSPORT6; Site:1: SalI; Site:2: NotI;  
This library was made from dt primed cDNA and cloned into  
Invitrogen pCMVSPORT6 vector. The work was done at DOE  
Joint Genome Institute. Poly A RNA were primed with 5'  
GACTACTTCTAGATCGGAG CGCGCGCCCTTTTCTTTT 3'. cDNA  
were ligated to SalI adapter (5' TCGACCCACCGGCGG and  
5' CGGACCGTGGG), digested with NotI, size fractionated in  
1.1% agarose gel electrophoresis and ligated into NotI and  
SalI digested pCMVSPORT6 vector."

#### ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 785;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCCGGGGTGCTC 22  
Db 493 GGAAGGCTGTCCGGGGTGCC 514

#### RESULT 96

DN524756  
LOCUS 800 bp mRNA linear EST 11-MAR-2005  
DEFINITION 1268443 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.  
ACCESSION DN524756  
VERSION DN524756.1 GI:60969064  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

#### REFERENCE

AUTHORS

#### TITLE

JOURNAL

COMMENT

Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 800)

Smith, T.P.L., Roberts, A.J., Echterkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.

Plate: RLK8048 row: A column: 22

Seq primer: TAGAAGGCACAGTCGAGG.

#### FEATURES

source

1. .800  
Location/Qualifiers  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 7BOV"  
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
Library made with RNA pooled from multiple tissues  
including ovary, hindbrain, uterus, and day-30 whole  
embryos."

#### ORIGIN

Query Match 78.2%; Score 17.2; DB 9; Length 800;  
Best Local Similarity 86.4%; Pred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCCGGGGTGCTC 22  
Db 428 GAAGGACCTTCGGGGATGCTC 449

#### RESULT 97

LOCUS

CA315865

DEFINITION

CA315865 806 bp mRNA linear EST 09-JUL-2003  
UI-M-FWO-cbo-e-01-0-UI.r1 NIH\_BMAP\_FWO Mus musculus cDNA clone  
IMAGE:6812234 5', mRNA sequence.

ACCESSION

CA315865

VERSION

CA315865.1 GI:24533989

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 806)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov

#### REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

#### FEATURES

source

1. .806  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"

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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6812234"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/notes="Organ: Brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGGAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
```

ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 806;  
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22  
|||||  
Db 138 GAAAGGCTTTTCGGATGAGCTC 159

RESULT 98  
BP434131/c

LOCUS BP434131 full-length enriched swine cDNA library, adult lung Sus  
DEFINITION scrofa cDNA clone LNG010001B03 5', mRNA sequence.  
ACCESSION BP434131 GI:40424198  
VERSION BP434131  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 829)  
Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H., Okumura,N., Hanasima,N. and Awata,T.  
PEDE (Pig EST Data Explorer): construction of a database for ESTs derived from porcine full-length cDNA libraries  
Nucleic Acids Res. 32 (1), D484-D488 (2004)

JOURNAL PUBLISHED 14681463

COMMENT Contact: Hirohide Uenishi  
Animal Genome Laboratory, Genome Research Department  
National Institute of Agrobiological Sciences  
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan  
Tel: +81-29-838-8627  
Fax: +81-29-838-8627  
Email: huenishi@affrc.go.jp  
EST project with full-length enriched cDNA libraries carried out in Animal Genome Research Program (Japan) by National Institute of Agrobiological Sciences and STAFF-Institute  
Single pass sequencing of clones derived from oligo-capped cDNA library  
Vector sequences were eliminated by RepeatMasker version 2002/07/13 and crossmatch version 0.990319  
Low quality bases were trimmed based on the quality values.

FEATURES  
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Location/Qualifiers  
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/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"

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/clone="LNG010001B03"  
/tissue_type="lung"  
/dev_stage="adult"  
/clone_lib="full-length enriched swine cDNA library, adult lung"
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ORIGIN

Query Match 78.2%; Score 17.2; DB 3; Length 829;  
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22  
|||||  
Db 304 GAAAGGCTTTTCAGGGTGCTC 283

RESULT 99  
BZ654405/c

LOCUS BZ654405 848 bp DNA linear GSS 29-JAN-2003  
DEFINITION OGCG587C ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBwa013919, genomic survey sequence.  
ACCESSION BZ654405  
VERSION BZ654405.1 GI:28123665  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 848)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGCG587M  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF  
Class: methylation filtered.  
Location/Qualifiers  
1..848  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBwa013919"  
/clone\_lib="ZM\_0.7\_1.5\_KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

Query Match 78.2%; Score 17.2; DB 12; Length 848;  
Best Local Similarity 86.4%; Pred. No. 3e+03; 3; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGTGCTC 22  
|||||  
Db 210 GAGAGGCTTTTCGGGGTGCTC 189

RESULT 100  
CV069365/c

LOCUS CV069365 849 bp mRNA linear EST 24-AUG-2004  
DEFINITION WPAshux1516F2\_B01\_430068T7\_A1.001.ab1 Preamplified custom cDNA library in pCMVSPORT6.1 (ResGen, Invitrogen Inc.) Emilia huxleyi cDNA, mRNA sequence.  
ACCESSION CV069365  
VERSION CV069365.1 GI:51532529

KEYWORDS EST.  
SOURCE Emiliana huxleyi  
ORGANISM Emiliana huxleyi  
REFERENCE Eukaryota; Haptophyceae; Isochrysidales; Emiliana.  
1 (bases 1 to 849)  
AUTHORS Wahlund, F.W., Zhang, X. and Read, B.A.  
TITLE Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying  
Cultures of Emiliana huxleyi  
JOURNAL Micropaleontology (2004) In press  
COMMENT Contact: Betsy Read  
Department of Biological Sciences  
California State University San Marcos  
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA  
Tel: 760 750 4129  
Email: bread@csusm.edu.

FEATURES  
source  
1..849 Location/Qualifiers  
/organism="Emiliana huxleyi"  
/mol\_type="mRNA"  
/strain="1516"  
/db\_xref="taxon:2903"  
/dev\_stage="Late log growth phase"  
/clone\_lib="Preamplified custom cDNA library in  
pcwvspor6.1 (ResGen, Invitrogen Inc.)"  
/note="Emiliana huxleyi grown in Artificial Seawater  
(Guillard's F/2 media)."

ORIGIN  
Query Match 78.2%; Score 17.2; DB 8; Length 849;  
Best Local Similarity 86.4%; Fred. No. 3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GAAAGGCCTTTTCGGGGTGCTC 22  
||| ||||| ||||| |||||  
Db 609 GAATGGCCTTCGAGGGGCTC 588

Search completed: May 19, 2006, 07:06:39  
Job time : 1492.35 secs

**This Page Blank (uspto)**



GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 67.3253 Seconds  
(without alignments)  
611.425 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22

Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents NA:\*

- 1: /EMC Celerra\_SIDS3/ptodata/2/ina/1 COMB.seq.\*
- 2: /EMC Celerra\_SIDS3/ptodata/2/ina/5 COMB.seq.\*
- 3: /EMC Celerra\_SIDS3/ptodata/2/ina/6A COMB.seq.\*
- 4: /EMC Celerra\_SIDS3/ptodata/2/ina/6B COMB.seq.\*
- 5: /EMC Celerra\_SIDS3/ptodata/2/ina/7 COMB.seq.\*
- 6: /EMC Celerra\_SIDS3/ptodata/2/ina/H COMB.seq.\*
- 7: /EMC Celerra\_SIDS3/ptodata/2/ina/PTUS COMB.seq.\*
- 8: /EMC Celerra\_SIDS3/ptodata/2/ina/PP COMB.seq.\*
- 9: /EMC Celerra\_SIDS3/ptodata/2/ina/RE COMB.seq.\*
- 10: /EMC Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	ID	Description
1	22	100.0	22	US-09-738-274-25
2	22	100.0	25	US-09-738-274-26
3	17.8	80.9	513	US-09-270-767-8270
4	17.8	80.9	513	US-09-270-767-23552
5	17.4	79.1	4637	US-09-221-017B-818
6	16.8	76.4	276	US-09-252-991A-15626
7	16.2	73.6	601	US-09-949-016-194496
8	16.2	73.6	601	US-09-949-016-194497
9	16.2	73.6	601	US-09-949-016-195241
10	16.2	73.6	771	US-09-252-991A-1476
11	16.2	73.6	828	US-09-252-991A-1701
12	16.2	73.6	909	US-09-573-080A-342
13	16.2	73.6	909	US-09-854-867-342
14	16.2	73.6	1239	US-09-252-991A-1603
15	16.2	73.6	8411	US-09-976-594-560
16	16.2	73.6	8412	US-09-919-039-223
17	16.2	73.6	28378	US-09-949-016-17281
18	16.2	73.6	119032	US-09-949-016-12160
19	16.2	73.6	119032	US-09-949-016-17268
20	16.2	73.6	4403765	US-09-103-840A-2
21	16.2	73.6	4411529	US-09-103-840A-1
22	15.8	71.8	579	US-09-328-352-161
23	15.8	71.8	601	US-09-949-016-54878

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479	70.9	15.6	3	US-09-471-276-779	Sequence 779, App
601	70.9	15.6	3	US-09-949-016-47594	Sequence 47594, A
601	70.9	15.6	3	US-09-949-016-83107	Sequence 83107, A
601	70.9	15.6	3	US-09-949-016-107747	Sequence 107747, A
601	70.9	15.6	3	US-09-949-016-107748	Sequence 107748, A
601	70.9	15.6	3	US-09-949-016-146881	Sequence 146881, A
601	70.9	15.6	3	US-09-949-016-166269	Sequence 166269, A
893	70.9	15.6	3	US-09-247-155-44	Sequence 44, Appl
893	70.9	15.6	3	US-09-903-190-44	Sequence 44, Appl
1098	70.9	15.6	3	US-09-748-264A-1	Sequence 1, Appli
1247	70.9	15.6	3	US-08-647-960-1	Sequence 1, Appli
1410	70.9	15.6	5	US-09-974-300-666	Sequence 666, App
1429	70.9	15.6	3	US-09-023-655-689	Sequence 689, App
1449	70.9	15.6	3	US-09-489-039A-2738	Sequence 2738, Ap
1746	70.9	15.6	3	US-09-422-936-58	Sequence 58, Appl
1862	70.9	15.6	3	US-10-104-047-900	Sequence 900, App
1990	70.9	15.6	3	US-09-016-434-1056	Sequence 1056, Ap
2297	70.9	15.6	4	US-10-094-749-421	Sequence 421, App
2895	70.9	15.6	3	US-09-422-936-52	Sequence 52, Appl
3995	70.9	15.6	3	US-09-917-254-18	Sequence 18, Appl
3995	70.9	15.6	3	US-09-919-497-9	Sequence 9, Appli
20076	70.9	15.6	3	US-09-949-016-13141	Sequence 13141, A
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37059	70.9	15.6	3	US-09-949-016-15865	Sequence 15865, A
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234884	70.9	15.6	3	US-09-949-016-16420	Sequence 16420, A
390890	70.9	15.6	3	US-09-949-016-14720	Sequence 14720, A
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668	70.0	15.4	3	US-09-533-559-4582	Sequence 4582, Ap
14438	70.0	15.4	3	US-09-949-016-12300	Sequence 12300, A
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600	69.1	15.2	3	US-09-370-838-264	Sequence 264, App
600	69.1	15.2	3	US-09-854-133-264	Sequence 264, App
601	69.1	15.2	3	US-09-949-016-76799	Sequence 76799, A
833	69.1	15.2	2	US-08-343-443B-97	Sequence 97, Appl
931	69.1	15.2	3	US-09-902-540-4292	Sequence 4292, Ap
1185	69.1	15.2	3	US-09-252-991A-7914	Sequence 7914, Ap
1320	69.1	15.2	3	US-09-248-796A-1866	Sequence 1866, Ap
1347	69.1	15.2	3	US-09-252-991A-7842	Sequence 7842, Ap
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1738	69.1	15.2	4	US-10-056-790-35	Sequence 35, Appl
1794	69.1	15.2	3	US-08-920-270-1	Sequence 1, Appli
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1794	69.1	15.2	5	US-10-229-346-10	Sequence 10, Appl
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1803	69.1	15.2	5	US-10-229-346-3	Sequence 3, Appli
1807	69.1	15.2	5	US-10-229-346-8	Sequence 8, Appli
1813	69.1	15.2	5	US-10-229-346-16	Sequence 16, Appl
1816	69.1	15.2	5	US-10-229-346-14	Sequence 14, Appl
1818	69.1	15.2	5	US-10-229-346-10	Sequence 10, Appl
1819	69.1	15.2	5	US-10-229-346-18	Sequence 18, Appl
1830	69.1	15.2	4	US-10-094-749-1246	Sequence 1246, Ap
1957	69.1	15.2	2	US-08-295-060-3	Sequence 3, Appli
2198	69.1	15.2	3	US-09-774-528-10	Sequence 10, Appl
2198	69.1	15.2	3	US-10-120-988-10	Sequence 10, Appl
2198	69.1	15.2	3	US-09-252-991A-7718	Sequence 7718, Ap
2256	69.1	15.2	3	US-09-774-528-11	Sequence 11, Appl
2256	69.1	15.2	3	US-10-120-988-11	Sequence 11, Appl
2426	69.1	15.2	3	US-09-028-327-2	Sequence 2, Appli
2426	69.1	15.2	3	US-09-571-078A-2	Sequence 2, Appli
2453	69.1	15.2	3	US-09-949-016-2230	Sequence 2230, Ap
2511	69.1	15.2	3	US-09-489-039A-530	Sequence 444, App
2742	69.1	15.2	3	US-09-008-697A-13	Sequence 13, Appl
2770	69.1	15.2	3	US-09-949-016-5461	Sequence 5461, Ap
3124	69.1	15.2	3	US-09-865-879-6	Sequence 6, Appli
3271	69.1	15.2	3	US-09-949-016-4008	Sequence 4008, Ap
4522	69.1	15.2	3	US-09-949-016-13972	Sequence 13972, A
6454	69.1	15.2	3	US-10-229-346-5	Sequence 5, Appli
7208	69.1	15.2	5	US-09-949-016-14771	Sequence 14771, A
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13438	69.1	15.2	3		

C 97	15.2	69.1	16287	3	US-09-949-016-17203	Sequence 17203, A	170	14.6	66.4	251	4	US-09-297-648-351	Sequence 351, App
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C 99	15.2	69.1	20444	3	US-09-949-016-15750	Sequence 15750, A	C 172	14.6	66.4	260	4	US-09-297-648-460	Sequence 460, App
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C 101	15.2	69.1	30569	3	US-09-949-016-12592	Sequence 12592, A	C 174	14.6	66.4	565	5	US-09-974-300-6342	Sequence 6342, App
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C 104	15.2	69.1	35784	3	US-09-949-016-16785	Sequence 16785, A	C 177	14.6	66.4	601	3	US-09-949-016-40575	Sequence 40575, A
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C 106	15.2	69.1	35881	3	US-08-311-731A-127	Sequence 127, App	C 179	14.6	66.4	601	3	US-09-949-016-40577	Sequence 40577, A
C 107	15.2	69.1	45587	3	US-09-949-016-15836	Sequence 15836, A	C 180	14.6	66.4	601	3	US-09-949-016-40578	Sequence 40578, A
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C 109	15.2	69.1	59076	3	US-09-949-016-15097	Sequence 15097, A	C 182	14.6	66.4	601	3	US-09-949-016-95005	Sequence 95005, A
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C 112	15.2	69.1	176006	3	US-09-949-016-16804	Sequence 16804, A	C 185	14.6	66.4	601	3	US-09-949-016-95118	Sequence 95118, A
C 113	15.2	69.1	253375	3	US-09-949-016-12849	Sequence 12849, A	C 186	14.6	66.4	601	3	US-09-949-016-117439	Sequence 117439, A
C 114	15	68.2	601	3	US-09-949-016-67429	Sequence 67429, A	C 187	14.6	66.4	601	3	US-09-949-016-117440	Sequence 117440, A
C 115	15	68.2	601	3	US-09-949-016-67429	Sequence 67429, A	C 188	14.6	66.4	601	3	US-09-949-016-117441	Sequence 117441, A
C 116	15	68.2	601	3	US-09-949-016-67569	Sequence 67569, A	C 189	14.6	66.4	601	3	US-09-949-016-131855	Sequence 131855, A
C 117	15	68.2	49931	3	US-09-949-016-13727	Sequence 13727, A	C 190	14.6	66.4	601	3	US-09-949-016-175826	Sequence 175826, A
C 118	15	68.2	49931	3	US-09-949-016-13728	Sequence 13728, A	C 191	14.6	66.4	601	3	US-09-949-016-175827	Sequence 175827, A
C 119	15	68.2	49931	3	US-09-949-016-13729	Sequence 13729, A	C 192	14.6	66.4	601	3	US-09-949-016-175828	Sequence 175828, A
C 120	14.8	67.3	409	3	US-09-513-999C-30157	Sequence 30157, A	C 193	14.6	66.4	601	3	US-09-949-016-177762	Sequence 177762, A
C 121	14.8	67.3	601	3	US-09-949-016-39725	Sequence 39725, A	C 194	14.6	66.4	601	3	US-09-949-016-181732	Sequence 181732, A
C 122	14.8	67.3	601	3	US-09-949-016-44240	Sequence 44240, A	C 195	14.6	66.4	601	3	US-09-949-016-181733	Sequence 181733, A
C 123	14.8	67.3	601	3	US-09-949-016-44241	Sequence 44241, A	C 196	14.6	66.4	601	3	US-09-949-016-181851	Sequence 181851, A
C 124	14.8	67.3	601	3	US-09-949-016-44242	Sequence 44242, A	C 197	14.6	66.4	601	3	US-09-949-016-181852	Sequence 181852, A
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C 126	14.8	67.3	601	3	US-09-949-016-70022	Sequence 70022, A	C 199	14.6	66.4	601	3	US-09-949-016-181971	Sequence 181971, A
C 127	14.8	67.3	601	3	US-09-949-016-177215	Sequence 177215, A	C 200	14.6	66.4	601	3	US-09-949-016-194577	Sequence 194577, A
C 128	14.8	67.3	636	4	US-09-605-703B-2657	Sequence 2657, App	C 201	14.6	66.4	601	3	US-09-949-016-194578	Sequence 194578, A
C 129	14.8	67.3	696	3	US-09-252-991A-13687	Sequence 13687, A	C 202	14.6	66.4	601	3	US-09-949-016-199356	Sequence 199356, A
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C 131	14.8	67.3	804	3	US-10-327-726-2	Sequence 2, Appli	C 204	14.6	66.4	721	3	US-09-533-559-5117	Sequence 5117, App
C 132	14.8	67.3	950	3	US-09-484-970B-31	Sequence 31, Appl	C 205	14.6	66.4	759	3	US-09-543-681A-2176	Sequence 2176, App
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C 134	14.8	67.3	1756	3	US-09-774-528-340	Sequence 340, App	C 207	14.6	66.4	979	4	US-09-297-648-2520	Sequence 2520, App
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C 136	14.8	67.3	1976	4	US-10-094-749-1455	Sequence 1465, App	C 209	14.6	66.4	1075	3	US-09-276-531-95	Sequence 95, Appli
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C 140	14.8	67.3	5391	3	US-08-811-519-2	Sequence 2, Appli	C 213	14.6	66.4	1458	3	US-09-252-991A-16310	Sequence 16310, A
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C 143	14.8	67.3	23673	3	US-09-773-816-1	Sequence 1, Appli	C 216	14.6	66.4	1558	3	US-09-311-021-79	Sequence 79, Appli
C 144	14.8	67.3	51049	3	US-09-949-016-15571	Sequence 15571, A	C 217	14.6	66.4	1599	3	US-09-252-991A-16536	Sequence 16536, A
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246	14.6	66.4	20513	3	US-09-949-016-13930	Sequence 13930, A
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260	14.6	66.4	87350	3	US-08-781-891-79	Sequence 79, A
261	14.6	66.4	87350	3	US-09-618-166-79	Sequence 79, A
262	14.6	66.4	87543	3	US-09-791-211-3	Sequence 3, A
263	14.6	66.4	91232	3	US-09-949-002-607	Sequence 607, A
264	14.6	66.4	94748	3	US-09-949-016-12648	Sequence 12648, A
265	14.6	66.4	94758	3	US-09-949-016-16741	Sequence 16741, A
266	14.6	66.4	114842	3	US-09-949-016-14993	Sequence 14993, A
267	14.6	66.4	123463	3	US-09-949-016-17078	Sequence 17078, A
268	14.6	66.4	126468	3	US-09-949-016-14418	Sequence 14418, A
269	14.6	66.4	131332	3	US-09-949-016-15535	Sequence 15535, A
270	14.6	66.4	131724	3	US-09-949-016-12893	Sequence 12893, A
271	14.6	66.4	146039	3	US-09-949-016-12449	Sequence 12449, A
272	14.6	66.4	152393	3	US-09-949-016-14514	Sequence 14514, A
273	14.6	66.4	152393	3	US-09-949-016-14515	Sequence 14515, A
274	14.6	66.4	156894	3	US-09-949-016-12765	Sequence 12765, A
275	14.6	66.4	156894	3	US-09-949-016-12766	Sequence 12766, A
276	14.6	66.4	156895	3	US-09-949-016-16957	Sequence 16957, A
277	14.6	66.4	156895	3	US-09-949-016-16958	Sequence 16958, A
278	14.6	66.4	156895	3	US-09-949-016-16959	Sequence 16959, A
279	14.6	66.4	162314	3	US-09-949-016-15578	Sequence 15578, A
280	14.6	66.4	185765	3	US-09-949-002-674	Sequence 674, A
281	14.6	66.4	185766	3	US-09-949-002-707	Sequence 707, A
282	14.6	66.4	194714	3	US-09-949-016-11869	Sequence 11869, A
283	14.6	66.4	227390	3	US-09-949-016-12201	Sequence 12201, A
284	14.6	66.4	227391	3	US-09-949-016-13365	Sequence 13365, A
285	14.6	66.4	228338	3	US-09-949-016-13506	Sequence 13506, A
286	14.6	66.4	343352	3	US-09-949-016-13498	Sequence 13498, A
287	14.6	66.4	611587	4	US-09-531-120-209	Sequence 209, A
288	14.6	66.4	767677	3	US-09-949-016-12147	Sequence 12147, A
289	14.6	66.4	767677	3	US-09-949-016-17361	Sequence 17361, A
290	14.6	65.5	563	3	US-09-621-976-18507	Sequence 18507, A
291	14.4	65.5	601	3	US-09-949-016-20864	Sequence 20864, A
292	14.4	65.5	601	3	US-09-949-016-74209	Sequence 74209, A

```

; ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; ; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; ; FILE REFERENCE: GP107-02.UT
; ; CURRENT APPLICATION NUMBER: US/09/738,274
; ; CURRENT FILING DATE: 2000-12-15
; ; PRIOR APPLICATION NUMBER: 60/172,190
; ; PRIOR FILING DATE: 1999-12-17
; ; NUMBER OF SEQ ID NOS: 42
; ; SOFTWARE: PatentIn Ver. 2.0
; ; SEQ ID NO 25
; ; LENGTH: 22
; ; TYPE: DNA
; ; ORGANISM: Artificial Sequence
; ; FEATURE:
; ; OTHER INFORMATION: Description of Artificial Sequence: primer
; ; OTHER INFORMATION: oligonucleotide
; ; US-09-738-274-25

```

```

RESULT 2
US-09-738-274-26
; Sequence 26, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: Gp107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-26

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RESULT 1  
US-09-738-274-25  
; Sequence 25, Application US/09738274  
; Patent No. 6664081  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus I.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc

RESULT 3  
US-09-270-767-8270/c  
; Sequence 8270, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8270  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-8270

Query Match 80.9%; Score 17.8; DB 3; Length 513;  
Best Local Similarity 90.5%; Pred. No. 19;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 383 ACAGGCTTTCGGGTGGTCTC 363

RESULT 4  
US-09-270-767-23552/c  
; Sequence 23552, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23552  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-23552

Query Match 80.9%; Score 17.8; DB 3; Length 513;  
Best Local Similarity 90.5%; Pred. No. 19;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 383 ACAGGCTTTCGGGTGGTCTC 363

RESULT 5  
US-09-221-017B-818/c  
; Sequence 818, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: Pp1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: Pp1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA: Pp2911  
; APPLICATION NUMBER: Pp2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141

; INFORMATION FOR SEQ ID NO: 818:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4637 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORYPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: 1...4637  
US-09-221-017B-818

Query Match 79.1%; Score 17.4; DB 3; Length 4637;  
Best Local Similarity 94.7%; Pred. No. 44;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4588 GAAAGGCCTTTCGGGGTG 4570

RESULT 6  
US-09-252-991A-15626/c  
; Sequence 15626, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 15626  
; LENGTH: 276  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-15626

Query Match 76.4%; Score 16.8; DB 3; Length 276;  
Best Local Similarity 90.0%; Pred. No. 56;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCT 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 87 AAAGGCCTTTCGTAGTGCT 68

RESULT 7

```

/ TITLE OF INVENTION: AEROGELGROSA FOR DIAGNOSIS AND THERAPEUTICS
/
/ FILE REFERENCE: 107196.136
/
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/
/ CURRENT FILING DATE: 1999-02-18
/
/ PRIOR APPLICATION NUMBER: US 60/074,788
/
/ PRIOR FILING DATE: 1998-02-18
/
/ PRIOR APPLICATION NUMBER: US 60/094,190
/

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; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1701
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1701

Query Match      73.6%; Score 16.2; DB 3; Length 828;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
   ||| ||||| ||||| |||||
Db 226 GAAGGGCCTTTCGGCGTGCT 246

RESULT 12
US-09-573-080A-342
; Sequence 342, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a
; NAME/KEY: misc feature
; OTHER INFORMATION: n is a, c, g or t
; PUBLICATION INFORMATION:
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE:
; DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-342

Query Match      73.6%; Score 16.2; DB 3; Length 909;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
   ||| ||||| ||||| |||||
Db 762 GAGAGGCCTTTCGGGGTGCT 782

RESULT 13
US-09-854-867-342
; Sequence 342, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
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; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 342
; LENGTH: 909
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat region
; LOCATION: (1)..(909)
; OTHER INFORMATION: l1me3a
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (647)..(647)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (657)..(658)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (705)..(705)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-342

Query Match      73.6%; Score 16.2; DB 5; Length 909;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
   ||| ||||| ||||| |||||
Db 762 GAGAGGCCTTTCGGGGTGCT 782

RESULT 14
US-09-252-991A-1603
; Sequence 1603, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1603
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1603

Query Match      73.6%; Score 16.2; DB 3; Length 1239;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTCGGGGTGCT 21
   ||| ||||| ||||| |||||
Db 1155 GAAGGGCCTTTCGGCGTGCT 1175

RESULT 15
US-09-976-594-560
; Sequence 560, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
```

```

; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 560
; LENGTH: 8411
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1327024.5
; NAME/KEY: unsure
; LOCATION: 8361, 8372, 8381, 8388, 8398, 8405-8406
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-560

```

```

Query Match          73.6%; Score 16.2; DB 3; Length 8411;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 AAAGGCTTTTCGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      4595 AAATGCCTTTGGGGAGTGCTC 4615

```

```

RESULT 16
US-09-919-039-223
; Sequence 223, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 223
; LENGTH: 8412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 380283.1
; NAME/KEY: unsure
; LOCATION: 4053-4099, 8362, 8373, 8382, 8389, 8399, 8406-8407
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-223

```

```

Query Match          73.6%; Score 16.2; DB 3; Length 8412;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 AAAGGCTTTTCGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      4595 AAATGCCTTTGGGGAGTGCTC 4615

```

```

RESULT 17
US-09-949-016-17281
; Sequence 17281, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307

```

```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17281
; LENGTH: 28378
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17281

```

```

Query Match          73.6%; Score 16.2; DB 3; Length 28378;
Best Local Similarity 85.7%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 GAAAGGCTTTTCGGGGTGCT 21
      ||| ||||| ||| |||||
Db      18269 GGAAGGCTTTCTGGGGAGCT 18289

```

```

RESULT 18
US-09-949-016-12160
; Sequence 12160, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12160
; LENGTH: 119032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(119032)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12160

```

```

Query Match          73.6%; Score 16.2; DB 3; Length 119032;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      2 AAAGGCTTTTCGGGGTGCTC 22
      ||| ||||| ||| |||||
Db      29218 ACAGGCTTTCTGGGGTGCTC 29238

```

```

RESULT 19
US-09-949-016-17268
; Sequence 17268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

```

GENERAL INFORMATION: J. Craig et al.  
APPLICANT: VENTER,  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF



```
; LOCATION: 73..231
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8000019073486
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV
US-09-471-276-779

Query Match          71.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTTCGGGGGTG 19
Db 158 GAAAGGCATTTCGGGGGTG 140

RESULT 24
US-09-949-016-13325/c
; Sequence 13325, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13325
; LENGTH: 17879
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13325

Query Match          71.8%; Score 15.8; DB 3; Length 17879;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTTCGGGGGTG 19
Db 5076 GAAAGGCATTTCGGGGGTG 5058

RESULT 25
US-09-471-276-779/c
; Sequence 779, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 779
; LENGTH: 479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 73..429
; NAME/KEY: sig_peptide
```

```
; LOCATION: 73..231
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.8000019073486
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV
US-09-471-276-779

Query Match          70.9%; Score 15.6; DB 3; Length 479;
Best Local Similarity 81.8%; Pred. No. 2.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTTCGGGGGTGCTC 22
Db 175 GAAAGGCCATTTCGGATGTCAC 154

RESULT 26
US-09-949-016-47594/c
; Sequence 47594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47594
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-47594

Query Match          70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTTTCGGGGGTGCTC 22
Db 170 GCAAGGGCATTTCGGGGGTGCGC 149

RESULT 27
US-09-949-016-83107/c
; Sequence 83107, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83107
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-83107
```



RESULT 32  
US-09-247-155-44/c  
; Sequence 44, Application US/09247155A  
; Patent No. 6312922  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/247,155A  
; PRIOR FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/074,121  
; EARLIER FILING DATE: 1998-02-09  
; EARLIER APPLICATION NUMBER: 60/081,563  
; EARLIER FILING DATE: 1998-04-13  
; EARLIER APPLICATION NUMBER: 60/096,116  
; EARLIER FILING DATE: 1998-08-10  
; EARLIER APPLICATION NUMBER: 60/099,273  
; EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 44  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 42..755  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 42..200  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 5.8  
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV  
; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 860..865  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 878..893  
US-09-247-155-44

Query Match 70.9%; Score 15.6; DB 3; Length 893;  
Best Local Similarity 81.8%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
Db 144 GAAAGGCCATTCGGATGTGCAC 123

RESULT 33  
US-09-903-190-44/c  
; Sequence 44, Application US/09903190  
; Patent No. 6936692  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
; APPLICANT: Duclert, Aymeric  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: Complementary DNAs  
; FILE REFERENCE: GENSET.021A  
; CURRENT APPLICATION NUMBER: US/09/903,190  
; PRIOR FILING DATE: 2001-07-11  
; PRIOR FILING DATE: 1999-02-09  
; PRIOR APPLICATION NUMBER: 60/074,121  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/081,563  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13  
; PRIOR APPLICATION NUMBER: 60/096,116  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10  
; PRIOR APPLICATION NUMBER: 60/099,273

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patent.pm  
; SEQ ID NO 44  
; LENGTH: 893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 42..755  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 42..200  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 5.8  
; OTHER INFORMATION: seq ILSLQVLLTTVTS/TV  
; FEATURE:  
; NAME/KEY: polyA\_signal  
; LOCATION: 860..865  
; FEATURE:  
; NAME/KEY: polyA\_site  
; LOCATION: 878..893  
US-09-903-190-44

Query Match 70.9%; Score 15.6; DB 3; Length 893;  
Best Local Similarity 81.8%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
Db 144 GAAAGGCCATTCGGATGTGCAC 123

RESULT 34  
US-09-748-264A-1/c  
; Sequence 1, Application US/09748264A  
; Patent No. 6642439  
; GENERAL INFORMATION:  
; APPLICANT: SECRETARY OF AGENCY OF INDUSTRIAL SCIENCE AND TECHNOLOGY  
; APPLICANT: Yosuke IIMURA  
; TITLE OF INVENTION: A BASIDIOMYCETE PEROXIDASE GENE-TRANSFERRED PLANT AND A METHOD FOR  
; FILE REFERENCE: 04853.0050  
; CURRENT APPLICATION NUMBER: US/09/748,264A  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: JP 2000-223653  
; PRIOR FILING DATE: 2000-07-26  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Corioliolus versicolor  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1095)  
US-09-748-264A-1

Query Match 70.9%; Score 15.6; DB 3; Length 1098;  
Best Local Similarity 81.8%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
Db 660 GAAAGGGGTTCCGGGATGCTC 639

RESULT 35  
US-08-647-960-1/c  
; Sequence 1, Application US/08647960  
; Patent No. 5908761  
; GENERAL INFORMATION:  
; APPLICANT: ZICK, Yehiel

; TITLE OF INVENTION: GALECTIN-8 AND GALECTIN-8-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/647,960  
 ; FILING DATE: 30-MAY-1996  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 107880  
 ; FILING DATE: 05-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: ZICK=1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3527  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1247 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 121..1068  
 ; US-08-647-960-1

Query Match 70.9%; Score 15.6; DB 2; Length 1247;  
 Best Local Similarity 81.8%; Pred. No. 2.9e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22  
 Db 408 GAAAGGCATGTCGTGGGTGATC 387

RESULT 36  
 US-09-974-300-666  
 ; Sequence 666, Application US/09974300  
 ; Patent No. 7018794  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Berk, Randy M.  
 ; APPLICANT: Clausen, Ib Groth  
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
 ; FILE REFERENCE: 10085.500-US  
 ; CURRENT APPLICATION NUMBER: US/09/974,300  
 ; CURRENT FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: 09/680,598  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: 60/279,526  
 ; PRIOR FILING DATE: 2001-03-27  
 ; NUMBER OF SEQ ID NOS: 8481  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 666  
 ; LENGTH: 1410  
 ; TYPE: DNA  
 ; ORGANISM: Bacillus licheniformis  
 ; US-09-974-300-666

Query Match 70.9%; Score 15.6; DB 5; Length 1410;  
 Best Local Similarity 81.8%; Pred. No. 3e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22  
 Db 390 GAAAGCCTTCGGGCATGATC 411

RESULT 37  
 US-09-023-655-689  
 ; Sequence 689, Application US/09023655  
 ; Patent No. 6607879  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cocks, Benjamin G.  
 ; APPLICANT: Susan G. Stuart  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1508  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/023,655  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0001 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 689:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1429 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: TLYMNOT02  
 ; CLONE: 450088  
 ; US-09-023-655-689

Query Match 70.9%; Score 15.6; DB 3; Length 1429;  
 Best Local Similarity 81.8%; Pred. No. 3e+02;  
 Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGCTC 22  
 Db 181 GAAAGCCTTCGATGGGCTC 202

RESULT 38  
 US-09-489-039A-2738  
 ; Sequence 2738, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al

```

RESULT 40
US-10-104-047-900/c
; Sequence 900, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104_047
; CURRENT FILING DATE: 2002-03-25

```

Query Match	70.9%	Score 15.6	DB 3	Length 1990
Best Local Similarity	81.8%	Pred. No. 3.1e+02		
Matches	19	Conservative 0	Mismatches 4	Indels 0
Gaps	0			
Qy	1	GAAGAGCGCTTTCGGGGGTGCTC	22	

```
Db      1197 GAAAGGCCTTTGGGACCTGCTC 1218

RESULT 42
US-10-094-749-421
; Sequence 421, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 421
; TYPE: DNA
; LENGTH: 2297
; ORGANISM: Homo sapiens
US-10-094-749-421

Query Match      70.9%; Score 15.6; DB 4; Length 2297;
Best Local Similarity 81.8%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      1277 GAAAGGCCTTTAGAGTGAGCTC 1298

RESULT 43
US-09-422-936-52
; Sequence 52, Application US/09422936
; Patent No. 6465213
; GENERAL INFORMATION:
; APPLICANT: Ekstrand, Jonas
; TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 06275-165002
; CURRENT APPLICATION NUMBER: US/09/422,936
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US 09/242,608
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: PCT/SE98/01947
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9703914-2
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: SWEDEN 9800864-2
; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: SWEDEN 9802575-2
; PRIOR FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0

Db      1197 GAAAGGCCTTTGGGACCTGCTC 1218

Query Match      70.9%; Score 15.6; DB 3; Length 2895;
Best Local Similarity 81.8%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      1470 GAGCGCGCTTCGGGGTGGC 1491

RESULT 44
US-09-917-254-18/c
; Sequence 18, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 3995
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-917-254-18

Query Match      70.9%; Score 15.6; DB 3; Length 3995;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
Db      2281 GAAACCCCTTTGGGGTGTCTC 2260

RESULT 45
US-09-919-497-9/c
; Sequence 9, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 3995
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-497-9

Query Match      70.9%; Score 15.6; DB 3; Length 3995;
Best Local Similarity 81.8%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTGGGGGTGCTC 22
```

Db 2281 GAAACCCCTTTGGGTGCTC 2260  
||||| ||||| ||||| ||||| |||||

## RESULT 46

US-09-949-016-13141/c  
; Sequence 13141, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 13141  
; LENGTH: 20076  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13141

Query Match 70.9%; Score 15.6; DB 3; Length 20076;  
Best Local Similarity 81.8%; Pred. No. 4.5e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
||||| ||||| ||||| ||||| |||||

Db 14656 GCAAGGCATTCGGGGTGCGC 14635

## RESULT 47

US-09-949-016-14140/c  
; Sequence 14140, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14140  
; LENGTH: 25973  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14140

Query Match 70.9%; Score 15.6; DB 3; Length 25973;  
Best Local Similarity 81.8%; Pred. No. 4.7e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
||||| ||||| ||||| ||||| |||||

Db 20553 GCAAGGCATTCGGGGTGCGC 20532

## RESULT 48

US-09-949-016-15865  
; Sequence 15865, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15865  
; LENGTH: 37059  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/Key: misc\_feature  
; LOCATION: (1)...(37059)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15865

Query Match 70.9%; Score 15.6; DB 3; Length 37059;  
Best Local Similarity 81.8%; Pred. No. 5e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
||||| ||||| ||||| ||||| |||||

Db 10641 GAAAGGCTTTCGTGTCTC 10662

## RESULT 49

US-09-949-016-15378  
; Sequence 15378, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 15378  
; LENGTH: 83516  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15378

Query Match 70.9%; Score 15.6; DB 3; Length 83516;  
Best Local Similarity 81.8%; Pred. No. 5.6e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
||||| ||||| ||||| ||||| |||||

Db 49986 GAAACGCTTTCGGGTCTC 50007

## RESULT 50

US-09-949-016-16420

```
; Sequence 16420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16420
; LENGTH: 234884
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(234884)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16420

Query Match          70.9%; Score 15.6; DB 3; Length 234884;
Best Local Similarity 81.8%; Pred. No. 6.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GAAAGGCTTTTCGGGGTGCTC 22
      ||||| ||||| ||||| ||||| |||||
Db      226956  GAATGGGTTTTCGGGGTGCTC 226977

RESULT 51
US-09-949-016-14720/c
; Sequence 14720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14720
; LENGTH: 390890
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(390890)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14720

Query Match          70.9%; Score 15.6; DB 3; Length 390890;
Best Local Similarity 81.8%; Pred. No. 6.7e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  GAAAGGCTTTTCGGGGTGCTC 22
      ||||| ||||| ||||| ||||| |||||
Db      101368  GAAAGGTTTTCGGGGTGCCC 101347
```

```
RESULT 52
US-09-497-855A-43/c
; Sequence 43, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 383
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-43

Query Match          70.0%; Score 15.4; DB 3; Length 383;
Best Local Similarity 94.1%; Pred. No. 3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GCCTTTCCGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      234  GCCTTTAGGGGGTGCTC 218

RESULT 53
US-09-533-559-4582
; Sequence 4582, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849,200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4582
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-4582

Query Match          70.0%; Score 15.4; DB 3; Length 668;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6  GCCTTTCCGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      422  GCCTTTCCGGGGTGCTC 438

RESULT 54
US-09-949-016-12300
; Sequence 12300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12300
; LENGTH: 14438
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(14438)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12300

Query Match          70.0%; Score 15.4; DB 3; Length 14438;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 GCCTTTCGGGGTGCTC 22
Db      5389 GCCTTTCGGGGTGCTC 5405

RESULT 55
US-09-949-016-14080
; Sequence 14080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14080
; LENGTH: 60990
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14080

Query Match          70.0%; Score 15.4; DB 3; Length 60990;
Best Local Similarity 94.1%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGG 17
Db      34457 GAAAGGCCTTTCGGGG 34473

RESULT 56
US-09-949-016-14080/c
; Sequence 14080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14080
; LENGTH: 60990
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14080

Query Match          70.0%; Score 15.4; DB 3; Length 60990;
Best Local Similarity 94.1%; Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGG 17
Db      34468 GAAAGGCCTTTCAGGGG 34452

RESULT 57
US-09-370-838-264
; Sequence 264, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)
; OTHER INFORMATION: n=A,T,C or G
US-09-370-838-264

Query Match          69.1%; Score 15.2; DB 3; Length 600;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGTGC 20
Db      120 GAAAGGCCTTTCGAGCTGC 139

RESULT 58
US-09-854-133-264
; Sequence 264, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
```

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; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)_feature
; OTHER INFORMATION: n=A,T,C or G
US-09-854-133-264

Query Match          69.1%; Score 15.2; DB 3; Length 600;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GAAAGGCCTTCGGGGTGTC 20
Db      120 GAAAGGCCTTCGGAGCTGC 139

RESULT 59
US-09-949-016-76799
; Sequence 76799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76799
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76799

Query Match          69.1%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2  AAAGGCCTTCGGGGTGCT 21
Db      209 AAATGCCTTCGAAGTGCT 228

RESULT 60
US-08-343-443B-97/c
; Sequence 97, Application US/08343443B
; Patent No. 5968734
; GENERAL INFORMATION:
; APPLICANT: Aurias, Alain
; APPLICANT: Delattre, Olivier
; APPLICANT: Desmaze, Chantal
; APPLICANT: Melot, Thomas
; APPLICANT: Peter, Martine
; APPLICANT: Ploougastel, Beatrice
; APPLICANT: Thomas, Gilles
.
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; APPLICANT: Zucman, Jessica
; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 264
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (32)_feature
; OTHER INFORMATION: n=A,T,C or G
US-09-854-133-264

Query Match          69.1%; Score 15.2; DB 3; Length 600;
Best Local Similarity 85.0%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GAAAGGCCTTCGGGGTGTC 20
Db      120 GAAAGGCCTTCGGAGCTGC 139

RESULT 59
US-09-949-016-76799
; Sequence 76799, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76799
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-76799

Query Match          69.1%; Score 15.2; DB 2; Length 833;
Best Local Similarity 85.0%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GAAAGGCCTTCGGGGTGTC 20
Db      37 GACCGCCTTCGGGGTGTC 18

RESULT 61
US-09-902-540-4292
; Sequence 4292, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4292
; LENGTH: 931
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
.
```

US-09-902-540-4292

Query Match 69.1%; Score 15.2; DB 3; Length 931;  
Best Local Similarity 85.0%; Pred. No. 4.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGGCCTTTCGGGGTGCT 21  
|||||  
Db 664 AAGGCCTTCGGGTGATGCT 683

RESULT 62

US-09-252-991A-7914  
; Sequence 7914, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7914  
; LENGTH: 1185  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7914

Query Match 69.1%; Score 15.2; DB 3; Length 1185;  
Best Local Similarity 85.0%; Pred. No. 4.6e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCT 22  
|||||  
Db 1058 AAGGCCTGCGGTGCTGCTC 1077

RESULT 63

US-09-248-796A-1866  
; Sequence 1866, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248.796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 1866  
; LENGTH: 1320  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-1866

Query Match 69.1%; Score 15.2; DB 3; Length 1320;  
Best Local Similarity 85.0%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCT 22  
|||||  
Db 500 ATGCGCTTTCGGGTGCTC 519

RESULT 64

US-09-252-991A-7642/c  
; Sequence 7642, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7642  
; LENGTH: 1347  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-7642

Query Match 69.1%; Score 15.2; DB 3; Length 1347;  
Best Local Similarity 85.0%; Pred. No. 4.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22  
|||||  
Db 185 AAGCCTGCGGTGCTC 166

RESULT 65

US-10-056-790-15  
; Sequence 15, Application US/10056790  
; Patent No. 6972179  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF  
; FILE REFERENCE: RRPPIP2002  
; CURRENT APPLICATION NUMBER: US/10/056.790  
; CURRENT FILING DATE: 2002-01-23  
; PRIOR APPLICATION NUMBER: US 09/908,419  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/219,289  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 60/277,487  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/277,471  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/304,863  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/305,017  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,491  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 1738  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-056-790-15

Query Match 69.1%; Score 15.2; DB 4; Length 1738;  
Best Local Similarity 85.0%; Pred. No. 4.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTCGGGGTGCT 20  
|||



```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1612)..(1623)
; OTHER INFORMATION: cathepsin G recognition site coding sequence
US-10-229-346-20

Query Match          69.1%; Score 15.2; DB 5; Length 1797;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 70
US-10-229-346-6/c
; Sequence 6, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1791)
; OTHER INFORMATION: Maize optimized modified cry3A054 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: cathepsin G recognition site coding sequence
US-10-229-346-6

Query Match          69.1%; Score 15.2; DB 5; Length 1801;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 71
US-10-229-346-3/c
; Sequence 3, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; NAME/KEY: CDS
; LOCATION: (1)..(1794)
; OTHER INFORMATION: Maize optimized cry3A coding sequence
US-10-229-346-3

Query Match          69.1%; Score 15.2; DB 5; Length 1803;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 72
US-10-229-346-8/c
; Sequence 8, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 1807
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1806)
; OTHER INFORMATION: Maize optimized modified cry3A055 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-8

Query Match          69.1%; Score 15.2; DB 5; Length 1807;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGTGCTC 22
    |||||  |||||  |||||  |||||
Db 185 AAGCCTTCCAGGGTGCTC 166

RESULT 73
US-10-229-346-16/c
; Sequence 16, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 1813
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
```

```
/ LOCATION: (1)..(1812)
; OTHER INFORMATION: Maize optimized modified cry3A057 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1618)..(1629)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
US-10-229-346-16

Query Match          69.1%; Score 15.2; DB 5; Length 1813;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCCGGGGTGCTC 22
Db 185 AAGGCCTTCCAGGGGTCTC 166

RESULT 74
US-10-229-346-14/c
; Sequence 14, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1812)
; OTHER INFORMATION: Maize optimized modified cry3A058 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1621)..(1632)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence
US-10-229-346-14

Query Match          69.1%; Score 15.2; DB 5; Length 1816;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCCGGGGTGCTC 22
Db 185 AAGGCCTTCCAGGGGTCTC 166

RESULT 75
US-10-229-346-10/c
; Sequence 10, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
```

```
/ SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 1818
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1818)
; OTHER INFORMATION: Maize optimized modified cry3A085 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (346)..(357)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-10

Query Match          69.1%; Score 15.2; DB 5; Length 1818;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCCGGGGTGCTC 22
Db 209 AAGGCCTTCCAGGGGTCTC 190

RESULT 76
US-10-229-346-18/c
; Sequence 18, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1818)
; OTHER INFORMATION: Maize optimized modified cry3A056 coding sequence.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (322)..(333)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
; NAME/KEY: misc feature
; LOCATION: (1624)..(1635)
; OTHER INFORMATION: Cathepsin G recognition site coding sequence.
US-10-229-346-18

Query Match          69.1%; Score 15.2; DB 5; Length 1819;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCCGGGGTGCTC 22
Db 185 AAGGCCTTCCAGGGGTCTC 166

RESULT 77
US-10-094-749-1246
; Sequence 1246, Application US/10094749
; Patent No. 6979557
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
```

```
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1246
; LENGTH: 1830
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-1246

Query Match          69.1%; Score 15.2; DB 4; Length 1830;
Best Local Similarity 85.0%; Pred. No. 4.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 1041 ATGGCCTTTCGTGTGCTC 1060

RESULT 78
US-08-295-060-3/c
; Sequence 3, Application US/08295060
; Patent No. 5659123
; GENERAL INFORMATION:
; APPLICANT: VAN RIE, Jeroen
; APPLICANT: JANSENS, Stefan
; APPLICANT: PERFEROEN, Marnix
; TITLE OF INVENTION: NEW DIABROTICA TOXINS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,060
; FILING DATE: 26-AUG-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Crane-Feury, Sharon E
; REGISTRATION NUMBER: 36,113
; REFERENCE/DOCKET NUMBER: 010830-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1957 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1947
US-08-295-060-3

Query Match          69.1%; Score 15.2; DB 2; Length 1957;
Best Local Similarity 85.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 341 AAGGCCTTTCAGGGTGCTC 322

RESULT 79
US-09-774-528-10
; Sequence 10, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: NO. 6743619el Nucleic Acids and
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 10
; LENGTH: 2198
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (124)..(891)
US-09-774-528-10

Query Match          69.1%; Score 15.2; DB 3; Length 2198;
Best Local Similarity 85.0%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 1398 ATGGCCTTTCGTGTGCTC 1417

RESULT 80
US-10-120-988-10
; Sequence 10, Application US/10120988
; Patent No. 6919193
; GENERAL INFORMATION:
```





RESULT 84  
US-09-028-327-2/c  
; Sequence 2, Application US/09028327  
; Patent No. 6130064  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/028,327  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0482 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2426 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT24  
; CLONE: 3769729  
US-09-028-327-2  
Query Match 69.1%; Score 15.2; DB 3; Length 2426;  
Best Local Similarity 85.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 257 GGAAGGCGTTTCGGGGATGC 238

RESULT 85  
US-09-571-078A-2/c  
; Sequence 2, Application US/09571078A  
; Patent No. 6620783  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl J.  
; TITLE OF INVENTION: HUMAN SMN-LIKE PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/571,078A  
FILING DATE: 15-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0482 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2426 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BRSTNOT24  
CLONE: 3769729  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-571-078A-2  
Query Match 69.1%; Score 15.2; DB 3; Length 2426;  
Best Local Similarity 85.0%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 257 GGAAGGCGTTTCGGGGATGC 238

RESULT 86  
US-09-949-016-2230/c  
; Sequence 2230, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2230  
; LENGTH: 2453  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-2230  
Query Match 69.1%; Score 15.2; DB 3; Length 2453;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTCGGGGTGC 21  
| | | | | | | | | | | | | | | | | | | | | |

Db 394 AATGCTTTTCGGAAGTGCT 375

## RESULT 87

US-09-489-039A-530  
; Sequence 530, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 530  
; LENGTH: 2511  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-530

Query Match 69.1%; Score 15.2; DB 3; Length 2511;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCTTTTCGGGGTGCTC 22

Db 169 AACGCTTTCGGGGTGCTC 188

## RESULT 88

US-09-489-039A-444  
; Sequence 444, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 444  
; LENGTH: 2742  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-444

Query Match 69.1%; Score 15.2; DB 3; Length 2742;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCTTTTCGGGGTGCTC 22

Db 2588 AACGCTTTCGGGGTGCTC 2607

## RESULT 89

US-09-008-697A-13/c  
; Sequence 13, Application US/09008697A  
; Patent No. 6197504  
; GENERAL INFORMATION:  
; APPLICANT: Chow, King Lau  
; TITLE OF INVENTION: USES OF MAB-21  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York

; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/008,697A  
; FILING DATE: January 19, 1998  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chan, Albert Wai-Kit  
; REGISTRATION NUMBER: 36,479  
; REFERENCE/DOCKET NUMBER: 50752-A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2770 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-008-697A-13

Query Match 69.1%; Score 15.2; DB 3; Length 2770;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGCCTTTTCGGGGTGCT 21

Db 695 AATGCTTTTCGGAAGTGCT 676

## RESULT 90

US-09-949-016-5461/c  
; Sequence 5461, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5461  
; LENGTH: 3124  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5461

Query Match 69.1%; Score 15.2; DB 3; Length 3124;  
Best Local Similarity 85.0%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGCCTTTTCGGGGTGCTC 22

Db 2546 AGGCATTTTCGAGGTGCTC 2527

## RESULT 91

US-09-865-879-6/c

```

; Sequence 6, Application US/09865879
; Patent No. 6767705
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Dokmanovic, Milos
; APPLICANT: Chang, Bev-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
; FILE REFERENCE: 99,216-H
; CURRENT APPLICATION NUMBER: US/09/865,879
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 3271
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Mac-2 BP promoter NCBI acc. number U91729.1
US-09-865-879-6

Query Match      69.1%; Score 15.2; DB 3; Length 3271;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAGGCTTCGGGGGTGC 20
Db 1496 GCAAGGCTTCGGGTGC 1477

RESULT 92
US-09-949-016-4008/c
; Sequence 4008, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4008
; LENGTH: 4522
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4008

Query Match      69.1%; Score 15.2; DB 3; Length 4522;
Best Local Similarity 85.0%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCTTCGGGGGTGCTC 22
Db 567 AGGCGCTTCGGGGCTGCTC 548

RESULT 93
US-09-949-016-13972/c
; Sequence 13972, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

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; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13972
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13972

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Best Local Similarity 85.0%; Pred. No. 6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTCGGGGGTGCT 21
Db 2394 AAATGCCTTCGGAAGTGT 2375

RESULT 94
US-10-229-346-5/c
; Sequence 5, Application US/10229346
; Patent No. 7030295
; GENERAL INFORMATION:
; APPLICANT: Chen, Eric
; APPLICANT: Stacy, Cheryl
; TITLE OF INVENTION: Modified Cry3A Toxins
; FILE REFERENCE: 60065A
; CURRENT APPLICATION NUMBER: US/10/229,346
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/316,421
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 7208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: pCIB6850
US-10-229-346-5

Query Match      69.1%; Score 15.2; DB 5; Length 7208;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGGCTTCGGGGGTGCTC 22
Db 193 AAGGCTTCAGGGGTCTC 174

RESULT 95
US-09-949-016-14771/c
; Sequence 14771, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17203
; LENGTH: 16287
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17203

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Best Local Similarity 85.0%; Pred. No. 7e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 AAGGCCTTCGGGGTGCTC 22
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Db      12708 AGGCGATTTCGGAGTGCTC 12689

RESULT 98
US-09-902-540-1213
; Sequence 1213, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1213
; LENGTH: 20250
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-1213

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Best Local Similarity 85.0%; Pred. No. 7.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTCGGGGGTGCT 21
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RESULT 99
US-09-949-016-15750/c
; Sequence 15750, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15750
; LENGTH: 20444
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature

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; LOCATION: (1)...(20444)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15750

Query Match      69.1%; Score 15.2; DB 3; Length 20444;
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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGCCTTCGGGGTGCTC 22
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RESULT 100
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; Sequence 15130, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15130
; LENGTH: 21831
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(21831)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15130

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Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db      1469 AACGCTTCGGGGAGCCC 1450

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Title: US-10-665-708-25

Perfect score: 22

Sequence: 1 gaagagccttcgggggtgtc 22

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# SUMMARIES

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4	22	100.0	25	10	US-10-665-708-26
5	18.8	85.5	493	8	US-10-424-599-34282
6	17.8	80.9	487	10	US-10-506-454-1690
7	17.8	80.9	688	4	US-09-925-065A-944213
8	17.8	80.9	688	5	US-09-925-065A-944213
9	17.8	80.9	3175	6	US-10-027-632-116247
10	17.8	80.9	3175	7	US-10-027-632-116247
11	17.8	80.9	40491	6	US-10-087-192-1426
12	17.8	80.9	25	13	US-11-036-317-122359
13	17.4	79.1	549	6	US-10-027-632-133700
14	17.4	79.1	549	7	US-10-027-632-133700
15	17.4	79.1	549	7	US-10-027-632-133700
16	17.4	79.1	4637	6	US-10-194-163-818
17	17.4	79.1	374849	6	US-10-087-192-1627

9	US-10-719-900-152165	25	78.2	17.2	c	18	Sequence 152165,
3	US-09-864-761-6845	569	78.2	17.2		19	Sequence 6845, Ap
682	US-10-424-599-34279	20	78.2	17.2		20	Sequence 34279, A
1440	US-10-282-122A-23975	21	78.2	17.2		21	Sequence 23975, A
58822	US-10-052-482-46	22	78.2	17.2		22	Sequence 46, Appl
63686	US-10-087-192-466	23	78.2	17.2		23	Sequence 466, App
195	US-10-425-115-69008	24	76.4	16.8	c	24	Sequence 69008, A
518	US-10-425-115-118256	25	76.4	16.8	c	25	Sequence 118256,
551	US-10-437-963-78913	26	76.4	16.8	c	26	Sequence 78913, A
601	US-10-021-323-8399	27	76.4	16.8	c	27	Sequence 8399, Ap
2107	US-10-282-122A-19508	28	76.4	16.8	c	28	Sequence 19508, A
289190	US-10-322-281-115	29	76.4	16.8	c	29	Sequence 115, App
309	US-10-106-698-3878	30	74.5	16.4	c	30	Sequence 3878, Ap
521	US-10-021-323-2667	31	74.5	16.4	c	31	Sequence 2667, Ap
47804	US-10-017-161-717	32	74.5	16.4	c	32	Sequence 717, App
47804	US-10-292-798-629	33	74.5	16.4	c	33	Sequence 629, App
82	US-10-990-355-32	34	73.6	16.2	c	34	Sequence 32, Appl
314	US-10-425-115-176343	35	73.6	16.2	c	35	Sequence 176343,
353	US-10-425-115-106353	36	73.6	16.2	c	36	Sequence 106353,
426	US-10-137-113-21	37	73.6	16.2	c	37	Sequence 21, Appl
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505	US-10-301-480-276883	39	73.6	16.2	c	39	Sequence 276883,
506	US-10-301-480-890292	40	73.6	16.2	c	40	Sequence 890292,
506	US-09-925-065A-186776	41	73.6	16.2	c	41	Sequence 186776,
511	US-10-029-386-9545	42	73.6	16.2	c	42	Sequence 9545, Ap
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567	US-08-925-065A-301026	46	73.6	16.2	c	46	Sequence 301026,
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592	US-09-925-065A-821134	49	73.6	16.2	c	49	Sequence 821134,
592	US-09-925-065A-821134	50	73.6	16.2	c	50	Sequence 821134,
600	US-10-750-185-19831	51	73.6	16.2	c	51	Sequence 19831, A
600	US-10-750-623-19831	52	73.6	16.2	c	52	Sequence 19831, A
607	US-09-925-065A-884151	53	73.6	16.2	c	53	Sequence 884151,
607	US-09-925-065A-884151	54	73.6	16.2	c	54	Sequence 884151,
623	US-10-027-632-268485	55	73.6	16.2	c	55	Sequence 268485,
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642	US-09-925-065A-674788	62	73.6	16.2	c	62	Sequence 674788,
825	US-10-750-185-32645	63	73.6	16.2	c	63	Sequence 32645, A
825	US-10-750-623-32645	64	73.6	16.2	c	64	Sequence 32645, A
909	US-09-854-867-342	65	73.6	16.2	c	65	Sequence 342, App
909	US-10-786-970A-342	66	73.6	16.2	c	66	Sequence 342, App
935	US-10-027-632-163064	67	73.6	16.2	c	67	Sequence 163064,
935	US-10-027-632-163064	68	73.6	16.2	c	68	Sequence 163064,
1014	US-09-864-761-20761	69	73.6	16.2	c	69	Sequence 20761, A
1218	US-09-864-761-20761	70	73.6	16.2	c	70	Sequence 20761, A
1377	US-10-282-122A-28246	71	73.6	16.2	c	71	Sequence 28246, A
1380	US-10-282-122A-28592	72	73.6	16.2	c	72	Sequence 28592, A
1704	US-10-240-965-33	73	73.6	16.2	c	73	Sequence 33, Appl
1740	US-09-349-015-30	74	73.6	16.2	c	74	Sequence 30, Appl
1740	US-10-219-664-22	75	73.6	16.2	c	75	Sequence 22, Appl
1954	US-09-864-761-4001	76	73.6	16.2	c	76	Sequence 4001, Ap
2772	US-10-264-049-815	77	73.6	16.2	c	77	Sequence 815, App
3135	US-10-175-523-151	78	73.6	16.2	c	78	Sequence 151, App
3258	US-11-099-266-151	79	73.6	16.2	c	79	Sequence 151, App
415	US-10-287-436A-1061	80	73.6	16.2	c	80	Sequence 1061, Ap
415	US-09-925-301-224	81	73.6	16.2	c	81	Sequence 224, App
415	US-10-137-113-23	82	73.6	16.2	c	82	Sequence 23, Appl
4758	US-09-842-777-9	83	73.6	16.2	c	83	Sequence 9, Appli
4831	US-10-334-143-116	84	73.6	16.2	c	84	Sequence 116, App
5594	US-10-205-219-136	85	73.6	16.2	c	85	Sequence 136, App
5994	US-10-173-999-122	86	73.6	16.2	c	86	Sequence 122, App
5994	US-10-723-860-1893	87	73.6	16.2	c	87	Sequence 1893, Ap
5994	US-10-723-860-1893	88	73.6	16.2	c	88	Sequence 1893, Ap
6332	US-10-756-149-1800	89	73.6	16.2	c	89	Sequence 1800, Ap
6332	US-10-276-774-1341	90	73.6	16.2	c	90	Sequence 1341, Ap
6332	US-10-960-414-82	91	73.6	16.2	c	91	Sequence 82, Appl





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C 241	15.6	70.9	1265	9	US-10-363-345A-15108	Sequence 15108, A
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C 243	15.6	70.9	1265	10	US-10-363-483A-15108	Sequence 15108, A
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C 245	15.6	70.9	1325	7	US-10-439-388-28	Sequence 28, Appl
C 246	15.6	70.9	1325	8	US-10-342-887-1599	Sequence 1599, Ap
C 247	15.6	70.9	1343	7	US-10-029-386-24092	Sequence 24092, A
C 248	15.6	70.9	1371	7	US-10-402-842-17	Sequence 17, Appl
C 249	15.6	70.9	1371	8	US-10-746-795-17	Sequence 17, Appl
C 250	15.6	70.9	1400	10	US-10-821-233-228	Sequence 228, App
C 251	15.6	70.9	1410	3	US-09-974-300-666	Sequence 666, App
C 252	15.6	70.9	1429	8	US-10-641-643-689	Sequence 689, App
C 253	15.6	70.9	1552	8	US-10-437-963-18968	Sequence 18968, A
C 254	15.6	70.9	1746	8	US-10-235-463-58	Sequence 58, Appl
C 255	15.6	70.9	1761	8	US-10-282-122A-1449	Sequence 1449, A
C 256	15.6	70.9	1811	8	US-10-437-963-86339	Sequence 86339, A
C 257	15.6	70.9	1862	7	US-10-104-047-900	Sequence 900, App
C 258	15.6	70.9	1862	16	US-11-072-512-900	Sequence 900, App
C 259	15.6	70.9	1898	10	US-10-750-185-46119	Sequence 46119, A
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C 262	15.6	70.9	1923	11	US-10-932-182A-75858	Sequence 75858, A
C 263	15.6	70.9	1935	8	US-10-437-963-85597	Sequence 85597, A
C 264	15.6	70.9	1990	7	US-10-305-720-1056	Sequence 1056, Ap
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C 274	15.6	70.9	2708	13	US-11-097-143-16156	Sequence 16156, A
C 275	15.6	70.9	2796	8	US-10-437-963-86274	Sequence 86274, A
C 276	15.6	70.9	2835	8	US-10-437-963-44350	Sequence 44350, A
C 277	15.6	70.9	2895	8	US-10-235-463-52	Sequence 52, Appl
C 278	15.6	70.9	2922	8	US-10-437-963-85997	Sequence 85997, A
C 279	15.6	70.9	2970	8	US-10-437-963-85652	Sequence 85652, A
C 280	15.6	70.9	3087	8	US-10-437-963-8562	Sequence 8562, Ap
C 281	15.6	70.9	3581	4	US-09-925-065A-676737	Sequence 676737, A
C 282	15.6	70.9	3581	4	US-09-925-065A-676738	Sequence 676738, A
C 283	15.6	70.9	3581	4	US-09-925-065A-676739	Sequence 676739, A
C 284	15.6	70.9	3581	4	US-09-925-065A-706965	Sequence 706965, A
C 285	15.6	70.9	3581	5	US-09-925-065A-676737	Sequence 676737, A
C 286	15.6	70.9	3581	5	US-09-925-065A-676738	Sequence 676738, A
C 287	15.6	70.9	3581	5	US-09-925-065A-676739	Sequence 676739, A
C 288	15.6	70.9	3581	5	US-09-925-065A-706965	Sequence 706965, A
C 289	15.6	70.9	3995	3	US-09-919-497-9	Sequence 9, Appl
C 290	15.6	70.9	3995	7	US-10-170-385-300	Sequence 300, App
C 291	15.6	70.9	4149	9	US-10-425-115-163575	Sequence 163575, A
C 292	15.6	70.9	4278	10	US-10-750-185-56237	Sequence 56237, A
C 293	15.6	70.9	4278	10	US-10-750-623-56237	Sequence 56237, A
C 294	15.6	70.9	4857	6	US-10-208-948-1	Sequence 1, Appl
C 295	15.6	70.9	4928	13	US-11-097-143-16157	Sequence 16157, A
C 296	15.6	70.9	5534	13	US-11-097-143-15530	Sequence 15530, A
C 297	15.6	70.9	5862	3	US-09-764-891-7363	Sequence 7363, Ap
C 298	15.6	70.9	6065	3	US-09-764-891-9652	Sequence 9652, Ap
C 299	15.6	70.9	7110	6	US-10-208-948-23	Sequence 23, Appl
C 300	15.6	70.9	7110	9	US-10-425-115-163573	Sequence 163573, A

ALIGNMENTS

RESULT 1  
US-09-738-274-25  
; Sequence 25, Application US/09738274  
; Publication No. US20030165824A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-25

Query Match 100.0%; Score 22; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22  
|||||  
Db 1 GAAAGGCTTCGGGGTGCTC 22  
|||||

RESULT 2

US-10-665-708-25  
; Sequence 25, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-25

Query Match 100.0%; Score 22; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTCGGGGTGCTC 22  
|||||  
Db 1 GAAAGGCTTCGGGGTGCTC 22  
|||||

RESULT 3

US-09-738-274-26  
 ; Sequence 26, Application US/09738274  
 ; Publication No. US20030165824A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BRENTANO, Steven T.  
 ; APPLICANT: JUCKER, Markus T.  
 ; APPLICANT: DELGADO, Francisco D.  
 ; APPLICANT: CLEUZAT, Philippe  
 ; APPLICANT: RODRIGUE, Marc  
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: GP107-02.UT  
 ; CURRENT APPLICATION NUMBER: US/09/738,274  
 ; CURRENT FILING DATE: 2000-12-15  
 ; PRIOR APPLICATION NUMBER: 60/172,190  
 ; PRIOR FILING DATE: 1999-12-17  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; OTHER INFORMATION: oligonucleotide

Query Match 100.0%; Score 22; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 1 GAAAGGCCCTTCGGGGTGCTC 22

RESULT 4  
 US-10-665-708-26  
 ; Sequence 26, Application US/10665708  
 ; Publication No. US20050100915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BRENTANO, Steven T.  
 ; APPLICANT: JUCKER, Markus T.  
 ; APPLICANT: DELGADO, Francisco D.  
 ; APPLICANT: CLEUZAT, Philippe  
 ; APPLICANT: RODRIGUE, Marc  
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: GP107-02.UT  
 ; CURRENT APPLICATION NUMBER: US/10/665,708  
 ; CURRENT FILING DATE: 2003-09-18  
 ; PRIOR APPLICATION NUMBER: US/09/738,274  
 ; PRIOR FILING DATE: 2000-12-15  
 ; PRIOR APPLICATION NUMBER: 60/172,190  
 ; PRIOR FILING DATE: 1999-12-17  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 26  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; OTHER INFORMATION: oligonucleotide

Query Match 100.0%; Score 22; DB 10; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 2.2;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 1 GAAAGGCCCTTCGGGGTGCTC 22

RESULT 5  
 US-10-424-599-34282  
 ; Sequence 34282, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J  
 ; APPLICANT: Kovalic, David K  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
 ; Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO 34282  
 ; LENGTH: 493  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_130960C.1  
 ; OTHER INFORMATION: US-10-424-599-34282  
 Query Match 85.5%; Score 18.8; DB 8; Length 493;  
 Best Local Similarity 90.9%; Pred. No. 56;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 321 GAAAGGCCCTTCGGGGTGCTC 342

RESULT 6  
 US-10-506-454-1690/c  
 ; Sequence 1690, Application US/10506454  
 ; Publication No. US20060068386A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Slesarev, Alexi I  
 ; APPLICANT: Mezhevaya, Katja V  
 ; APPLICANT: Polushin, Nikolai N  
 ; APPLICANT: Shcherbinina, Olga V  
 ; APPLICANT: Shakhova, Vera V  
 ; APPLICANT: Malykh, Andrei G  
 ; APPLICANT: Kozyavkin, Sergei A  
 ; TITLE OF INVENTION: The Complete Genome and Protein Sequences of the Hyperthermophile  
 ; Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens  
 ; TITLE OF INVENTION: Methanopyrus Kandleri AV19 and Monophyly of Archaeal Methanogens  
 ; FILE REFERENCE: FID001  
 ; CURRENT APPLICATION NUMBER: US/10/506,454  
 ; CURRENT FILING DATE: 2004-08-31  
 ; PRIOR APPLICATION NUMBER: PCT/US03/06664  
 ; PRIOR FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: 60/361,742  
 ; PRIOR FILING DATE: 2002-03-04  
 ; NUMBER OF SEQ ID NOS: 1722  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1690  
 ; LENGTH: 1694969  
 ; TYPE: DNA  
 ; ORGANISM: Methanopyrus kandleri  
 ; OTHER INFORMATION: US-10-506-454-1690  
 Query Match 85.5%; Score 18.8; DB 12; Length 1694969;  
 Best Local Similarity 90.9%; Pred. No. 27;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
 |||||  
 Db 54678 GAAAGGCCCTTCGGGGTGATC 54657

```
RESULT 7
US-10-287-436A-794
; Sequence 794, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287.436A
; PRIOR FILING DATE: 2002-10-31
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 794
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-287-436A-794

Query Match      80.9%; Score 17.8; DB 10; Length 487;
Best Local Similarity 90.5%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
Db 79 GACAGGCTTTCGGGGTGCT 99

RESULT 8
US-09-925-065A-944213
; Sequence 944213, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 944213
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-944213

Query Match      80.9%; Score 17.8; DB 4; Length 688;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
Db 76 GACAGGCTTTCGGGGTGCT 96

RESULT 9
US-09-925-065A-944213
; Sequence 944213, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116247
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-116247

Query Match      80.9%; Score 17.8; DB 6; Length 3175;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
Db 1073 GACAGGCTTTCGGGGTGCT 1093
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 944213
; LENGTH: 688
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-944213

Query Match      80.9%; Score 17.8; DB 5; Length 688;
Best Local Similarity 90.5%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
Db 76 GACAGGCTTTCGGGGTGCT 96

RESULT 10
US-10-027-632-116247
; Sequence 116247, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-09-28
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116247
; LENGTH: 3175
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-116247

Query Match      80.9%; Score 17.8; DB 6; Length 3175;
Best Local Similarity 90.5%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTCGGGGTGCT 21
Db 1073 GACAGGCTTTCGGGGTGCT 1093
```



Db 100 GAAAGCCTTCCTGGGGTGCT 120

RESULT 15

US-10-027-632-133700

; Sequence 133700, Application US/10027632

; Publication No. US20030204075A9

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108927.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218,006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198,676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193,483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167,363

; PRIOR FILING DATE: 1998-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 133700

; LENGTH: 549

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-133700

Query Match 79.1%; Score 17.4; DB 7; Length 549;

Best Local Similarity 85.7%; Pred. No. 2.5e+02;

Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCCTGGGGTGCT 21

Db 100 GAAAGCCTTCCTGGGGTGCT 120

RESULT 16

US-10-194-163-818/c

; Sequence 818, Application US/10194163

; Publication No. US20020172976A1

; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce Carter

; TITLE OF INVENTION: PORPHYROMONAS GINGIVALIS POLYNUCLEOTIDES

; AND USES THEREOF

; NUMBER OF SEQUENCES: 1120

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 PAGE MILL ROAD

; CITY: PALO ALTO

; STATE: CA

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/194,163

; FILING DATE: 04-Nov-2002

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Baeu, Shantanu

; REGISTRATION NUMBER: 43,318

REFERENCE/DOCKET NUMBER: 529282000101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-813-5995

TELEFAX: 650-494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 818

SEQUENCE CHARACTERISTICS:

LENGTH: 4637 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: UNKNOWN

ORIGINAL SOURCE:

ORGANISM: PORPHYROMONAS GINGIVALIS

FEATURE:

NAME/KEY: misc feature

LOCATION: 1...4637

SEQUENCE DESCRIPTION: SEQ ID NO: 818

US-10-194-163-818

Query Match 79.1%; Score 17.4; DB 6; Length 4637;

Best Local Similarity 94.7%; Pred. No. 2.1e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGCCTTCCTGGGGTGCT 19

Db 4588 GAAAGCCTTCCTGGGGTGCT 4570

RESULT 17

US-10-087-192-1627

; Sequence 1627, Application US/10087192

; Publication No. US20020182586A1

; GENERAL INFORMATION:

; APPLICANT: Morris, David W.

; APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER

; FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1627

; LENGTH: 374849

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(374849)

; OTHER INFORMATION: n = A,T,C or G

US-10-087-192-1627

Query Match 79.1%; Score 17.4; DB 6; Length 374849;

Best Local Similarity 94.7%; Pred. No. 1.4e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 AAGGCCTTCCTGGGGTGCT 21

Db 353594 AAGGCCTTCCTGGGGTGCT 353612

RESULT 18

US-10-719-900-152165/c

; Sequence 152165, Application US/10719900

; Publication No. US20050026164A1

; GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
; FILE REFERENCE: 3528.1  
; CURRENT APPLICATION NUMBER: US/10/719,900  
; CURRENT FILING DATE: 2003-11-20  
; PRIOR APPLICATION NUMBER: 60/427,808  
; PRIOR FILING DATE: 2002 11 20  
; NUMBER OF SEQ ID NOS: 982914  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 152165  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-719-900-152165

Query Match 78.2%; Score 17.2; DB 9; Length 25;  
Best Local Similarity 86.4%; Pred. No. 4.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 23 GCAAGGCCCTTCGGGGTTGCTC 2

## RESULT 19

US-09-864-761-6845  
; Sequence 6845, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aeomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 6845  
; LENGTH: 569  
; TYPE: DNA  
; ORGANISM: Homo sapiens

FEATURE:  
; OTHER INFORMATION: MAP TO AL333354.8  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1  
US-09-864-761-6845

Query Match 78.2%; Score 17.2; DB 3; Length 569;  
Best Local Similarity 86.4%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 290 GAAAGGCCCTTCAGGGTGCTC 311

## RESULT 20

US-10-424-599-34279  
; Sequence 34279, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 34279  
; LENGTH: 682  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(682)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_130958C.1  
US-10-424-599-34279

Query Match 78.2%; Score 17.2; DB 8; Length 682;  
Best Local Similarity 86.4%; Pred. No. 3.1e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 332 GAAAGGCCCTTCGGGTGCTC 353

## RESULT 21

US-10-282-122A-23975  
; Sequence 23975, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari

```
; APPLICANT: Zykkind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23975
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-23975

Query Match      78.2%; Score 17.2; DB 8; Length 1440;
Best Local Similarity 86.4%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
Db 141 GAAAGGCCTGGCCGGGTGCTC 162

RESULT 22
US-10-052-482-46
; Sequence 46, Application US/10052482
; Publication No. US20040072264A1
; GENERAL INFORMATION:
; APPLICANT: Engelhard, Eric
; APPLICANT: Morris, David
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71087/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/052,482
; CURRENT FILING DATE: 2002-08-15
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 58822
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4679)..(5145)
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; OTHER INFORMATION: "n" at positions 4679 to 5145 can be any base
US-10-052-482-46

Query Match      78.2%; Score 17.2; DB 8; Length 58822;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
Db 26859 GACAGGCCTTTGGGGGTCTC 26880

RESULT 23
US-10-087-192-466
; Sequence 466, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 466
; LENGTH: 63686
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-466

Query Match      78.2%; Score 17.2; DB 6; Length 63686;
Best Local Similarity 86.4%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGGTGCTC 22
Db 45915 GAAAGGCCTCTCAGGGGTGCTC 45936

RESULT 24
US-10-425-115-69008/c
; Sequence 69008, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69008
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(195)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_162929C.1
US-10-425-115-69008

Query Match      76.4%; Score 16.8; DB 9; Length 195;
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Best Local Similarity 90.0%; Pred. No. 5.4e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AAGAGCCTTCGGGGGTGC 21  
 Db 63 AAGAGCCTTCGGGGGGGCT 44

RESULT 25  
 US-10-425-115-118256/c  
 ; Sequence 118256, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53222)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 118256  
 ; LENGTH: 518  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(518)  
 ; OTHER INFORMATION: unsure at all n locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_39339C.1  
 US-10-425-115-118256

Query Match 76.4%; Score 16.8; DB 9; Length 518;  
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCTTCGGGGGTGC 20  
 Db 311 GAAAGGCCATTCGGGGGGGC 292

RESULT 26  
 US-10-437-963-78913  
 ; Sequence 78913, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 78913  
 ; LENGTH: 551  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_78674C.1  
 US-10-437-963-78913

Query Match 76.4%; Score 16.8; DB 8; Length 551;  
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCTTCGGGGGTGC 20  
 Db 176 GAAAGGCCTTCGGGGGGTTC 195

RESULT 27  
 US-10-021-323-8399/c  
 ; Sequence 8399, Application US/10021323  
 ; Publication No. US20040123340A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deikman, Jill  
 ; APPLICANT: Peng, Paul C.C.  
 ; APPLICANT: Fincher, Karen L.  
 ; APPLICANT: Ziegler, Todd E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(52274)B  
 ; CURRENT APPLICATION NUMBER: US/10/021,323  
 ; CURRENT FILING DATE: 2001-12-12  
 ; PRIOR APPLICATION NUMBER: US 60/255, 619  
 ; PRIOR FILING DATE: 2000-12-14  
 ; NUMBER OF SEQ ID NOS: 17880  
 ; SEQ ID NO 8399  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Gossypium hirsutum  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: LIB3828-009-Q1-K6-G5  
 US-10-021-323-8399

Query Match 76.4%; Score 16.8; DB 8; Length 601;  
 Best Local Similarity 90.0%; Pred. No. 4.9e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGGCCTTCGGGGGTGC 20  
 Db 525 GAAAGGCCTTCGGGGGGGC 506

RESULT 28  
 US-10-282-122A-19508  
 ; Sequence 19508, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578



; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19508  
; LENGTH: 2107  
; TYPE: DNA  
; ORGANISM: Enterobacter cloacae  
US-10-282-122A-19508

Query Match 76.4%; Score 16.8; DB 8; Length 2107;  
Best Local Similarity 90.0%; Pred. No. 4.4e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGCGCTTCGGGGTGCTC 22  
Db 113 AAGCGGTTCGGGGTGCTC 132

## RESULT 29

US-10-322-281-115  
; Sequence 115, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 115  
; LENGTH: 289190  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(289190)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-322-281-115

Query Match 76.4%; Score 16.8; DB 8; Length 289190;  
Best Local Similarity 90.0%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGCGCTTCGGGGTGCT 21  
Db 116861 AAGCGCTTCGTGTGTGCT 116880

## RESULT 30

US-10-106-698-3878  
; Sequence 3878, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides  
; FILE REFERENCE: PA005P1  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PCT APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 3878  
; LENGTH: 309  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28)...(28)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (98)...(98)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (128)...(128)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (139)...(139)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (153)...(153)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (159)...(160)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (207)...(207)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (219)...(219)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (240)...(240)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (250)...(250)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (263)...(263)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (265)...(265)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-106-698-3878

Query Match 74.5%; Score 16.4; DB 6; Length 309;  
Best Local Similarity 94.4%; Pred. No. 8e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGCGCTTCGGGGGTG 19  
Db 74 AAGCGCTTCGGGGGTG 91

## RESULT 31

US-10-021-323-2667  
; Sequence 2667, Application US/10021323  
; Publication No. US20040123340A1  
; GENERAL INFORMATION:  
; APPLICANT: Deikman, Jill  
; APPLICANT: Peng, Paul C.C.  
; APPLICANT: Fincher, Karen L.  
; APPLICANT: Ziegler, Todd E.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(52274)B  
; CURRENT APPLICATION NUMBER: US/10/021,323  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: US 60/255, 619  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 17880

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/ SEQ ID NO 2667
/ LENGTH: 521
/ TYPE: DNA
/ ORGANISM: Gossypium hirsutum
/ FEATURE:
/ OTHER INFORMATION: Clone ID: LIB3825-016-Q1-N6-D3
US-10-021-323-2667

Query Match          74.5%; Score 16.4; DB 8; Length 521;
Best Local Similarity 94.4%; Pred. No. 7.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AAAGGCGCTTCGGGGGTG 19
      |||||
Db       232 AAAGGCGCTTCGGGGGAG 249

RESULT 32
US-10-017-161-717/c
/ Sequence 717, Application US/10017161
/ Publication No. US2003014368A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 084335/0152
/ CURRENT APPLICATION NUMBER: US/10/017,161
/ CURRENT FILING DATE: 2002-12-18
/ PRIOR APPLICATION NUMBER: JP 2001/246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2430
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 717
/ LENGTH: 47804
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: source
/ LOCATION: (1)..(47804)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (201)..(1022)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1093)..(1208)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1871)..(2040)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3227)..(3386)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (3492)..(3698)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (5159)..(5424)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (5651)..(6504)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (18486)..(18612)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (19045)..(19140)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (25901)..(26126)
/ FEATURE:
/ NAME/KEY: CDS

/ LOCATION: (26658)..(26848)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (30445)..(30482)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (37501)..(37634)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (38681)..(38889)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (46474)..(46682)
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (46867)..(47604)
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (7478)..(7577)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (17033)..(17132)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (24561)..(24660)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (33542)..(33641)
/ OTHER INFORMATION: a, t, c, g, unknown or other
/ FEATURE:
/ NAME/KEY: modified base
/ LOCATION: (41424)..(41523)
/ OTHER INFORMATION: a, t, c, g, unknown or other
US-10-017-161-717

Query Match          74.5%; Score 16.4; DB 7; Length 47804;
Best Local Similarity 94.4%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGCCTTTCGGGGTGCTC 22
      |||||
Db       47345 GGCCTTTCGGGGTTCTC 47328

RESULT 33
US-10-292-798-629/c
/ Sequence 629, Application US/10292798
/ Publication No. US2003023583A1
/ GENERAL INFORMATION:
/ APPLICANT: SUWA, MAKIKO
/ APPLICANT: ASAI, KIYOSHI
/ APPLICANT: AKIYAMA, YUTAKA
/ APPLICANT: ABURATANI, HIROYUKI
/ TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
/ FILE REFERENCE: 084335/166
/ CURRENT APPLICATION NUMBER: US/10/292,798
/ CURRENT FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: 10/017,161
/ PRIOR FILING DATE: 2001-12-18
/ PRIOR APPLICATION NUMBER: JP 2001-246789
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 2070
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 629
/ LENGTH: 47804
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ LOCATION: source
/ FEATURE:
```

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; LOCATION: (1)..(47804)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(1022)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1093)..(1208)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1871)..(2040)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3227)..(3386)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3492)..(3698)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5159)..(5424)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (5651)..(6504)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18486)..(18612)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19045)..(19140)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (25901)..(26126)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26658)..(26848)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30445)..(30482)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37501)..(37634)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (38681)..(38889)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46474)..(46682)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46867)..(47604)
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (7478)..(7577)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (17033)..(17132)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (24561)..(24660)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (33542)..(33641)
; OTHER INFORMATION: a, t, c, g, unknown or other
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (41424)..(41523)
; OTHER INFORMATION: a, t, c, g, unknown or other
US-10-292-798-629
```

Query Match 74.5%; Score 16.4; DB 7; Length 47804;  
Best Local Similarity 94.4%; Pred. No. 5.1e+02;

```
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 GGCCTTTCGGGGTGCTC 22
|||||
Db 47345 GGCCTTTCGGGGTTCTC 47328

RESULT 34
US-10-990-355-32
; Sequence 32, Application US/10990355
; Publication No. US20050158741A1
; GENERAL INFORMATION:
; APPLICANT: Mulligan, Richard
; APPLICANT: Yen, Laising
; TITLE OF INVENTION: SELF-CLEAVING RIBOZYMES AND USES THEREOF
; FILE REFERENCE: CHME-P01-001
; CURRENT APPLICATION NUMBER: US/10/990,355
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,941
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: RNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: modified schistosome ribozyme partial sequence
US-10-990-355-32
```

Query Match 73.6%; Score 16.2; DB 10; Length 82;  
Best Local Similarity 61.9%; Pred. No. 1.1e+03;  
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 GAAAGGCCTTTCGGGGTGCT 21
|||||
Db 43 GAAAGCCUUUCGGGCUCCU 63
```

## RESULT 35

```
US-10-425-115-176343/c
; Sequence 176343, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 176343
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_92418C.1
US-10-425-115-176343
```

Query Match 73.6%; Score 16.2; DB 9; Length 314;  
Best Local Similarity 85.7%; Pred. No. 1e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 GAAAGGCCTTTCGGGGTGCT 21
|||||
Db 105 GAAAGGCCTTACGGTTGTCT 85
```

RESULT 36  
US-10-425-115-106353/c

; Sequence 106353, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 106353  
; LENGTH: 353  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_28496C.1  
US-10-425-115-106353

Query Match 73.6%; Score 16.2; DB 9; Length 353;  
Best Local Similarity 85.7%; Pred. No. 9.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 AAAGGCCTTTCGGGGTGCTC 22  
Db 152 AAAGGCCTTTCGGGGTGCTC 132

RESULT 37  
US-10-137-113-21  
; Sequence 21, Application US/10137113  
; Publication No. US20030175725A1  
; GENERAL INFORMATION:  
; APPLICANT: Kepur, Vivek  
; TITLE OF INVENTION: Mycobacterial Diagnostics  
; FILE REFERENCE: 09531-112001  
; CURRENT APPLICATION NUMBER: US/10/137,113  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/362,396  
; PRIOR FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Mycobacterium paratuberculosis  
US-10-137-113-21

Query Match 73.6%; Score 16.2; DB 7; Length 426;  
Best Local Similarity 85.7%; Pred. No. 9.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 AAAGGCCTTTCGGGGTGCTC 22  
Db 77 AAAGACCTGTCGGGGTGCCCC 97

RESULT 38  
US-10-437-963-2250/c  
; Sequence 2250, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 2250  
; LENGTH: 483  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_102039C.1  
US-10-437-963-2250

Query Match 73.6%; Score 16.2; DB 8; Length 483;  
Best Local Similarity 85.7%; Pred. No. 9.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GAAAGGCCTTTCGGGGTGCT 21  
Db 435 GAAAGGCCTTTCGGGGTGCT 415

RESULT 39  
US-10-301-480-276883  
; Sequence 276883, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 276883  
; LENGTH: 505  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-276883

Query Match 73.6%; Score 16.2; DB 12; Length 505;  
Best Local Similarity 85.7%; Pred. No. 9.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GAAAGGCCTTTCGGGGTGCT 21  
Db 360 GTAAGGCCTTTCGGGATGCT 380

RESULT 40  
US-10-301-480-890292  
; Sequence 890292, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 890292

```

; LENGTH: 505
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890292

Query Match      73.6%; Score 16.2; DB 12; Length 505;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 360 GTAAGGCCTTTCGGGATGCT 380

RESULT 41
US-09-925-065A-186776
; Sequence 186776, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186776
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-186776

Query Match      73.6%; Score 16.2; DB 4; Length 506;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 361 GTAAGGCCTTTCGGGATGCT 381

RESULT 42
US-09-925-065A-186776
; Sequence 186776, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09

```

```

; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186776
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-186776

Query Match      73.6%; Score 16.2; DB 5; Length 506;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 361 GTAAGGCCTTTCGGGATGCT 381

RESULT 43
US-10-029-386-9545
; Sequence 9545, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9545
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHRI.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.8
; OTHER INFORMATION: SWISSPROT HIT: Q01956, EVALUAE 1.60e+00
; OTHER INFORMATION: NT HIT: G16679159, EVALUAE 9.00e-49
; OTHER INFORMATION: EST_HUMAN HIT: AW752727.1, EVALUAE 4.00e-36
US-10-029-386-9545

Query Match      73.6%; Score 16.2; DB 7; Length 511;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCT 21
   ||||| ||||| ||||| |||||
Db 187 GTAAGGCCTTTCGGGATGCT 207

RESULT 44
US-10-437-963-84361
; Sequence 84361, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B

```

```
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 84361
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_83604C.1
US-10-437-963-84361

Query Match      73.6%; Score 16.2; DB 8; Length 528;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 279 AAGGGACTTTGGGGGGTGCTC 299

RESULT 45
US-09-925-065A-301027
; Sequence 301027, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2000-11-30
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301027
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301027

Query Match      73.6%; Score 16.2; DB 4; Length 561;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 238 AAAGGTCTTTTCGGGTGCTC 258

RESULT 46
US-09-925-065A-301027
; Sequence 301027, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301027
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301027

Query Match      73.6%; Score 16.2; DB 4; Length 561;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 238 AAAGGTCTTTTCGGGTGCTC 258

RESULT 47
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026

Query Match      73.6%; Score 16.2; DB 4; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 146 AAAGGTCTTTTCGGGTGCTC 166

RESULT 48
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026
```

```
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301027
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301027

Query Match      73.6%; Score 16.2; DB 5; Length 561;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 238 AAAGGTCTTTTCGGGTGCTC 258

RESULT 47
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026

Query Match      73.6%; Score 16.2; DB 4; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTTCGGGGTGCTC 22
Db 146 AAAGGTCTTTTCGGGTGCTC 166

RESULT 48
US-09-925-065A-301026
; Sequence 301026, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026
```

```

; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 301026
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-301026

Query Match      73.6%; Score 16.2; DB 5; Length 567;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      146 AAAGTCTTCGGTGGTCTC 166

RESULT 49
US-09-925-065A-821134/c
; Sequence 821134, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821134
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-821134

Query Match      73.6%; Score 16.2; DB 4; Length 592;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGCCTTCGGGGGTGCTC 21
Db      65 GAAAGGCCTCCCTGGGGTCTC 45

RESULT 50
US-09-925-065A-821134/c
; Sequence 821134, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135

```

```

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 821134
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-821134

Query Match      73.6%; Score 16.2; DB 5; Length 592;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGCCTTCGGGGGTGCTC 21
Db      65 GAAAGGCCTCCCTGGGGTCTC 45

RESULT 51
US-10-750-185-19831/c
; Sequence 19831, Application US/10/750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19831
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine
MMBT00837
US-10-750-185-19831

Query Match      73.6%; Score 16.2; DB 10; Length 600;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGCCTTCGGGGGTGCTC 22
Db      159 AATGGCCTTCGGGGGAATC 139

RESULT 52
US-10-750-623-19831/c
; Sequence 19831, Application US/10/750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David

```

```

; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19831
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT00837
US-10-750-623-19831
```

```

Query Match      73.6%; Score 16.2; DB 10; Length 600;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 AAAGGCCCTTTCGGGGTGCTC 22
Db      159 AATGGCCCTTTCGGGGGAATC 139
```

```

RESULT 53
US-09-925-065A-884151
; Sequence 884151, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 884151
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-884151
```

```

Query Match      73.6%; Score 16.2; DB 4; Length 607;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GAAAGCCCTTTCGGGGTGCT 21
Db      197 GAAAGCCCTTTCGGAGGTGAT 217
```

```

RESULT 54
US-09-925-065A-884151
; Sequence 884151, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```

; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 884151
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-884151
```

```

Query Match      73.6%; Score 16.2; DB 5; Length 607;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 GAAAGCCCTTTCGGGGTGCT 21
Db      197 GAAAGCCCTTTCGGAGGTGAT 217
```

```

RESULT 55
US-10-027-632-268485
; Sequence 268485, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268485
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-268485
```

```

Query Match      73.6%; Score 16.2; DB 6; Length 623;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 AAAGCCCTTTCGGGGTGCTC 22
Db      517 AAAGCCCTTTCGGTGAGCTC 537
```

```

RESULT 56
US-10-027-632-268485
```



```
; Sequence 268485, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027.632
; CURRENT FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2002-04-30
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 268485
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-268485

Query Match          73.6%; Score 16.2; DB 7; Length 623;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCGCTTTTCGGGGTGCTC 22
Db      517 AAAGGCGCTTTTCGGTGAGCTC 537

RESULT 57
US-09-925-065A-818614/c
; Sequence 818614, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 818614
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-818614

Query Match          73.6%; Score 16.2; DB 4; Length 626;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 GAAAGGCGCTTTTCGGGGTGCT 21
Db      568 GGAAGGCGCTTTTCGGGGTGTT 548

RESULT 58
US-09-925-065A-818614/c
; Sequence 818614, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 818614
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-818614

Query Match          73.6%; Score 16.2; DB 5; Length 626;
Best Local Similarity 85.7%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GAAAGGCGCTTTTCGGGGTGCT 21
Db      568 GGAAGGCGCTTTTCGGGGTGTT 548

RESULT 59
US-09-925-065A-848383/c
; Sequence 848383, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 848383
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848383

Query Match          73.6%; Score 16.2; DB 4; Length 631;
```



US-10-750-185-32645

Query Match 73.6%; Score 16.2; DB 10; Length 825;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTCGGGGTGCTC 22  
Db 306 AATGGCCTTTCGGGGGAATC 286

RESULT 64

US-10-750-623-32645/c  
; Sequence 32645, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10750.623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64322  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 32645  
; LENGTH: 825  
; TYPE: DNA  
; ORGANISM: Bovine 19866880690787

US-10-750-623-32645  
Query Match 73.6%; Score 16.2; DB 10; Length 825;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTCGGGGTGCTC 22  
Db 306 AATGGCCTTTCGGGGGAATC 286

RESULT 65

US-09-854-867-342  
; Sequence 342, Application US/09854867  
; Publication No. US20030224356A1  
; GENERAL INFORMATION:  
; APPLICANT: JOAN, KNOLL H  
; APPLICANT: ROGAN, PETER K  
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING  
; FILE REFERENCE: 30307  
; CURRENT APPLICATION NUMBER: US/09/854.867  
; CURRENT FILING DATE: 2003-05-08  
; NUMBER OF SEQ ID NOS: 613  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 342  
; LENGTH: 909  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: repeat\_region  
; LOCATION: (1)..(909)  
; OTHER INFORMATION: l1me3a  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (647)..(647)  
; OTHER INFORMATION: n is a, c, g or t  
; FEATURE:  
; NAME/KEY: misc\_feature

; LOCATION: (657)..(658)  
; FEATURE:  
; OTHER INFORMATION: n is a, c, g or t  
; NAME/KEY: misc\_feature  
; LOCATION: (705)..(705)  
; OTHER INFORMATION: n is a, c, g or t  
US-09-854-867-342

Query Match 73.6%; Score 16.2; DB 3; Length 909;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTCGGGGTGCT 21  
Db 762 GAGAGGCTTTCGGGGTGCT 782

RESULT 66

US-10-786-970A-342  
; Sequence 342, Application US/10786970A  
; Publication No. US2005006449A1  
; GENERAL INFORMATION:  
; APPLICANT: JOAN, KNOLL  
; APPLICANT: ROGAN, PETER  
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING  
; FILE REFERENCE: 30307  
; CURRENT APPLICATION NUMBER: US/10786.970A  
; CURRENT FILING DATE: 2004-02-24  
; PRIOR APPLICATION NUMBER: US/09/573,080  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 479  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 342  
; LENGTH: 909  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: repeat\_region  
; LOCATION: (1)..(909)  
; OTHER INFORMATION: l1me3a  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: n is a, c, g or t  
; PUBLICATION INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A  
; TITLE: Prototypic sequences for human repetitive DNA  
; JOURNAL: Journal of Molecular Evolution  
; VOLUME: 35  
; ISSUE: 4  
; PAGES: 286-291  
; DATE: 1992-10-  
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)  
; DATABASE ENTRY DATE: 1996-01-26  
; DATABASE ENTRY DATE: 1996-01-26

US-10-786-970A-342  
Query Match 73.6%; Score 16.2; DB 10; Length 909;  
Best Local Similarity 85.7%; Pred. No. 9.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTCGGGGTGCT 21  
Db 762 GAGAGGCTTTCGGGGTGCT 782

RESULT 67

US-10-027-632-163064  
; Sequence 163064, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 163064  
 ; LENGTH: 935  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-027-632-163064

Query Match 73.6%; Score 16.2; DB 6; Length 935;  
 Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 3;

QY 2 AAAGGCCTTTCGGGGTGCTC 22  
 |||||  
 Db 519 AAAGGCCTTTCGGTGAGTC 539

RESULT 68  
 US-10-027-632-163064  
 ; Sequence 163064, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 163064  
 ; LENGTH: 935  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-027-632-163064

Query Match 73.6%; Score 16.2; DB 7; Length 935;  
 Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 3;

QY 2 AAAGGCCTTTCGGGGTGCTC 22

Db 519 AAAGGCCTTTCGGTGAGTC 539  
 |||||  
 |||||

RESULT 69  
 US-10-437-963-29828/c  
 ; Sequence 29828, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 29828  
 ; LENGTH: 1014  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (1)..(1014)  
 ; OTHER INFORMATION: unsure at all n locations  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_34292C.1  
 ; US-10-437-963-29828

Query Match 73.6%; Score 16.2; DB 8; Length 1014;  
 Best Local Similarity 85.7%; Pred. No. 9e+02; 3; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 3;

QY 1 GAAAGGCCTTTCGGGGTGCT 21  
 |||||  
 Db 944 GAAGGCCCATTCGGGGGGCT 924

RESULT 70  
 US-09-864-761-20761/c  
 ; Sequence 20761, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; FILE REFERENCE: Aeonica-X-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664

;  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 20761  
; LENGTH: 1218  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AC006115.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.5  
; OTHER INFORMATION: NT HIT: AF208980.1, EVALUE 0.00e+00  
; OTHER INFORMATION: EST HUMAN HIT: AU137741.1, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: P52742, EVALUE 2.00e-17  
US-09-864-761-20761

Query Match 73.6%; Score 16.2; DB 3; Length 1218;  
Best Local Similarity 85.7%; Pred. No. 8.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTCCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 139 AAATGCCTTTGGGGAGTGCTC 119

## RESULT 71

US-10-282-122A-26246  
; Sequence 26246, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A

;  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26246  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Mycobacterium bovis  
US-10-282-122A-26246  
  
Query Match 73.6%; Score 16.2; DB 8; Length 1377;  
Best Local Similarity 85.7%; Pred. No. 8.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 2 AAAGCCTTTCCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 538 AAAGCGCGTCCGGGGTGCTC 558  
  
RESULT 72  
US-10-282-122A-28592  
; Sequence 28592, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625

RESULT 74

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; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US 09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4001
; LENGTH: 1954
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006115.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.9
US-09-864-761-4001

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; Sequence 815, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133p1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 815
; LENGTH: 2772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1253)..(1253)
; OTHER INFORMATION: n equals a,t,g, or c
;
US-10-264-049-815

Query Match 73.6%; Score 16.2; DB 7; Length 2772;
Best Local Similarity 85.7%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGTGCTC 22
||| ||||| ||||| |||||
Db 1526 AAATGCCTTTGGGGAGTGCTC 1546

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RESULT 78
US-10-175-523-151
; Sequence 151, Application US/10175523
; Publication No. US20030096264A1
; GENERAL INFORMATION:
; APPLICANT: Brockman, Jeffrey
; APPLICANT: Evans, David
; APPLICANT: Hook, Derek
; APPLICANT: Klimczak, Leszek
; APPLICANT: Laeng, Pascal
; APPLICANT: Palfreyman, Michael
; APPLICANT: Rajan, Prithi
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
; FILE REFERENCE: 3235/1J795-US3
; CURRENT APPLICATION NUMBER: US/10/175,523
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/299,151
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/317,828
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/325,150
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/333,047
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 60/349,936
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/361,834
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 3135
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-175-523-151

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RESULT 77  
US-10-264-049-815  
Best Local Similarity 83.7%, Freq. NO. 0.16702,  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 1689 AAATGCCTTTGGGAGTGCTC 1709

## RESULT 79

US-11-099-266-151  
; Sequence 151, Application US/11099266  
; Publication No. US20050181433A1  
; GENERAL INFORMATION:  
; APPLICANT: Brockman, Jeffrey  
; APPLICANT: Evans, David  
; APPLICANT: Hook, Derek  
; APPLICANT: Klimczak, Leszek  
; APPLICANT: Laeng, Pascal  
; APPLICANT: Palfreyman, Michael  
; APPLICANT: Rajan, Prithi  
; TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)  
; FILE REFERENCE: 03235/100J795-US4  
; CURRENT APPLICATION NUMBER: US/11/099,266  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: US 10/175,523  
; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,151  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/317,828  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/325,150  
; PRIOR FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: US 60/333,047  
; PRIOR FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 60/349,936  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/361,834  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 151  
; LENGTH: 3135  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-099-266-151

Query Match 73.6%; Score 16.2; DB 13; Length 3135;  
Best Local Similarity 85.7%; Pred. No. 8.1e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 1689 AAATGCCTTTGGGAGTGCTC 1709

## RESULT 80

US-10-287-436A-1061  
; Sequence 1061, Application US/10287436A  
; Publication No. US20050202421A1  
; GENERAL INFORMATION:  
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER  
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF  
; FILE REFERENCE: 10872.514696  
; CURRENT APPLICATION NUMBER: US/10/287,436A  
; CURRENT FILING DATE: 2002-10-31  
; PRIOR APPLICATION NUMBER: US 60/336,220  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 1446  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1061  
; LENGTH: 4258  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-287-436A-1061

Query Match 73.6%; Score 16.2; DB 10; Length 4258;  
Best Local Similarity 85.7%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCT 21  
||| ||||| ||| |||||  
Db 12 GACAGGCCTTCGGGGATGCT 32

## RESULT 81

US-09-925-301-224  
; Sequence 224, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 224  
; LENGTH: 4395  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (325)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (4382)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (4391)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-224

Query Match 73.6%; Score 16.2; DB 3; Length 4395;  
Best Local Similarity 85.7%; Pred. No. 7.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGCCTTTCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 603 AAATGCCTTTGGGAGTGCTC 623

## RESULT 82

US-10-137-113-23/c  
; Sequence 23, Application US/10137113  
; Publication No. US20030175725A1  
; GENERAL INFORMATION:  
; APPLICANT: Kepur, Vivek  
; APPLICANT: Rannantine, John P.  
; TITLE OF INVENTION: Mycobacterial Diagnostics  
; FILE REFERENCE: 09531-112001  
; CURRENT APPLICATION NUMBER: US/10/137,113  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/362,396  
; PRIOR FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 4415  
; TYPE: DNA  
; ORGANISM: Mycobacterium paratuberculosis  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 44  
; OTHER INFORMATION: n = A,T,C or G



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US-10-137-113-23
Query Match      73.6%; Score 16.2; DB 7; Length 4415;
Best Local Similarity 85.7%; Pred. No. 7.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      625 AAAGACCTGTCGGGGGTGCC 605

RESULT 83
US-09-842-777-9
; Sequence 9, Application US/09842777
; Publication No. US20020182669A1
; GENERAL INFORMATION:
; APPLICANT: Surani, Azim
; APPLICANT: Szeto, Yuk Y
; TITLE OF INVENTION: Human PEG3 Gene and Uses Thereof
; FILE REFERENCE: 41657
; CURRENT APPLICATION NUMBER: US/09/842,777
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-842-777-9

Query Match      73.6%; Score 16.2; DB 3; Length 4758;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      4599 AAATGCCTTTGGGGAGTGCTC 4619

RESULT 84
US-10-334-143-116
; Sequence 116, Application US/10334143
; Publication No. US20040009549A1
; GENERAL INFORMATION:
; APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
; APPLICANT: SUDARSANAM, SUCHA
; TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL
; TITLE OF INVENTION: KINASES IDENTIFIED WITH THE METHOD
; FILE REFERENCE: 038602/1543
; CURRENT APPLICATION NUMBER: US/10/334,143
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: 60/343,169
; PRIOR FILING DATE: 2001-12-31
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 4831
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-334-143-116

Query Match      73.6%; Score 16.2; DB 7; Length 4831;
Best Local Similarity 85.7%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      4672 AAATGCCTTTGGGGAGTGCTC 4692

RESULT 85
US-10-205-219-136
; Sequence 136, Application US/10205219
; Publication No. US20030138803A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pincock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018200
; CURRENT APPLICATION NUMBER: US/10/205,219
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: KIAA0287
US-10-205-219-136

Query Match      73.6%; Score 16.2; DB 7; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      4591 AAATGCCTTTGGGGAGTGCTC 4611

RESULT 86
US-10-173-999-122
; Sequence 122, Application US/10173999
; Publication No. US20040005583A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Ovarian Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Ovarian
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002420US
; CURRENT APPLICATION NUMBER: US/10/173,999
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: US 60/299,234
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/315,287
; PRIOR FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2001-04-12
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-173-999-122

Query Match      73.6%; Score 16.2; DB 7; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTCGGGGGTGCTC 22
Db      4591 AAATGCCTTTGGGGAGTGCTC 4611

RESULT 87
US-10-723-860-1893
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; Sequence 1893, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1893
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1893

Query Match 73.6%; Score 16.2; DB 9; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 4591 AAATGCTTTGGGAGTGCTC 4611

RESULT 88
US-10-756-149-1800
; Sequence 1800, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1800
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-1800

Query Match 73.6%; Score 16.2; DB 10; Length 5994;
Best Local Similarity 85.7%; Pred. No. 7.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 4591 AAATGCTTTGGGAGTGCTC 4611

RESULT 89
US-10-276-774-1341
; Sequence 1341, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914

; Sequence 1893, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1893
; LENGTH: 5994
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-1893

Query Match 73.6%; Score 16.2; DB 8; Length 6332;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 4899 AAATGCTTTGGGAGTGCTC 4919

RESULT 90
US-10-960-414-82
; Sequence 82, Application US/10960414
; Publication No. US200600074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINCENTIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82
; LENGTH: 6371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-82

Query Match 73.6%; Score 16.2; DB 12; Length 6371;
Best Local Similarity 85.7%; Pred. No. 7.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGTGCTC 22
Db 4972 AAATGCTTTGGGAGTGCTC 4992

RESULT 91
US-09-919-039-223
; Sequence 223, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 223
; LENGTH: 8412
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 380283.1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 4053-4099, 8362, 8373, 8382, 8389, 8399, 8406-8407
; OTHER INFORMATION: a, t, c, g, or other
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## US-09-919-039-223

Query Match 73.6%; Score 16.2; DB 3; Length 8412;  
Best Local Similarity 85.7%; Pred. No. 7.5e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTTCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 4595 AAATGCCTTTGGGGAGTGCTC 4615

## RESULT 92

US-10-062-674-1976  
; Sequence 1976, Application US/10062674  
; Publication No. US2004000559A1  
; GENERAL INFORMATION:  
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.  
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS  
; FILE REFERENCE: PA-0026-1 CIP  
; CURRENT APPLICATION NUMBER: US/10/062,674  
; CURRENT FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: US 09/625,102  
; PRIOR FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 2217  
; SOFTWARE: PERL Program  
; SEQ ID NO 1976  
; LENGTH: 8682  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US2004000559A1 380283.5  
; FEATURE:  
; LOCATION: (1).... (8682)  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-062-674-1976

Query Match 73.6%; Score 16.2; DB 7; Length 8682;  
Best Local Similarity 85.7%; Pred. No. 7.4e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGCCTTTTCGGGGTGCTC 22  
||| ||||| ||| |||||  
Db 4771 AAATGCCTTTGGGGAGTGCTC 4791

## RESULT 93

US-10-388-934-556  
; Sequence 556, Application US/10388934  
; Publication No. US20040005547A1  
; GENERAL INFORMATION:  
; APPLICANT: Boess, Franziska  
; APPLICANT: Suter-Dick, Laura  
; TITLE OF INVENTION: Biomarkers and Expression Profiles for Toxicology  
; FILE REFERENCE: 21199  
; CURRENT APPLICATION NUMBER: US/10/388,934  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 02005336.9  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: 02015657.6  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 862  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 556  
; LENGTH: 25759  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus (No. US20040005547A1way rat)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7).... (7)  
; OTHER INFORMATION: n

; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8).... (8)  
; OTHER INFORMATION: n  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9).... (9)  
; OTHER INFORMATION: n  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10).... (10)  
; OTHER INFORMATION: n  
US-10-388-934-556

Query Match 73.6%; Score 16.2; DB 7; Length 25759;  
Best Local Similarity 85.7%; Pred. No. 6.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTTCGGGGTGCT 21  
||| ||||| ||| |||||  
Db 21445 GAAAGCATTAGTGGTGCT 21465

## RESULT 94

US-11-224-663-556  
; Sequence 556, Application US/11224663  
; Publication No. US20060078921A1  
; GENERAL INFORMATION:  
; APPLICANT: BOESS, FRANZISKA  
; APPLICANT: SUTER-DICK, LAURA  
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY  
; FILE REFERENCE: 21199 US2  
; CURRENT APPLICATION NUMBER: US/11/224,663  
; CURRENT FILING DATE: 2005-09-12  
; PRIOR APPLICATION NUMBER: 10/388,934  
; PRIOR FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: EP 02005336.9  
; PRIOR FILING DATE: 2002-03-14  
; PRIOR APPLICATION NUMBER: EP 02015657.6  
; PRIOR FILING DATE: 2002-07-17  
; NUMBER OF SEQ ID NOS: 862  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 556  
; LENGTH: 25759  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (7).... (10)  
; OTHER INFORMATION: a, t, c, g, other or unknown  
US-11-224-663-556

Query Match 73.6%; Score 16.2; DB 16; Length 25759;  
Best Local Similarity 85.7%; Pred. No. 6.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTTTCGGGGTGCT 21  
||| ||||| ||| |||||  
Db 21445 GAAAGCATTAGTGGTGCT 21465

## RESULT 95

US-11-224-525-556  
; Sequence 556, Application US/11224525  
; Publication No. US20060084096A1  
; GENERAL INFORMATION:  
; APPLICANT: BOESS, FRANZISKA  
; APPLICANT: SUTER-DICK, LAURA  
; TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY  
; FILE REFERENCE: 21199 US1  
; CURRENT APPLICATION NUMBER: US/11/224,525

CURRENT APPLICATION NUMBER: US/10/175,523

Db 37462 GATATGCCCTTTTCGGGTGCT 37442  
|||||

RESULT 99  
US-10-012-697-422/c  
; Sequence 422, Application US/10012697  
; Publication No. US20030215803A1  
; GENERAL INFORMATION:  
; APPLICANT: Escobedo, Jaime  
; APPLICANT: Garcia, Pablo Dominguez  
; APPLICANT: Kassam, Altaf  
; APPLICANT: Lamson, George  
; APPLICANT: Scott, Beth  
; APPLICANT: Drmanac, Radoje  
; APPLICANT: Crkvenjakov, Radomir  
; APPLICANT: Dickson, Mark  
; APPLICANT: Drmanac, Snezana  
; APPLICANT: Labat, Ivan  
; APPLICANT: Leshkowitz, Dena  
; APPLICANT: Kita, David  
; APPLICANT: Garcia, Veronica  
; APPLICANT: Jones, Lee William  
; APPLICANT: Stache-Crain, Birgit  
; TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS  
; FILE REFERENCE: 2300-16252  
; CURRENT APPLICATION NUMBER: US/10/012,697  
; PRIOR FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: 60/254,648  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: 60/275,668  
; PRIOR FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 1568  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 422  
; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
US-10-012-697-422

Query Match 72.7%; Score 16; DB 7; Length 297;  
Best Local Similarity 100.0%; Pred.No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTTCGGGG 16  
|||||  
Db 74 GAAAGGCCTTTTCGGGG 59

RESULT 100  
US-10-779-543-22422/c  
; Sequence 22422, Application US/10779543  
; Publication No. US20050227917A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams et al  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
; FILE REFERENCE: 2300-21302  
; CURRENT APPLICATION NUMBER: US/10/779,543  
; PRIOR FILING DATE: 2004-02-12  
; PRIOR APPLICATION NUMBER: 10/076,555  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: 09/217,471  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/068,755  
; PRIOR FILING DATE: 1997-12-23  
; PRIOR APPLICATION NUMBER: 60/080,664  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/105,234  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 09/297,648  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: PCT/US99/01619  
; PRIOR FILING DATE: 1999-01-28  
; PRIOR APPLICATION NUMBER: 60/072,910  
; PRIOR FILING DATE: 1998-01-28  
; PRIOR APPLICATION NUMBER: 60/075,954  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/080,114  
; PRIOR FILING DATE: 1998-03-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 23767  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22422  
; LENGTH: 297  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,  
; LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297  
; OTHER INFORMATION: n = A,T,C or G  
US-10-779-543-22422

Query Match 72.7%; Score 16; DB 10; Length 297;  
Best Local Similarity 100.0%; Pred.No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTTCGGGG 16  
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Db 74 GAAAGGCCTTTTCGGGG 59

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 13.6506 Seconds  
(without alignments)  
113.711 Million cell updates/sec

Title: US-10-665-708-25

Perfect score: 22

Sequence: 1 gaaagcccttcgggggtgctc 22

Scoring table: IDENTITY NUC

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Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA New.\*

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- 2: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US06\_NEW\_PUB.seq.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US07\_NEW\_PUB.seq.\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US08\_NEW\_PUB.seq.\*
- 5: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/PCT\_NEW\_PUB.seq.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US10\_NEW\_PUB.seq.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US11\_NEW\_PUB.seq.\*
- 8: /EMC\_Celerra\_SID33/ptodata/2/pubnpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	70.9	1923	7	US-11-217-529-75858
2	14.8	67.3	51	7	US-11-143-642-1563
3	14.6	66.4	352	6	US-10-488-619-487
4	14.6	66.4	4896	7	US-11-258-767-61
5	14.6	66.4	394191	6	US-10-506-549-3
6	14.2	64.5	415	6	US-10-473-173-344
7	14.2	64.5	597	6	US-10-488-619-2783
8	14.2	64.5	1869	7	US-11-217-529-76833
9	14.2	64.5	2063	6	US-10-196-749-329
10	14.2	64.5	2063	7	US-11-101-316-111
11	14.2	64.5	2104	7	US-11-145-307A-34
12	14.2	64.5	963	7	US-11-217-529-80486
13	14.2	64.5	1122	7	US-11-217-529-81650
14	14.2	64.5	1938	7	US-11-217-529-82499
15	14.2	64.5	2384	7	US-11-145-307A-259
16	14.2	64.5	3401	6	US-10-505-928-717
17	14.2	64.5	4277	6	US-10-196-749-439
18	14.2	64.5	4933	6	US-10-505-928-15
19	14.2	64.5	4933	6	US-10-505-928-88
20	14.2	64.5	135090	6	US-10-505-928-607
21	13.8	62.7	76	7	US-11-267-871-477
22	13.8	62.7	76	7	US-11-267-871-477
23	13.8	62.7	76	7	US-11-267-871-478
24	13.8	62.7	76	7	US-11-267-871-478
25	13.8	62.7	76	7	US-11-267-871-479

Sequence 479, App	76	62.7	13.8	7	US-11-267-871-479
Sequence 577, App	3432	62.7	13.8	6	US-10-505-928-577
GENERAL INFORMATI	6	62.7	13.8	6	US-10-489-730-10
Sequence 2651, Ap	50	61.8	13.6	7	US-10-511-937-2651
Sequence 480, App	76	61.8	13.6	7	US-11-267-871-480
Sequence 480, App	76	61.8	13.6	7	US-11-267-871-480
Sequence 2876, Ap	282	61.8	13.6	7	US-11-217-529-2876
Sequence 1040, Ap	393	61.8	13.6	6	US-10-488-619-1040
Sequence 167012,	420	61.8	13.6	6	US-11-217-529-167012
Sequence 76, Appl	1170	61.8	13.6	6	US-10-541-993-76
Sequence 598, App	1458	61.8	13.6	6	US-10-511-937-598
Sequence 398, App	1631	61.8	13.6	6	US-10-511-937-398
Sequence 77050, A	1950	61.8	13.6	7	US-11-217-529-77050
Sequence 462, App	2615	61.8	13.6	6	US-10-511-937-462
Sequence 2820, Ap	3003	61.8	13.6	6	US-10-511-937-2820
Sequence 989, App	3435	61.8	13.6	7	US-11-217-529-989
Sequence 319, App	462	60.9	13.4	6	US-10-488-619-319
Sequence 1868, Ap	20	60.0	13.2	6	US-10-511-937-1868
Sequence 185666,	25	60.0	13.2	7	US-11-217-529-185666
Sequence 397, App	64	60.0	13.2	7	US-11-267-871-397
Sequence 397, App	64	60.0	13.2	7	US-11-267-871-397
Sequence 300, App	185	60.0	13.2	7	US-11-301-554-300
Sequence 1087, Ap	253	60.0	13.2	6	US-10-488-619-1087
Sequence 81832, A	330	60.0	13.2	7	US-11-217-529-81832
Sequence 13, Appl	339	60.0	13.2	7	US-11-217-529-82742
Sequence 373, App	467	60.0	13.2	6	US-11-301-554-373
Sequence 79160, A	574	60.0	13.2	6	US-10-514-738-19
Sequence 1381, Ap	723	60.0	13.2	6	US-11-217-529-79160
Sequence 447, App	894	60.0	13.2	7	US-11-217-529-447
Sequence 1664, Ap	999	60.0	13.2	7	US-11-301-554-1664
Sequence 613, App	1263	60.0	13.2	6	US-10-511-937-613
Sequence 2966, Ap	1284	60.0	13.2	7	US-11-217-529-2966
Sequence 3591, Ap	1902	60.0	13.2	6	US-11-217-529-3591
Sequence 605, App	2338	60.0	13.2	6	US-10-511-937-605
Sequence 1652, Ap	2436	60.0	13.2	6	US-11-217-529-1652
Sequence 99, Appl	2579	60.0	13.2	6	US-10-196-749-95
Sequence 80783, A	2760	60.0	13.2	7	US-11-217-529-80783
Sequence 836, App	2976	60.0	13.2	6	US-11-217-529-80319
Sequence 346, App	3269	60.0	13.2	6	US-10-505-928-836
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Sequence 105, App	2610	59.1	13	7	US-11-217-529-105

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ALIGNMENTS

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; Sequence 75858, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Sequence 1719, Ap  
Sequence 81843, A  
Sequence 205, App  
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Sequence 71, Appl  
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Sequence 5833, Ap  
Sequence 179, App  
Sequence 77238, A  
Sequence 78638, A  
Sequence 261, App  
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Sequence 3, Appl

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; CURRENT APPLICATION NUMBER: US/11/217,529  
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; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
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; LENGTH: 1923  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-75858

Query Match 70.9%; Score 15.6; DB 7; Length 1923;  
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RESULT 2

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; Sequence 1563, Application US/11143642  
; Publication No. US20060099610A1  
; GENERAL INFORMATION:  
; APPLICANT: Jukka T. SALONEN et al.  
; TITLE OF INVENTION: METHOD AND KIT FOR DETECTING A RISK OF ACUTE MYOCARDIAL INFARCTION  
; FILE REFERENCE: 0933-0245PUS1  
; CURRENT APPLICATION NUMBER: US/11/143,642  
; CURRENT FILING DATE: 2005-06-03  
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US-11-143-642-1563

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Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 AGGCCCTTCGGGGTGCT 21  
DB 32 AGGCCCTTCGGGGTGCT 49

RESULT 3

US-10-488-619-487  
; Sequence 487, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 487  
; LENGTH: 352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-488-619-487

Query Match 66.4%; Score 14.6; DB 6; Length 352;  
Best Local Similarity 81.0%; Pred. No. 36;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGCCCTTCGGGGTGCT 21

Db 168 GGAAGGCTCCGGGGTGCT 188  
| | | | | | | | | | | | | | | | | |

RESULT 4  
US-11-258-767-61  
; Sequence 61, Application US/11258767  
; Publication No. US20060094082A1  
; GENERAL INFORMATION:  
; APPLICANT: Varadhachary, Atul  
; APPLICANT: Glynn, Peter  
; APPLICANT: Petrak, Karei  
; APPLICANT: Engelmayer, Jose  
; TITLE OF INVENTION: COMPOSITIONS OF LACTOFERRIN RELATED PEPTIDES AND USES THEREOF  
; FILE REFERENCE: HO-P02915US1  
; CURRENT APPLICATION NUMBER: US/11/258,767  
; PRIOR FILING DATE: 2005-10-26  
; PRIOR APPLICATION NUMBER: US 60/622,176  
; PRIOR FILING DATE: 2004-10-26  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 61  
; LENGTH: 4896  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-11-258-767-61

Query Match 66.4%; Score 14.6; DB 7; Length 4896;  
Best Local Similarity 81.0%; Pred. No. 52;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGCTC 22  
| | | | | | | | | | | | | | | | | |  
Db 336 AATGGCCTTCAGGGGTGCTC 356

RESULT 5  
US-10-506-549-3/c  
; Sequence 3, Application US/10506549  
; Publication No. US20060100417A1  
; GENERAL INFORMATION:  
; APPLICANT: APPLERA CORPORATION  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001361-US  
; CURRENT APPLICATION NUMBER: US/10/506,549  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 60/361,343  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 394191  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(394191)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-506-549-3

Query Match 66.4%; Score 14.6; DB 6; Length 394191;  
Best Local Similarity 81.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTGCT 21  
| | | | | | | | | | | | | | | | | |  
Db 348930 GAGAGGCTTTCTGATGCT 348910

RESULT 6  
US-10-473-173-344/c

; Sequence 344, Application US/10473173  
; Publication No. US20060088823A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN ANDEL INSTITUTE  
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell  
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification  
; FILE REFERENCE: 38345-170094  
; CURRENT APPLICATION NUMBER: US/10/473,173  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/279,411  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 498  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 344  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (186)..(186)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (235)..(235)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (242)..(242)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (257)..(257)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (319)..(319)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (372)..(372)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (385)..(385)  
; OTHER INFORMATION: n can be a, c, g or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (410)..(410)  
; OTHER INFORMATION: n can be a, c, g or t  
US-10-473-173-344

Query Match 64.5%; Score 14.2; DB 6; Length 415;  
Best Local Similarity 84.2%; Pred. No. 58;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGTG 19  
| | | | | | | | | | | | | | | | | |  
Db 228 GAGAGCCCTTCAGGGTG 210

RESULT 7  
US-10-488-619-2783  
; Sequence 2783, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1

```

; SEQ ID NO 2783
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2783

Query Match      64.5%; Score 14.2; DB 6; Length 597;
Best Local Similarity 84.2%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAAGGCCTTCGGGGGTGC 20
      ||||| ||||| |||||
Db      312 AAAGGCCTTAGGGGTCC 330

RESULT 8
US-11-217-529-76833/c
; Sequence 76833, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76833
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76833

Query Match      64.5%; Score 14.2; DB 7; Length 1869;
Best Local Similarity 84.2%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGGTG 19
      ||||| ||||| |||||
Db      1085 GAAAGACATTCGGGTG 1067

RESULT 9
US-10-196-749-329/c
; Sequence 329, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263

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Db      509 AGGCCCTTCGGGAAGCTC 491
||||| ||||| ||||| |||||
RESULT 11
US-11-145-307A-34/c
; Sequence 34, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 2104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-34
Query Match      64.5%; Score 14.2; DB 7; Length 2104;
Best Local Similarity 84.2%; Pred. No. 73;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      4 AGGCCCTTCGGGGTGCTC 22
||||| ||||| ||||| |||||
Db      532 AGGCCCTTCGGGAAGCTC 514

RESULT 12
US-11-217-529-80486/c
; Sequence 80486, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80486
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80486
Query Match      63.6%; Score 14; DB 7; Length 963;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| ||||| |||||
Db      275 GTATAGCCTTCGAGGGTGCTC 254

RESULT 13
US-11-217-529-81650
; Sequence 81650, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81650
; LENGTH: 1122
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81650
Query Match      63.8%; Score 14; DB 7; Length 1122;
Best Local Similarity 77.3%; Pred. No. 84;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| ||||| |||||
Db      526 GTRAGCCCTTCGGGGATACAC 547

RESULT 14
US-11-217-529-82499/c
; Sequence 82499, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82499
; LENGTH: 1938
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82499
Query Match      63.6%; Score 14; DB 7; Length 1938;
Best Local Similarity 77.3%; Pred. No. 91;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTCGGGGTGCTC 22
||||| ||||| ||||| |||||
Db      504 GAAGAGCCTTCGGGGGAAGCTC 483

RESULT 15
US-11-145-307A-259
; Sequence 259, Application US/11145307A
; Publication No. US20060094035A1
; GENERAL INFORMATION:
; APPLICANT: Arcturus Bioscience, Inc.
; APPLICANT: Erlander, Mark G.
; APPLICANT: Ma, Xiao-Jun
; TITLE OF INVENTION: Identification of Tumors
```

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; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: US/11/145,307A
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 60/577,084
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-145-307A-259

Query Match      63.6%; Score 14; DB 7; Length 2384;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 CCTTCCGGGGTGTC 20
Db      2244 CCTTCCGGGGTGTC 2257

RESULT 16
US-10-505-928-717
; Sequence 717, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 717
; LENGTH: 3401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-717

Query Match      63.6%; Score 14; DB 6; Length 3401;
Best Local Similarity 77.3%; Pred. No. 99;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      2758 GAAAGGCCTTTCACGGCTGCTC 2779

RESULT 17
US-10-196-749-439/c
; Sequence 439, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
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; FILE REFERENCE: 022041-002020US
; CURRENT APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 439
; LENGTH: 4277
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-439

Query Match      63.6%; Score 14; DB 6; Length 4277;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      3465 GACAGGACTGTGCGGGCTCTC 3444

RESULT 18
US-10-505-928-15/c
; Sequence 15, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 15
; LENGTH: 4933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-15

Query Match      63.6%; Score 14; DB 6; Length 4933;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 GAAAGGCCTTTCGGGGTGCTC 22
Db      1852 GAGAGGCCGTTGGGTGGGCTC 1831

RESULT 19
US-10-505-928-88/c
; Sequence 88, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
```

```
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 88
; LENGTH: 4933
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-88

Query Match      63.6%; Score 14; DB 6; Length 4933;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGTCTC 22
Db 1852 GAGAGGCCGTTGGGGTGGGCTC 1831

RESULT 20
US-10-505-928-607/c
; Sequence 607, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 607
; LENGTH: 135090
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-607

Query Match      63.6%; Score 14; DB 6; Length 135090;
Best Local Similarity 77.3%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGTCTC 22
Db 33663 GATAGGCCCTTGGCAGTTGCTC 33642

RESULT 21
US-11-267-871-477
; Sequence 477, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-477

Query Match      62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCGGGGT 18
Db 43 AAAGGCCTTAGGAGGT 27

RESULT 23
US-11-267-871-478
; Sequence 478, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-477
```

```
; OTHER INFORMATION: Primer
US-11-267-871-478

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGT 18
    |||||
Db 34 AAAGGCCTTTAGGAGT 50

RESULT 24
US-11-267-871-478/c
; Sequence 478, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 478
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-478

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGT 18
    |||||
Db 43 AAAGGCCTTTAGGAGT 27

RESULT 25
US-11-267-871-479
; Sequence 479, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-479

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGT 18
    |||||
Db 43 AAAGGCCTTTAGGAGT 27

RESULT 26
US-11-267-871-479/c
; Sequence 479, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Dittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 76
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-11-267-871-479

Query Match          62.7%; Score 13.8; DB 7; Length 76;
Best Local Similarity 88.2%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTTCGGGGT 18
    |||||
Db 43 AAAGGCCTTTAGGAGT 27

RESULT 27
US-10-505-928-577
; Sequence 577, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Patentin 3.2
; SEQ ID NO 577
; LENGTH: 3432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-577

Query Match          62.7%; Score 13.8; DB 6; Length 3432;
Best Local Similarity 88.2%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGGCCTTTCGGGGTG 19
    |||||
```

Db 2782 AAGGCCTTGGGGGGTG 2798

RESULT 28

US-10-489-730-10

GENERAL INFORMATION:

APPLICANT: Melino, Gennaro

APPLICANT: Hayes, Ian

APPLICANT: de Laurenzi, Vincenzo

APPLICANT: Barcaroli, Daniela

APPLICANT: Candi, Eleonora

APPLICANT: Bernassola, Francesca

APPLICANT: Tobler, Andreas

APPLICANT: Novak, Urban

TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof

FILE REFERENCE: 19319.002

CURRENT APPLICATION NUMBER: US/10/489,730

CURRENT FILING DATE: 2004-03-16

PRIOR APPLICATION NUMBER: PCT/GB02/04238

PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: US 60/322,436

PRIOR FILING DATE: 2001-09-17

NUMBER OF SEQ ID NOS: 39

OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A

US-10-489-730-10

Query Match 62.7%; Score 13.8; DB 6; Length 138941;

Best Local Similarity 88.2%; Pred. No. 1.8e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AAGGCCTTTCGGGGGTG 19

Db 81269 AAGGCCTATCTGGGGTG 81285

RESULT 29

US-10-511-937-2651/c

Sequence 2651, Application US/10511937

Publication No. US20060088836A1

GENERAL INFORMATION:

APPLICANT: EXPRESSION DIAGNOSTICS, INC.

APPLICANT: Wohlgenuth, Jay

APPLICANT: Fry, Kirk

APPLICANT: Woodward, Robert

APPLICANT: Ly, Ngoc

APPLICANT: Prentice, James

APPLICANT: Morris, MacDonald

APPLICANT: Rosenberg, Steven

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

FILE REFERENCE: 506612000104

CURRENT APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: PCT/US2003/012946

PRIOR FILING DATE: 2003-04-24

PRIOR APPLICATION NUMBER: US 10/131,831

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: Patent in version 3.2

SEQ ID NO 2651

LENGTH: 50

TYPE: DNA

ORGANISM: Homo sapiens

US-10-511-937-2651

Query Match 61.8%; Score 13.6; DB 6; Length 50;

Best Local Similarity 80.0%; Pred. No. 85;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTGCT 21

Db 43 AAAGGCCTTTAGGAGCTGAT 24

Db 24 AAAGCCATTGGGTGGGCT 5

RESULT 30

US-11-267-871-480

Sequence 480, Application US/11267871

Publication No. US20060094655A1

GENERAL INFORMATION:

APPLICANT: Guyon, Thierry

APPLICANT: Borrelly, Gilles

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: MODIFIED GROWTH HORMONES

FILE REFERENCE: 17109-015001/925

CURRENT APPLICATION NUMBER: US/11/267,871

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: 60/706,697

PRIOR FILING DATE: 2005-08-08

PRIOR APPLICATION NUMBER: 60/625,652

PRIOR FILING DATE: 2004-11-04

NUMBER OF SEQ ID NOS: 719

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 480

LENGTH: 76

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-11-267-871-480

Query Match 61.8%; Score 13.6; DB 7; Length 76;

Best Local Similarity 80.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGCCTTTCGGGGGTGCT 21

Db 34 AAAGCCTTTAGGAGCTGAT 53

RESULT 31

US-11-267-871-480/c

Sequence 480, Application US/11267871

Publication No. US20060094655A1

GENERAL INFORMATION:

APPLICANT: Guyon, Thierry

APPLICANT: Borrelly, Gilles

APPLICANT: Drittanti, Lila

APPLICANT: Vega, Manuel

TITLE OF INVENTION: MODIFIED GROWTH HORMONES

FILE REFERENCE: 17109-015001/925

CURRENT APPLICATION NUMBER: US/11/267,871

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: 60/706,697

PRIOR FILING DATE: 2005-08-08

PRIOR APPLICATION NUMBER: 60/625,652

PRIOR FILING DATE: 2004-11-04

NUMBER OF SEQ ID NOS: 719

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 480

LENGTH: 76

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Primer

US-11-267-871-480

Query Match 61.8%; Score 13.6; DB 7; Length 76;

Best Local Similarity 80.0%; Pred. No. 90;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGCCTTTCGGGGGTGCT 21

Db 43 AAAGCCTTTAGGAGCTGAT 24



```

; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 167012
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-167012

Query Match          61.8%; Score 13.6; DB 7; Length 420;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  313 AAAGCCCTTTGGGGCGTT 294

RESULT 35
US-10-541-993-76/c
; Sequence 76, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 1170
; TYPE: DNA
; ORGANISM: Thermus thermophilus
US-10-541-993-76

Query Match          61.8%; Score 13.6; DB 6; Length 1170;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3 AAGCCCTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db  482 AGGCCCTTAAGGGCGTGCTC 463

RESULT 36
US-10-511-937-598
; Sequence 598, Application US/10511937
; Publication No. US20060089836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James

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; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2676
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2676

Query Match          61.8%; Score 13.6; DB 7; Length 282;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  74 AAAGCCCTTTGGGGCGCTT 55

RESULT 33
US-10-488-619-1040
; Sequence 1040, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1040
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1040

Query Match          61.8%; Score 13.6; DB 6; Length 393;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAAGCCCTTCGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db  73 AAAGGTCTCTGGAGGTGCT 92

RESULT 34
US-11-217-529-167012/c
; Sequence 167012, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO

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; APPLICANT: Morris, MacDonald  
 ; APPLICANT: Rosenberg, Steven  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
 ; FILE REFERENCE: 506612000104  
 ; CURRENT APPLICATION NUMBER: US/10/511,937  
 ; PRIOR FILING DATE: 2004-10-19  
 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 ; PRIOR FILING DATE: 2003-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/131,831  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/325,899  
 ; PRIOR FILING DATE: 2002-12-20  
 ; NUMBER OF SEQ ID NOS: 3117  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 598  
 ; LENGTH: 1458  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-511-937-598

Query Match 61.8%; Score 13.6; DB 6; Length 1458;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGTC 20  
 |||||  
 Db 1225 GTAAAGCCTTCGGGTGTC 1244

RESULT 37  
 US-10-511-937-398/c  
 ; Sequence 398, Application US/10511937  
 ; Publication No. US20060088836A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; APPLICANT: Prentice, James  
 ; APPLICANT: Morris, MacDonald  
 ; APPLICANT: Rosenberg, Steven  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
 ; FILE REFERENCE: 506612000104  
 ; CURRENT APPLICATION NUMBER: US/10/511,937  
 ; CURRENT FILING DATE: 2004-10-19  
 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 ; PRIOR FILING DATE: 2003-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/131,831  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/325,899  
 ; PRIOR FILING DATE: 2002-12-20  
 ; NUMBER OF SEQ ID NOS: 3117  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 398  
 ; LENGTH: 1631  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-511-937-398

Query Match 61.8%; Score 13.6; DB 6; Length 1631;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGTGCT 21  
 |||||  
 Db 1379 AATGGCCTTCCAGTGTCT 1360

RESULT 38  
 US-11-217-529-77050

; Sequence 77050, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHIRO  
 ; APPLICANT: KODAMA, YUKIO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 77050  
 ; LENGTH: 1950  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-77050

Query Match 61.8%; Score 13.6; DB 7; Length 1950;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 AAGGCCTTCGGGGTGCTC 22  
 |||||  
 Db 364 AAGGCCTTCGGAGTTCTC 383

RESULT 39  
 US-10-511-937-462/c  
 ; Sequence 462, Application US/10511937  
 ; Publication No. US20060088836A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; APPLICANT: Prentice, James  
 ; APPLICANT: Morris, MacDonald  
 ; APPLICANT: Rosenberg, Steven  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
 ; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
 ; FILE REFERENCE: 506612000104  
 ; CURRENT APPLICATION NUMBER: US/10/511,937  
 ; CURRENT FILING DATE: 2004-10-19  
 ; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
 ; PRIOR FILING DATE: 2003-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/131,831  
 ; PRIOR FILING DATE: 2002-04-24  
 ; PRIOR APPLICATION NUMBER: US 10/325,899  
 ; PRIOR FILING DATE: 2002-12-20  
 ; NUMBER OF SEQ ID NOS: 3117  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 462  
 ; LENGTH: 2615  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-511-937-462

Query Match 61.8%; Score 13.6; DB 6; Length 2615;  
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAAGGCCTTCGGGGTGTC 20  
 |||||  
 Db 994 GAAGGCATTCGGGGCTCC 975

RESULT 40

US-10-511-937-2820/c  
; Sequence 2820, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2820  
; LENGTH: 3003  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-511-937-2820

Query Match 61.8%; Score 13.6; DB 6; Length 3003;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCT 21

Db 2918 AAAGCCATTGGGTGGGCT 2899

RESULT 41

US-11-217-529-989  
; Sequence 989, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 989  
; LENGTH: 3435  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-989

Query Match 61.8%; Score 13.6; DB 7; Length 3435;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAAGCCTTCGGGGTGCT 21

Db 53 ATAGGCCTTCGGCGGTGT 72

RESULT 42

US-10-488-619-319/c  
; Sequence 319, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 319  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(462)  
; OTHER INFORMATION: n is g, c, a or t  
US-10-488-619-319

Query Match 60.9%; Score 13.4; DB 6; Length 462;  
Best Local Similarity 93.3%; Pred. No. 1.5e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAAGCCTTCGGG 15

Db 92 GAAAGCCTTCGGG 78

RESULT 43

US-10-511-937-1868  
; Sequence 1868, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgenuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR APPLICATION NUMBER: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1868  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-511-937-1868

Query Match 60.0%; Score 13.2; DB 6; Length 20;  
Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCTTCGGGGTGCTC 22

Db 3 GGCCTTCGGGGTGCTC 20

RESULT 46

PRIOR FILING DATE: 2000-10-30  
PRIOR APPLICATION NUMBER: US 09/677,419

```
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 300
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-300

Query Match      60.0%; Score 13.2; DB 7; Length 185;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTCGGGGTG 19
Db  130 AATGGCCTTCGTGGTG 147

RESULT 48
US-10-488-619-1087/c
; Sequence 1087, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1087
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1087

Query Match      60.0%; Score 13.2; DB 6; Length 253;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAAGGCCTTCGGGGTG 19
Db  223 AAAGGCCTTCGGGGGGG 206

RESULT 49
US-11-217-529-81832
; Sequence 81832, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81832
; LENGTH: 330
; TYPE: DNA
```

```
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81832

Query Match      60.0%; Score 13.2; DB 7; Length 330;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 GAAAGCCTTCGGGGT 18
Db  244 GAAAGGCATTTGGGTG 261

RESULT 50
US-11-217-529-82742
; Sequence 82742, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82742
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82742

Query Match      60.0%; Score 13.2; DB 7; Length 399;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4 AGGCCTTCGGGGTGCT 21
Db  323 AAGCCTTCAGCGGTCT 340

RESULT 51
US-11-301-554-373/c
; Sequence 373, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
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; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-301-554-373

Query Match          60.0%; Score 13.2; DB 7; Length 467;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTG 19
Db 148 AAAGCTCTCTCGGGGTG 131

RESULT 52
US-10-514-738-19
; Sequence 19, Application US/10514738
; Publication No. US2006009353A1
; GENERAL INFORMATION:
; APPLICANT: DANG, NAM HOANG
; APPLICANT: MORIMOTO, CHIKAO
; TITLE OF INVENTION: CD26-BASED THERAPIES FOR CANCERS AND IMMUNE DISEASE
; FILE REFERENCE: UTSC:7500S
; CURRENT APPLICATION NUMBER: US/10/514,738
; PRIOR FILING DATE: 2004-11-18
; PRIOR APPLICATION NUMBER: PCT/US03/15499
; PRIOR FILING DATE: 2003-05-15
; PRIOR APPLICATION NUMBER: 60/381,606
; PRIOR FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-514-738-19

Query Match          60.0%; Score 13.2; DB 6; Length 574;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTG 19
Db 159 AATGGCTTCTCGGGGTG 176

RESULT 53
US-11-217-529-79160/c
; Sequence 79160, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; APPLICANT: NAKAO, YOSHIHIRO
```

```
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79160
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-79160

Query Match          60.0%; Score 13.2; DB 7; Length 723;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTG 19
Db 95 AAAGGACTTCAGGGTTG 78

RESULT 54
US-10-488-619-1381/c
; Sequence 1381, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations and Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1381
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-488-619-1381

Query Match          60.0%; Score 13.2; DB 6; Length 813;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCCTTCGGGGGTG 19
Db 457 AAAGCTCTCTCGGGGTG 440

RESULT 55
US-11-217-529-447/c
; Sequence 447, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 447
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-447

Query Match      60.0%; Score 13.2; DB 7; Length 894;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY   1  GAAGGCGCTTTCGGGGGT 18
    ||| ||||| |||||
DB   79  GAATGGCCTTTTGGGGT 62

RESULT 56
US-11-301-554-1664
; Sequence 1664, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1664
; LENGTH: 999
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2_5_10, 22, 83, 150, 176, 189, 264, 275, 283, 286, 302,
; LOCATION: 311, 318, 339, 374, 524, 528, 531, 536, 541, 606, 611, 614,
; LOCATION: 616, 621, 634, 635, 636, 644, 659, 682, 702, 715, 723,
; LOCATION: 726, 768, 777, 779, 789, 796, 802, 810, 819, 831, 836
; OTHER INFORMATION: n = A,T,C or G

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 853, 854, 869, 874, 893, 900, 903, 911, 989, 999
; OTHER INFORMATION: n = A,T,C or G
US-11-301-554-1664

Query Match      60.0%; Score 13.2; DB 7; Length 999;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY   2  AAAGGCGCTTTCGGGGTG 19
    ||| ||||| |||||
DB   956  AAAGACCTTTGGGGGGG 973

RESULT 57
US-10-511-937-613/c
; Sequence 613, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 613
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-613

Query Match      60.0%; Score 13.2; DB 6; Length 1263;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY   5  GGCCCTTTCGGGGTGCTC 22
    ||||| ||||| |||||
DB   261  GGCCCTTAGGGGCTCCTC 244

RESULT 58
US-11-217-529-2966/c
; Sequence 2966, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAWA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIOHKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
```

```

; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2966
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2966

Query Match      60.0%; Score 13.2; DB 7; Length 1284;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 185 AAAGCTCTTCGGGGGTG 168
||||| ||||| |||||

RESULT 59
US-11-217-529-3591/c
; Sequence 3591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3591
; LENGTH: 1902
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3591

Query Match      60.0%; Score 13.2; DB 7; Length 1902;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGT 18
||||| ||||| |||||
Db 1039 GAATGGCTTTCTTGGGT 1022
||||| ||||| |||||

RESULT 60
US-10-511-937-605
; Sequence 605, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24

; NUMBER OF SEQ ID NOS: 10196749
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 605
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-605

Query Match      60.0%; Score 13.2; DB 6; Length 2338;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 1285 AAAGCTCTTCGGGGGTG 1302
||||| ||||| |||||

RESULT 61
US-11-217-529-1652
; Sequence 1652, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1652
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1652

Query Match      60.0%; Score 13.2; DB 7; Length 2436;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AAAGGCTTTTCGGGGGTG 19
||||| ||||| |||||
Db 1480 AATGGCTTTTCAGGTTG 1497
||||| ||||| |||||

RESULT 62
US-10-196-749-95
; Sequence 95, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
```



; CURRENT FILING DATE: 2002-07-16  
 ; PRIOR APPLICATION NUMBER: 10/052586  
 ; PRIOR FILING DATE: 2002-01-15  
 ; PRIOR APPLICATION NUMBER: 60/059263  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/059266  
 ; PRIOR FILING DATE: 1997-09-18  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063120  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063121  
 ; PRIOR FILING DATE: 1997-10-24  
 ; PRIOR APPLICATION NUMBER: 60/063486  
 ; PRIOR FILING DATE: 1997-10-21  
 ; PRIOR APPLICATION NUMBER: 60/063540  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063541  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/063544  
 ; PRIOR FILING DATE: 1997-10-28  
 ; Prior Application data removed - See File Wrapper or PALM.  
 ; SEQ ID NO 95  
 ; LENGTH: 2579  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-196-749-95

Query Match 60.0%; Score 13.2; DB 6; Length 2579;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 AAAGCCCTTCGGGGGTG 19  
 ||||| ||||| |||||  
 Db 1570 AAAGTCTTCAGGGATG 1587

RESULT 63  
 US-11-217-529-80783/c  
 ; Sequence 80783, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 80783  
 ; LENGTH: 2760  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 ; FEATURE:  
 ; NAME/KEY: modified base  
 ; LOCATION: (2094)..(2094)  
 ; OTHER INFORMATION: a, c, g, t, unknown, or other  
 US-11-217-529-80783

Query Match 60.0%; Score 13.2; DB 7; Length 2760;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 AAGCCCTTCGGGGGTGC 20  
 ||||| ||||| |||||

Db 567 AAGCCATTTGGGAGTGC 550  
 RESULT 64  
 US-11-217-529-80319/c  
 ; Sequence 80319, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 80319  
 ; LENGTH: 2976  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-80319

Query Match 60.0%; Score 13.2; DB 7; Length 2976;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAAAGCCCTTCGGGGGTG 18  
 ||||| ||||| |||||  
 Db 1484 GAAGCGCTTTCGTCGCT 1467

RESULT 65  
 US-10-505-928-836/c  
 ; Sequence 836, Application US/10505928  
 ; Publication No. US20060088532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 836  
 ; LENGTH: 3269  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-836

Query Match 60.0%; Score 13.2; DB 6; Length 3269;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 AGCCCTTTCGGGGGTGCT 21  
 ||||| ||||| |||||  
 Db 963 AGGCCTTTCGCGGGGCT 946

RESULT 66  
 US-10-505-928-346/c  
 ; Sequence 346, Application US/10505928  
 ; Publication No. US20060088532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

```
/ FILE REFERENCE: 28967/39178
/ CURRENT APPLICATION NUMBER: US/10/505,928
/ PRIOR FILING DATE: 2004-08-27
/ PRIOR APPLICATION NUMBER: US 60/363,019
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: PatentIn 3.2
/ SEQ ID NO 346
/ LENGTH: 3396
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-505-928-346

Query Match          60.0%   Score 13.2;   DB 6;   Length 3396;
Best Local Similarity 83.3%;   Pred. No. 2.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY  2  AAAGGCCTTTTCGGGGGTG 19
    |||||
Db   1193 AAAGGCCTATTGTGGGTG 1176

RESULT 67
US-11-145-307A-255/c
/ Sequence 255, Application US/11/145307A
/ Publication No. US20060094035A1
/ GENERAL INFORMATION:
/ APPLICANT: Arcturus Bioscience, Inc.
/ APPLICANT: Erlander, Mark G.
/ APPLICANT: Ma, Xiao-Jun
/ TITLE OF INVENTION: Identification of Tumors
/ FILE REFERENCE: 022041-002020US
/ CURRENT APPLICATION NUMBER: US/11/145,307A
/ CURRENT FILING DATE: 2005-06-03
/ PRIOR APPLICATION NUMBER: US 60/577,084
/ PRIOR FILING DATE: 2004-06-04
/ NUMBER OF SEQ ID NOS: 268
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 255
/ LENGTH: 3487
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-11-145-307A-255

Query Match          60.0%   Score 13.2;   DB 7;   Length 3487;
Best Local Similarity 83.3%;   Pred. No. 2.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY  1  GAAAGGCCTTTTCGGGGGT 18
    |||||
Db   1872 GACAGACCTTTTCAGGGGT 1855

RESULT 68
US-11-312-958-59
/ Sequence 59, Application US/11/312958
/ Publication No. US20060100152A1
/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc.
/ APPLICANT: Rosenfeld, Julie Beth
/ APPLICANT: Silos-Santiago, Immaculada
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
/ TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
/ TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
/ TITLE OF INVENTION: 13424 MOLECULES
/ FILE REFERENCE: MPI02-027PIRNOINM
/ CURRENT APPLICATION NUMBER: US/11/312,958
/ CURRENT FILING DATE: 2005-12-20
/ PRIOR APPLICATION NUMBER: US/10/369,022
/ PRIOR FILING DATE: 2003-02-19
/ PRIOR APPLICATION NUMBER: US 60/360,495
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/ PRIOR FILING DATE: 2002-02-28
/ PRIOR APPLICATION NUMBER: US 60/370,121
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/373,010
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/373,908
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/377,717
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US 60/379,949
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US 60/382,409
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/385,280
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 60/386,879
/ PRIOR FILING DATE: 2002-06-06
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FastSEQ for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 3650
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (118)...(2013)
/ US-11-312-958-59

Query Match          60.0%   Score 13.2;   DB 7;   Length 3650;
Best Local Similarity 83.3%;   Pred. No. 2.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY  5  GGCCTTTCGGGGGTGCTC 22
    |||||
Db   2304 GGCCATTTCAGGGGTGCAC 2321

RESULT 69
US-10-505-928-679/c
/ Sequence 679, Application US/10505928
/ Publication No. US20060088532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ludwig Institute for Cancer Research et al.
/ TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
/ FILE REFERENCE: 28967/39178
/ CURRENT APPLICATION NUMBER: US/10/505,928
/ CURRENT FILING DATE: 2004-08-27
/ PRIOR APPLICATION NUMBER: US 60/363,019
/ PRIOR FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 866
/ SOFTWARE: PatentIn 3.2
/ SEQ ID NO 679
/ LENGTH: 3711
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-505-928-679

Query Match          60.0%   Score 13.2;   DB 6;   Length 3711;
Best Local Similarity 83.3%;   Pred. No. 2.5e+02;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY  4  AGGCCCTTTCGGGGGTGCT 21
    |||||
Db   756 AGGCCCTTCGGGGGTGCT 739

RESULT 70
US-10-473-173-18
/ Sequence 18, Application US/10473173
/ Publication No. US2006008823A1
/ GENERAL INFORMATION:
/ APPLICANT: VAN ANDEL INSTITUTE
```

```
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 3806
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-18

Query Match      60.0%; Score 13.2; DB 6; Length 3806;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAAGGCTTTTCGGGGT 18
    ||||| ||| |||||
Db 852 GAAAGGCTTTCTCGGGT 869

RESULT 71
US-11-066-633-3/c
; Sequence 3, Application US/11066633
; Publication No. US2006094031A1
; GENERAL INFORMATION:
; APPLICANT: Stowers Institute for Medical Research
; APPLICANT: Sauer, Brian L.
; TITLE OF INVENTION: Alpha-subscript L-Arabinofuranosidase Histochemical Reporter Gene
; FILE REFERENCE: 097287
; CURRENT APPLICATION NUMBER: US/11/066,633
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 4122
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-11-066-633-3

Query Match      60.0%; Score 13.2; DB 7; Length 4122;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 AGGCTTTTCGGGGTGTCT 21
    ||||| ||||| |||||
Db 1855 AAGCTCCCGGGGTGTCT 1838

RESULT 72
US-10-511-937-629
; Sequence 629, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
```

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; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 629
; LENGTH: 7391
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-629

Query Match      60.0%; Score 13.2; DB 6; Length 7391;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCTTTTCGGGGTGTCT 22
    ||||| ||||| |||||
Db 7105 GGCCTTTTCGGGTCTC 7122

RESULT 73
US-10-511-937-2852/c
; Sequence 2852, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2852
; LENGTH: 7603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2852

Query Match      60.0%; Score 13.2; DB 6; Length 7603;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAAGGCTTTTCGGGGTGTG 19
    ||||| ||||| |||||
Db 670 AGATGCTTTTCGGGTGTG 653

RESULT 74
US-10-519-335-37
; Sequence 37, Application US/10519335
; Publication No. US2006009210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
```

APPLICANT: Elias, Isabelle  
TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN THE TREATMENT OF MENTAL DISORDERS  
FILE REFERENCE: G-194US03PCT  
CURRENT APPLICATION NUMBER: US/10/519,335  
CURRENT FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: US 60/391,359  
PRIOR FILING DATE: 2002-06-25  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 37  
LENGTH: 151830  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10)..(10)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (60402)..(60402)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (61110)..(61110)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (98207)..(98207)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (98208)..(98208)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (98209)..(98209)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (98210)..(98210)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (98211)..(98211)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (99743)..(99743)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (108055)..(108055)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (109094)..(109094)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (109125)..(109125)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (118900)..(118900)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (119052)..(119052)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (119112)..(119112)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (119123)..(119123)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (141674)..(141674)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (142063)..(142063)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (142137)..(142137)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (142967)..(142967)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (143077)..(143077)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (143506)..(143506)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (143587)..(143587)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (143629)..(143629)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (149079)..(149079)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (5363)..(5363)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8080)..(8080)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (10296)..(10296)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (14528)..(14528)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15336)..(15336)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15457)..(15457)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (16288)..(16288)  
OTHER INFORMATION: n = a or c or g or t

FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (16306)..(16307)  
; OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (16316)..(16316)  
; OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (16397)..(16397)  
; OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (56012)..(56012)  
; OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (57662)..(57662)  
; OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
; NAME/KEY: 5'UTR  
; LOCATION: (1)..(54)  
; OTHER INFORMATION: exon 1  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (55)..(124)  
; OTHER INFORMATION: exon 1  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (91147)..(91244)  
; OTHER INFORMATION: exon 2  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (93669)..(93834)  
; OTHER INFORMATION: exon 3  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (96310)..(96422)  
; OTHER INFORMATION: exon 4  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (99546)..(99723)  
; OTHER INFORMATION: exon 5  
FEATURE:  
; NAME/KEY: exon  
; LOCATION: (125441)..(125605)

Query Match 60.0%; Score 13.2; DB 6; Length 151830;  
Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GGCCCTTCGGGGTGCTC 22

Db 40233 GGCCCTTCGGAGGTGCTC 40250

## RESULT 75

US-11-217-529-48200  
; Sequence 48200, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 110861  
; LENGTH: 25

; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 48200  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-48200

Query Match 59.1%; Score 13; DB 7; Length 25;  
Best Local Similarity 76.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGTGCTC 22

Db 2 AAAGTCTTCAGCGATGGTC 22

## RESULT 76

US-11-217-529-95163/c  
; Sequence 95163, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95163  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-95163

Query Match 59.1%; Score 13; DB 7; Length 25;  
Best Local Similarity 76.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAAGGCCTTCGGGGTGCTC 22

Db 24 ACAGGCCTTCGAGGGTTTC 4

## RESULT 77

US-11-217-529-110861/c  
; Sequence 110861, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 110861  
; LENGTH: 25

```

; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110861

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2 AAAGGCCTTCGGGGGTGCTC 22
    ||||| ||| ||||| |||||
Db   21 AAAGTCAATTAGGGGATTC 1

RESULT 78
US-11-217-529-193133/c
; Sequence 193133, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 193133
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-193133

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTCGGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db   24 GAAAGTATTTCGGCGTGCT 4

RESULT 79
US-10-473-173-422
; Sequence 422, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 422
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-422

Query Match      59.1%; Score 13; DB 6; Length 455;
Best Local Similarity 76.2%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTCGGGGGTGCT 21

```

```

Db   321 GCAAGGCATTTTCAGGGATGCT 341
    ||||| ||||| ||||| ||||| |||||

RESULT 80
US-11-217-529-3817
; Sequence 3817, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3817
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3817

Query Match      59.1%; Score 13; DB 7; Length 519;
Best Local Similarity 76.2%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  2 AAAGGCCTTCGGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db   26 AAAGTCTTTTCAGCGATGCTC 46

RESULT 81
US-10-488-619-772/c
; Sequence 772, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 772
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-772

Query Match      59.1%; Score 13; DB 6; Length 524;
Best Local Similarity 76.2%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTCGGGGGTGCT 21
    ||||| ||||| ||||| |||||
Db   465 GAAAGCCCTCTTGGGGGCACT 445

RESULT 82
US-10-488-619-2860/c
; Sequence 2860, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations

```

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RESULT 84
US-11-217-529-190988/c
; Sequence 190988, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190988
; LENGTH: 838
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-190988

```

QY 2 AAAGGCCTTTCCGGGGTGCTC 22  
||||| ||| ||| ||| |||  
Db 714 AAAGTCCATTAGGGGATTCTC 694

## RESULT 87

US-11-217-529-591/c  
; Sequence 591, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 591  
; LENGTH: 966  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-591

Query Match 59.1%; Score 13; DB 7; Length 966;  
Best Local Similarity 76.2%; Pred. No. 2.6e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCCGGGGTGCTC 22  
||||| ||| ||| ||| |||  
Db 94 ACAGCCCTTTACGGGGAGCGC 74

## RESULT 88

US-11-217-529-77610/c  
; Sequence 77610, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77610  
; LENGTH: 975  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-77610

Query Match 59.1%; Score 13; DB 7; Length 975;  
Best Local Similarity 76.2%; Pred. No. 2.6e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCCGGGGTGCTC 22  
||| ||| ||| ||| ||| |||  
Db 54 AAGAACTTTCCGGGGTGCTC 34

## RESULT 89

US-11-301-554-1664/c  
; Sequence 1664, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.478C21  
; CURRENT APPLICATION NUMBER: US/11/301,554  
; CURRENT FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1664  
; LENGTH: 999  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 2, 5, 10, 22, 83, 150, 176, 189, 264, 275, 283, 286, 302,  
; LOCATION: 311, 318, 338, 374, 524, 528, 531, 536, 541, 606, 611, 614,  
; LOCATION: 616, 621, 634, 635, 636, 644, 659, 682, 688, 702, 715, 723,  
; LOCATION: 726, 768, 777, 779, 789, 796, 802, 810, 819, 831, 836  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 853, 854, 869, 874, 893, 900, 903, 911, 989, 999  
; OTHER INFORMATION: n = A,T,C or G  
US-11-301-554-1664

Query Match 59.1%; Score 13; DB 7; Length 999;  
Best Local Similarity 76.2%; Pred. No. 2.6e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAAGGCCTTTCCGGGGTGCTC 22  
||||| ||| ||| ||| |||  
Db 965 AAAGTCTTTTGGGGTTACCC 945

## RESULT 90



```
US-11-217-529-3014
; Sequence 3014, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3014
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3014

Query Match          59.1%; Score 13; DB 7; Length 1299;
Best Local Similarity 76.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      841 AATGGTCTTTTGGCGGTGATC 861

RESULT 91
US-11-217-529-76451/c
; Sequence 76451, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76451
; LENGTH: 1329
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76451

Query Match          59.1%; Score 13; DB 7; Length 1329;
Best Local Similarity 76.2%; Pred. No. 2.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      986 ACAGGCCTTTGAGGGGTTTC 966

RESULT 92
US-11-242-505A-11/c
; Sequence 11, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
```

```
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; FILE REFERENCE: MPI2001-288P1RCP10MNM
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 1431
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1431)
US-11-242-505A-11

Query Match          59.1%; Score 13; DB 7; Length 1431;
Best Local Similarity 76.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GAAAGGCCTTTCGGGGTGCT 21
      ||||| ||||| ||||| |||||
Db      977 GAAAGACCTGTGCGGGTCTCT 957

RESULT 93
US-10-508-063A-2/c
; Sequence 2, Application US/10508063A
; Publication No. US20060088832A1
; GENERAL INFORMATION:
; APPLICANT: Deutsches Krebsforschungszentrum
; APPLICANT: ANGEL, Peter
; APPLICANT: FURSTENBERGER, Gerhard
; APPLICANT: BREITENBACH, Ute
; APPLICANT: RICHTER, Harmut
; APPLICANT: HESS, Jochen
; APPLICANT: TUCKERMAN, Jan
; TITLE OF INVENTION: TAP-70, A NOVEL MARKER FOR EPITHELIAL TUMORS
; FILE REFERENCE: 31304-701.831
; CURRENT APPLICATION NUMBER: US/10/508,063A
; CURRENT FILING DATE: 2004-09-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-508-063A-2

Query Match          59.1%; Score 13; DB 6; Length 1695;
Best Local Similarity 76.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 AAAGGCCTTTCGGGGTGCTC 22
      ||||| ||||| ||||| |||||
Db      616 AAAGGCCTTCAGGAGGCCTC 596

RESULT 94
US-11-217-529-77917
; Sequence 77917, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US 10/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77917
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (1323)..(1373)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-77917

Query Match          59.1%; Score 13; DB 7; Length 1731;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCT 21
   ||||| ||||| |||||
Db 202 GCAGGGCCTTTTGGTGGTGT 222

RESULT 95
US-11-242-505A-10/c
; Sequence 10, Application US/11242505A
; Publication No. US20060099656A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; TITLE OF INVENTION: Methods and Compositions for Treating
; TITLE OF INVENTION: Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
; FILE REFERENCE: 14395, 14618, 17692, 58874, 252, 304, 1980, 14717, 9941, 19310,
; CURRENT APPLICATION NUMBER: US/11/242,505A
; CURRENT FILING DATE: 2005-10-03
; PRIOR APPLICATION NUMBER: US 10/290,078
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/347,949
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 10/320,351
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-242-505A-10

Query Match          59.1%; Score 13; DB 7; Length 1821;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCT 21
   ||||| ||||| |||||
Db 1011 GAAAGACCTGTGCGGGTTCT 991

RESULT 96
US-11-217-529-76600/c
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```
; Sequence 76600, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76600
; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76600

Query Match          59.1%; Score 13; DB 7; Length 2007;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db 1665 GAAAGCGCTTTGAGTGTGAT 1645

RESULT 97
US-10-511-937-384/c
; Sequence 384, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 384
; LENGTH: 2106
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-384

Query Match          59.1%; Score 13; DB 6; Length 2106;
Best Local Similarity 76.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAAGCCTTTCGGGGTGCT 21
   ||||| ||||| |||||
Db 1955 GATAGCCACGCGGGGTACT 1935
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## ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

**This Page Blank (uspto)**

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 1887.72 Seconds  
(without alignments)  
1829.273 Million cell updates/sec

Title: US-10-665-708-11

Perfect score: 54

Sequence: 1 gaaattaatatcgactacta.....tgtgcaaatattccccactgc 54

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

GenEmbl.\*

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2: gb\_pat.\*

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4: gb\_pl.\*

5: gb\_pr.\*

6: gb\_ro.\*

7: gb\_sts.\*

8: gb\_sy.\*

9: gb\_un.\*

10: gb\_vi.\*

11: gb\_ov.\*

12: gb\_htg.\*

13: gb\_in.\*

14: gb\_om.\*

15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	41	75.9	57	2	AR438642 Sequence
6	41	75.9	57	2	AX166844 Sequence
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9	37.6	69.6	54	2	AR344820 Sequence
10	37.6	69.6	54	2	AR720137 Sequence
11	37.6	69.6	54	2	AX397775 Sequence
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13	37	68.5	53	2	AR720170 Sequence
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15	37	68.5	57	2	CS072196 Sequence
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247	33	61.1	3153	2	A68112	A58104 Sequence 13	Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA	
248	33	61.1	3160	2	A68104	Sequence 13	Location/Qualifiers	
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DEFINITION

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AR438643

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Sequence 54 from patent US 6664081.

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Sequence 11 from patent US 6664081.

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AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 115

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 120

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 125

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 130

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 135

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 140

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 145

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 150

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 155

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 160

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 165

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 170

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 175

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 180

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 185

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 190

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 195

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 200

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 205

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 210

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 215

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 220

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 225

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 230

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 235

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 240

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 245

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 250

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 255

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 260

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 265

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 270

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 275

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 280

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 285

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 290

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 295

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 300

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 305

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 310

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 315

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

AR438643

ALIGNMENTS

RESULT 320

AR438643

LOCUS

DEFINITION

ACCESSION

Sequence 54 bp DNA

AR438643

Sequence 11 from patent US 6664081.

TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 8 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source  
1. .58  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 77.8%; Score 42; DB 2; Length 58;  
Best Local Similarity 98.1%; Pred. No. 5.8e+04;  
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA-TGTGCAATATTTCCCACTGC 53

## RESULT 4

AXI166842  
LOCUS AXI166842 58 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 8 from Patent WO0144510.  
ACCESSION AXI166842  
VERSION AXI166842.1 GI:14596445

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

## REFERENCE

1 Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 8 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

## FEATURES

source  
Location/Qualifiers

1. .58  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="primer oligonucleotide"  
1. .33

## promoter

## ORIGIN

Query Match 77.8%; Score 42; DB 2; Length 58;  
Best Local Similarity 98.1%; Pred. No. 5.8e+04;  
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA-TGTGCAATATTTCCCACTGC 53

## RESULT 5

AXI166842  
LOCUS AXI166842 57 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 10 from patent US 6664081.  
ACCESSION AR438642  
VERSION AR438642.1 GI:42663566

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

## REFERENCE

1 (bases 1 to 57)  
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 10 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
source  
1. .57  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 75.9%; Score 41; DB 2; Length 57;  
Best Local Similarity 94.7%; Pred. No. 7.9e+04;  
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACACCATTTGTGCAATATTTCCCACTGC 57

## RESULT 6

AXI166844  
LOCUS AXI166844 57 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 10 from Patent WO0144510.  
ACCESSION AXI166844  
VERSION AXI166844.1 GI:14596447

KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

## REFERENCE

1 Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 10 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

## FEATURES

source  
Location/Qualifiers

1. .57  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="primer oligonucleotide"  
1. .33

## promoter

## ORIGIN

Query Match 75.9%; Score 41; DB 2; Length 57;  
Best Local Similarity 94.7%; Pred. No. 7.9e+04;  
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACACCATTTGTGCAATATTTCCCACTGC 57

## RESULT 7

AR438641  
LOCUS AR438641 59 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 9 from patent US 6664081.  
ACCESSION AR438641  
VERSION AR438641.1 GI:42663565

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

## REFERENCE

1 (bases 1 to 59)  
Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 9 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

## FEATURES

source  
1. .59  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 74.1%; Score 40; DB 2; Length 59;  
Best Local Similarity 93.1%; Pred. No. 1e+05;  
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACCCCATTTGTGCAATATTTCCCACTGC 58



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RESULT 8
LOCUS      AX166843
DEFINITION Sequence 9 from Patent WO0144510.
ACCESSION  AX166843
VERSION     AX166843.1  GI:14596446
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL     Patent: WO 0144510-A 9 21-JUN-2001;
            Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES   .
            Location/Qualifiers
            source
            1
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="primer oligonucleotide"
            1..33
            promoter
            1..33
            ORIGIN
            Query Match      74.1%; Score 40; DB 2; Length 59;
            Best Local Similarity 93.1%; Pred. No. 1e+05;
            Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy      1  GAAATTAATACGACTCACTATAGGAGACCA----CATGTGCAATATTTCCCACTGC 54
        |||||||
Db      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACTGC 58
        |||||||

RESULT 9
LOCUS      AR344820
DEFINITION Sequence 9 from patent US 6582920.
ACCESSION  AR344820
VERSION     AR344820.1  GI:33740901
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 54)
AUTHORS     Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE       Amplification of HIV-1 RT sequences for detection of sequences
            associated with drug-resistance mutations
JOURNAL     Patent: US 6582920-A 9 24-JUN-2003;
            Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES   .
            Location/Qualifiers
            source
            1..54
            /organism="unknown"
            /mol_type="genomic DNA"
            ORIGIN
            Query Match      69.6%; Score 37.6; DB 2; Length 54;
            Best Local Similarity 90.9%; Pred. No. 2.3e+05;
            Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 44
        |||||||
Db      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTT 44
        |||||||

RESULT 10
LOCUS      AR720137
DEFINITION Sequence 9 from patent US 6946254.
ACCESSION  AR720137
VERSION     AR720137.1  GI:77371202
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KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 54)
AUTHORS     Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE       Amplification of HIV-1 gag sequences for detection of sequences
            associated with drug-resistance mutations
JOURNAL     Patent: US 6946254-A 9 20-SEP-2005;
            Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES   .
            Location/Qualifiers
            source
            1..54
            /organism="unknown"
            /mol_type="genomic DNA"
            ORIGIN
            Query Match      69.6%; Score 37.6; DB 2; Length 54;
            Best Local Similarity 90.9%; Pred. No. 2.3e+05;
            Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 44
        |||||||
Db      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTT 44
        |||||||

RESULT 11
LOCUS      AX397775
DEFINITION Sequence 9 from Patent WO0220852.
ACCESSION  AX397775
VERSION     AX397775.1  GI:21260649
KEYWORDS   .
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE       Amplification of hiv-1 sequences for detection of sequences
            associated with drug-resistance mutations
JOURNAL     Patent: WO 0220852-A 9 14-MAR-2002;
            Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES   .
            Location/Qualifiers
            source
            1..54
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide primer for Reverse Transcriptase
            target sequence"
            1..33
            promoter
            1..33
            ORIGIN
            Query Match      69.6%; Score 37.6; DB 2; Length 54;
            Best Local Similarity 90.9%; Pred. No. 2.3e+05;
            Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 44
        |||||||
Db      1  GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTT 44
        |||||||

RESULT 12
LOCUS      AR344853
DEFINITION Sequence 42 from patent US 6582920.
ACCESSION  AR344853
VERSION     AR344853.1  GI:33740934
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 53)
AUTHORS     Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE       Amplification of HIV-1 RT sequences for detection of sequences
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associated with drug-resistance mutations  
Patent: US 6582920-A 42 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

JOURNAL  
FEATURES  
source

ORIGIN

Query Match 68.5%; Score 37; DB 2; Length 53;  
Best Local Similarity 88.9%; Pred. No. 2.8e+05;  
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45

RESULT 13  
LOCUS ART20170 53 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 42 from patent US 6946254.  
ACCESSION ART20170  
VERSION ART20170.1 GI:77371235  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 42 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source 1..53  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 68.5%; Score 37; DB 2; Length 53;  
Best Local Similarity 88.9%; Pred. No. 2.8e+05;  
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45

RESULT 14  
LOCUS AX397808 53 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 42 from Patent WO0220852.  
ACCESSION AX397808  
VERSION AX397808.1 GI:21260682  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 42 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)  
FEATURES  
source 1..53  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer for Reverse Transcriptase target sequence"

promoter 1..33

ORIGIN

Query Match 68.5%; Score 37; DB 2; Length 53;  
Best Local Similarity 88.9%; Pred. No. 2.8e+05;  
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATCTTGATAAATT 45

RESULT 15  
LOCUS CS072196 57 bp DNA linear PAT 05-MAY-2005  
DEFINITION Sequence 3 from Patent WO2001044511.  
ACCESSION CS072196  
VERSION CS072196.1 GI:63089421  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Brentano, S.T. and Lankford, R.L.  
TITLE Methods and compositions for detection of mycobacterium avium complex species  
JOURNAL Patent: WO 2001044511-A 3 21-JUN-2001;  
Gen-Probe Incorporated (US)  
FEATURES  
source 1..57  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: synthetic promoter-primer"

ORIGIN

Query Match 68.5%; Score 37; DB 2; Length 57;  
Best Local Similarity 91.2%; Pred. No. 2.7e+05;  
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATCCCCACT 52  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCATATCCCCACT 57

RESULT 16  
LOCUS CS072206/c 57 bp DNA linear PAT 05-MAY-2005  
DEFINITION Sequence 13 from Patent WO2001044511.  
ACCESSION CS072206  
VERSION CS072206.1 GI:63089431  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Brentano, S.T. and Lankford, R.L.  
TITLE Methods and compositions for detection of mycobacterium avium complex species  
JOURNAL Patent: WO 2001044511-A 13 21-JUN-2001;  
Gen-Probe Incorporated (US)  
FEATURES  
source 1..57  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: synthetic probe"

ORIGIN

Query Match 68.5%; Score 37; DB 2; Length 57;  
Best Local Similarity 91.2%; Pred. No. 2.7e+05;  
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCATATCCCCACT 52  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCATATCCCCACT 57

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Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCCACT 52
|||||
Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTCCCACT 1

RESULT 17
AR438639
LOCUS AR438639 57 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 7 from patent US 6664081.
ACCESSION AR438639
VERSION AR438639.1 GI:42663563
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 7 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source
1..57
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCCACT 52
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTCCCACT 57

RESULT 18
AR559011
LOCUS AR559011 57 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 3 from patent US 6747141.
ACCESSION AR559011
VERSION AR559011.1 GI:53966350
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T. and Lankford,R.L.
TITLE Methods and compositions for detection of mycobacterium avium
complex species
JOURNAL Patent: US 6747141-A 3 08-JUN-2004;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source
1..57
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCCACT 52
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Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTCCCACT 57

RESULT 19
AR559021/c
LOCUS AR559021 57 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 13 from patent US 6747141.
ACCESSION AR559021
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AR559021.1 GI:53966360
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS Brentano,S.T. and Lankford,R.L.
TITLE Methods and compositions for detection of mycobacterium avium
complex species
JOURNAL Patent: US 6747141-A 13 08-JUN-2004;
Gen-Probe Incorporated; San Diego, CA
FEATURES
source
1..57
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCCACT 52
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Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTCCCACT 1

RESULT 20
AX166841
LOCUS AX166841 57 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 7 from Patent WO0144510.
ACCESSION AX166841
VERSION AX166841.1 GI:14596444
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 7 21-JUN-2001;
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)
FEATURES
source
1..57
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer oligonucleotide"
1..33
promoter

ORIGIN
Query Match 68.5%; Score 37; DB 2; Length 57;
Best Local Similarity 91.2%; Pred. No. 2.7e+05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCCACT 52
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCAGCCATTGTGCAATATTCCCACT 57

RESULT 21
AR344813
LOCUS AR344813 37 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6582920.
ACCESSION AR344813
VERSION AR344813.1 GI:33740894
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 37)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
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associated with drug-resistance mutations
Patent: US 6582920-A 2 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source
        Location/Qualifiers
            1..37
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match      66.7%; Score 36; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||

RESULT 22
AR720130
LOCUS AR720130 37 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 2 from patent US 6946254.
ACCESSION AR720130
VERSION AR720130.1 GI:77371195
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 37)
    Yang, Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
    Amplification of HIV-1 gag sequences for detection of sequences
    associated with drug-resistance mutations
JOURNAL
    Patent: US 6946254-A 2 20-SEP-2005;
    Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source
        Location/Qualifiers
            1..37
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match      66.7%; Score 36; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||

RESULT 23
AX397768
LOCUS AX397768 37 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 2 from Patent WO220852.
ACCESSION AX397768
VERSION AX397768.1 GI:21260642
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1
    Yang, Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
    Amplification of hiv-1 sequences for detection of sequences
    associated with drug-resistance mutations
JOURNAL
    Patent: WO 0220852-A 2 14-MAR-2002; (US) ; Biomerieux S.A. (FR)
    Gen-Probe Incorporated Patent Dept (US)
FEATURES
    source
        Location/Qualifiers
            1..37
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="T7 promoter sequence"
            1..29
                promoter
ORIGIN
associated with drug-resistance mutations
Patent: US 6582920-A 2 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source
        Location/Qualifiers
            1..37
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match      66.7%; Score 36; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||

RESULT 24
AR344817
LOCUS AR344817 54 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 6 from patent US 6582920.
ACCESSION AR344817
VERSION AR344817.1 GI:33740898
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 54)
    Yang, Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
    Amplification of HIV-1 RT sequences for detection of sequences
    associated with drug-resistance mutations
JOURNAL
    Patent: US 6582920-A 6 24-JUN-2003;
    Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source
        Location/Qualifiers
            1..54
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match      66.7%; Score 36; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||

RESULT 25
AR720134
LOCUS AR720134 54 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 6 from patent US 6946254.
ACCESSION AR720134
VERSION AR720134.1 GI:77371199
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1 (bases 1 to 54)
    Yang, Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
    Amplification of HIV-1 gag sequences for detection of sequences
    associated with drug-resistance mutations
JOURNAL
    Patent: US 6946254-A 6 20-SEP-2005;
    Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source
        Location/Qualifiers
            1..54
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
Query Match      66.7%; Score 36; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.7e+05;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||||

RESULT 26
AX397768
LOCUS AX397768 37 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 2 from Patent WO220852.
ACCESSION AX397768
VERSION AX397768.1 GI:21260642
KEYWORDS
SOURCE
ORGANISM
REFERENCE
    1
    Yang, Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
    Amplification of hiv-1 sequences for detection of sequences
    associated with drug-resistance mutations
JOURNAL
    Patent: WO 0220852-A 2 14-MAR-2002; (US) ; Biomerieux S.A. (FR)
    Gen-Probe Incorporated Patent Dept (US)
FEATURES
    source
        Location/Qualifiers
            1..37
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="T7 promoter sequence"
            1..29
                promoter
ORIGIN
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AX397772  
LOCUS AX397772 54 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 6 from Patent WO220852.  
ACCESSION AX397772  
VERSION AX397772.1 GI:21260646  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 6 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)  
FEATURES  
source  
1..54  
Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer for Gag target sequence"  
promoter 1..33  
modified\_base 46  
/note="Nebularine"  
/mod\_base=OTHER  
ORIGIN  
Query Match 66.7%; Score 36; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.7e+05;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
RESULT 27  
AR344845  
LOCUS AR344845 53 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 34 from patent US 6582920.  
ACCESSION AR344845  
VERSION AR344845.1 GI:33740926  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 34 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source  
1..53  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 66.3%; Score 35.8; DB 2; Length 53;  
Best Local Similarity 94.9%; Pred. No. 4e+05;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39  
|||||  
RESULT 28  
AR344847  
LOCUS AR344847 53 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 36 from patent US 6582920.  
ACCESSION AR344847  
VERSION AR344847.1 GI:33740928  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 36 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
Location/Qualifiers

KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 36 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source  
1..53  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 66.3%; Score 35.8; DB 2; Length 53;  
Best Local Similarity 94.9%; Pred. No. 4e+05;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39  
|||||  
RESULT 29  
AR720162  
LOCUS AR720162 53 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 34 from patent US 6946254.  
ACCESSION AR720162  
VERSION AR720162.1 GI:77371227  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 34 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source  
1..53  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 66.3%; Score 35.8; DB 2; Length 53;  
Best Local Similarity 94.9%; Pred. No. 4e+05;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGATGC 39  
|||||  
RESULT 30  
AR720164  
LOCUS AR720164 53 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 36 from patent US 6946254.  
ACCESSION AR720164  
VERSION AR720164.1 GI:77371229  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 36 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
Location/Qualifiers

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source          1. .53
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||

RESULT 31
AX397800
LOCUS          AX397800          53 bp          DNA          linear          PAT 27-MAY-2002
DEFINITION    Sequence 36 from Patent WO0220852.
ACCESSION     AX397800
VERSION       AX397800.1 GI:21260674
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Yang,Y.Y., Brentano,S.T., Babola O., Tran,N. and Vernet,G.
TITLE         Amplification of hiv-1 sequences for detection of sequences
              associated with drug-resistance mutations
JOURNAL       Patent: WO 0220852-A 36 14-MAR-2002;
              Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES      Location/Qualifiers
source        1. .53
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide primer for Gag target sequence"
promoter      1. .33
modified_base 45
              /note="Nebularine"
              /mod_base=OTHER

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||

RESULT 32
AX397802
LOCUS          AX397802          53 bp          DNA          linear          PAT 27-MAY-2002
DEFINITION    Sequence 36 from Patent WO0220852.
ACCESSION     AX397802
VERSION       AX397802.1 GI:21260676
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Yang,Y.Y., Brentano,S.T., Babola O., Tran,N. and Vernet,G.
TITLE         Amplification of hiv-1 sequences for detection of sequences
              associated with drug-resistance mutations
JOURNAL       Patent: WO 0220852-A 36 14-MAR-2002;
              Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES      Location/Qualifiers
source        1. .53
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Oligonucleotide primer for Gag target sequence"

promoter      1. .33
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match          66.3%; Score 35.8; DB 2; Length 53;
Best Local Similarity 94.9%; Pred. No. 4e+05;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 45
|||||

RESULT 33
DD177972
LOCUS          DD177972          53 bp          DNA          linear          PAT 19-DEC-2005
DEFINITION    Method for the detection and/or identification of the original
              animal species in animal matter contained in a sample.
ACCESSION     DD177972
VERSION       DD177972.1 GI:83962997
KEYWORDS      JP 2005514037-A/241.
SOURCE        unidentified
ORGANISM      unclassified sequences.
REFERENCE     1 (bases 1 to 53)
AUTHORS       Pijemu,N.B., Babola,O., Douvaren,S., Lacroix,B. and Mabilat,C.
TITLE         Method for the detection and/or identification of the original
              animal species in animal matter contained in a sample
JOURNAL       Patent: JP 2005514037-A 241 19-MAY-2005;
              Bio Merieux
COMMENT       OS amorce sequence CBHT7 20
              PN JP 2005514037-A/241
              PD 19-MAY-2005
              PF 10-JAN-2003 JP 2003558206
              PI 10-JAN-2002 FR 02/00265
              PI nathalie bero pijemu,odile babola,sabine douvaren,bruno PI
              lacroix,
              PI claudie mabilat
              CC
              FH Key Location/Qualifiers.
FEATURES      Location/Qualifiers
source        1. .53
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

ORIGIN
Query Match          65.6%; Score 35.4; DB 2; Length 53;
Best Local Similarity 86.7%; Pred. No. 4.6e+05;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCATATT 45
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAGAAATGATATT 45
|||||

RESULT 34
AX802102
LOCUS          AX802102          53 bp          DNA          linear          PAT 24-NOV-2003
DEFINITION    Sequence 241 from Patent WO03057913.
ACCESSION     AX802102
VERSION       AX802102.1 GI:38501026
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Mabilat,C., Desvarenne,S., Babola,O., Lacroix,B. and bello Pigem,N.
TITLE         Method for the detection and/or identification of the original
              animal species in animal matter contained in a sample
JOURNAL       Patent: WO 03057913-A 241 17-JUL-2003;
              BIO MERIEUX (FR)
FEATURES      Location/Qualifiers
source        1. .53
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

ORIGIN
Query Match          65.6%; Score 35.4; DB 2; Length 53;
Best Local Similarity 86.7%; Pred. No. 4.6e+05;
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCATATT 45
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAGAAATGATATT 45
|||||

RESULT 34
AX802102
LOCUS          AX802102          53 bp          DNA          linear          PAT 24-NOV-2003
DEFINITION    Sequence 241 from Patent WO03057913.
ACCESSION     AX802102
VERSION       AX802102.1 GI:38501026
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      synthetic construct
              other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Mabilat,C., Desvarenne,S., Babola,O., Lacroix,B. and bello Pigem,N.
TITLE         Method for the detection and/or identification of the original
              animal species in animal matter contained in a sample
JOURNAL       Patent: WO 03057913-A 241 17-JUL-2003;
              BIO MERIEUX (FR)
FEATURES      Location/Qualifiers
source        1. .53
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"
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[illegible]

RESULT 3 /	AR5941174	AR5941174	LOCUS	AR5941174	Sequence 49 from patent US 6811985.	54 bp	DNA	linear	PAT 15-DEC-2004
			DEFINITION	AR5941174					
			ACCESSION	AR5941174					
			VERSION	AR5941174.1	GI:56643679				
			KEYWORDS	.					
			SOURCE	Unknown.					
			ORGANISM	Unknown.					
			REFERENCE	Unclassified.					
			AUTHORS	1 (bases 1 to 54)					
			TITLE	Harvey,R.C. and Clark,T.J. Jr.					
				Nucleic acid sequences for detecting genetic markers for cancer in a biological sample					
			JOURNAL	Patent: US 6811985-A 49 02-NOV-2004;					
				Gen-Probe Incorporated; San Diego, CA					

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source
1. .54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match      65.6%;   Score 35.4;   DB 2;   Length 54;
Best Local Similarity 79.2%;   Pred. No. 4.5e+03;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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AR344821	LOCUS	AR344821	55 bp	DNA	linear	PAT 17-AUG-2003
	DEFINITION	Sequence 10 from patent US 6582920.				
	ACCESSION	AR344821				
	VERSION	AR344821.1	GI:33740902			
	KEYWORDS					
	SOURCE	Unknown.				
	ORGANISM	Unknown.				
		Unclassified.				

```

Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 10 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
FEATURES
    source          Location/Qualifiers
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN
Query Match          65.6%; Score 35.4; DB 2; Length 55;
Best Local Similarity 97.3%; Pred. No. 4.4e+09;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37

RESULT 39  
AR720138  
LOCUS AR720138 55 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 10 from patent US 6946254.  
ACCESSION AR720138  
VERSION AR720138.1 GI:77371203  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 10 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source  
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/organism="unknown"  
/mol\_type="genomic DNA"

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Query Match 65.6%; Score 35.4; DB 2; Length 55;  
Best Local Similarity 97.3%; Pred. No. 4.4e+05;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37  
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37

RESULT 40  
AX397776  
LOCUS AX397776 55 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 10 from Patent WO0220852.  
ACCESSION AX397776  
VERSION AX397776.1 GI:21260650  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 10 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)  
FEATURES  
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Location/Qualifiers  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer for Reverse Transcriptase target sequence"

promoter  
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ORIGIN  
Query Match 65.6%; Score 35.4; DB 2; Length 55;  
Best Local Similarity 97.3%; Pred. No. 4.4e+05;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37

RESULT 41  
AR344854

LOCUS AR344854 52 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 43 from patent US 6582920.  
ACCESSION AR344854  
VERSION AR344854.1 GI:33740935  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 43 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
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1..52  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 64.8%; Score 35; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 5.2e+05;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35  
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

RESULT 42  
AR438644  
LOCUS AR438644 52 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 12 from patent US 6664081.  
ACCESSION AR438644  
VERSION AR438644.1 GI:42663568  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodrigue, M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 12 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source  
1..52  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 64.8%; Score 35; DB 2; Length 52;  
Best Local Similarity 80.4%; Pred. No. 5.2e+05;  
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTCGCCAC 51  
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCATCAGGCTTGCCCC 51

RESULT 43  
AR720171  
LOCUS AR720171 52 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 43 from patent US 6946254.  
ACCESSION AR720171  
VERSION AR720171.1 GI:77371236  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 52)  
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences



associated with drug-resistance mutations  
 Patent: US 6946254-A 43 20-SEP-2005;  
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

# JOURNAL

FEATURES  
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ORIGIN  
 Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="genomic DNA"

Query Match 64.8%; Score 35; DB 2; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+05;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATT 35  
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 Db 1 GAAATTAATACGACTCACTATAGGAGACACATT 35

RESULT 44  
 AX166846  
 LOCUS 52 bp DNA linear PAT 04-JUL-2001  
 DEFINITION Sequence 12 from Patent WO0144510.  
 ACCESSION AX166846  
 VERSION AX166846.1 GI:14596449  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodrigue, M.  
 TITLE Nucleic acid amplification and detection of mycobacterium species  
 JOURNAL Patent: WO 0144510-A 12 21-JUN-2001;  
 Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
 FEATURES  
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 1..52  
 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
 /db\_xref="taxon:32630"  
 /note="primer oligonucleotide"

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 ORIGIN

Query Match 64.8%; Score 35; DB 2; Length 52;  
 Best Local Similarity 80.4%; Pred. No. 5.2e+05;  
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 51  
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 Db 1 GAAATTAATACGACTCACTATAGGAGACACATGCATGCGTTC 51

RESULT 45  
 AX397809  
 LOCUS 52 bp DNA linear PAT 27-MAY-2002  
 DEFINITION Sequence 43 from Patent WO0220852.  
 ACCESSION AX397809  
 VERSION AX397809.1 GI:21260683  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE 1  
 AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
 TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
 JOURNAL Patent: WO 0220852-A 43 14-MAR-2002;  
 Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)  
 FEATURES  
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 /organism="synthetic construct"  
 /mol\_type="unassigned DNA"  
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/note="Oligonucleotide primer for Reverse Transcriptase target sequence"  
 1..33

# promoter

ORIGIN  
 Location/Qualifiers  
 64.8%; Score 35; DB 2; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+05;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATT 35  
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 Db 1 GAAATTAATACGACTCACTATAGGAGACACATT 35

RESULT 46  
 AR344846  
 LOCUS 53 bp DNA linear PAT 17-AUG-2003  
 DEFINITION Sequence 35 from patent US 6582920.  
 ACCESSION AR344846  
 VERSION AR344846.1 GI:33740927  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 53)  
 AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
 TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
 JOURNAL Patent: US 6582920-A 35 24-JUN-2003;  
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
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 source  
 1..53  
 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Location/Qualifiers  
 64.4%; Score 34.8; DB 2; Length 53;  
 Best Local Similarity 84.8%; Pred. No. 5.5e+05;  
 Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 46  
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 Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGTGCTCCTTC 46

RESULT 47  
 AR720163  
 LOCUS 53 bp DNA linear PAT 07-OCT-2005  
 DEFINITION Sequence 35 from patent US 6946254.  
 ACCESSION AR720163  
 VERSION AR720163.1 GI:77371228  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 53)  
 AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.  
 TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
 JOURNAL Patent: US 6946254-A 35 20-SEP-2005;  
 Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
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 /mol\_type="genomic DNA"

ORIGIN  
 Location/Qualifiers  
 64.4%; Score 34.8; DB 2; Length 53;  
 Best Local Similarity 84.8%; Pred. No. 5.5e+05;  
 Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTCGAATATTC 46  
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Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGGTGGCTCCTTC 46

RESULT 48  
AX397801  
LOCUS  
DEFINITION Sequence 35 from Patent WO220852.  
ACCESSION AX397801  
VERSION AX397801.1 GI:21260675  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 35 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer for Gag target sequence"  
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promoter  
ORIGIN

Query Match 64.4%; Score 34.8; DB 2; Length 53;  
Best Local Similarity 84.8%; Pred. No. 5.5e+05;  
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACACATGTCATATTC 46  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACACAGGGTGGCTCCTTC 46  
|||||

RESULT 49  
AR344844  
LOCUS  
DEFINITION Sequence 33 from patent US 6582920.  
ACCESSION AR344844  
VERSION AR344844.1 GI:33740925  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 33 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source Location/Qualifiers  
1..54  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.7%; Score 34.4; DB 2; Length 54;  
Best Local Similarity 97.2%; Pred. No. 6.1e+05;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACACATG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACACAGTG 36  
|||||

RESULT 50  
AR720161  
LOCUS  
DEFINITION Sequence 33 from patent US 6946254.  
ACCESSION AR720161

VERSION AR720161.1 GI:77371226  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 33 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.7%; Score 34.4; DB 2; Length 54;  
Best Local Similarity 97.2%; Pred. No. 6.1e+05;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACACATG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACACAGTG 36  
|||||

RESULT 51  
AX397799  
LOCUS  
DEFINITION Sequence 33 from Patent WO220852.  
ACCESSION AX397799  
VERSION AX397799.1 GI:21260673  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.  
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 33 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide primer for Gag target sequence"  
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promoter  
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Query Match 63.7%; Score 34.4; DB 2; Length 54;  
Best Local Similarity 97.2%; Pred. No. 6.1e+05;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACACATG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACACAGTG 36  
|||||

RESULT 52  
AR719674  
LOCUS  
DEFINITION Sequence 48 from patent US 6943242.  
ACCESSION AR719674  
VERSION AR719674.1 GI:77370598  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 62)  
AUTHORS Samartzidou, H., Turner, L., Daniel, S. and Houts, T.  
TITLE Design of artificial genes for use as controls in gene expression

Query Match 63.0%; Score 34; DB 2; Length 53;  
Best Local Similarity 88.1%; Pred. No. 7e+05;

/db\_xref="taxon:32630"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;  
Best Local Similarity 80.0%; Pred. No. 6.9e+05;  
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 2 AAATTAATACGACTCCTATAGGGAGCCACATTGTGCAATATCCCCAC 51  
|||||  
Db 2 AAATTAATACGACTCCTATAGGGAGCCACAGGGTGAACCTGGCGCAC 51  
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RESULT 57  
LOCUS AR307441 54 bp DNA linear PAT 12-JUN-2003  
DEFINITION Sequence 30 from patent US 6551778.  
ACCESSION AR307441  
VERSION AR307441.1 GI:31697980  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6551778-A 30 22-APR-2003;  
FEATURES Gen-Probe Incorporated; San Diego, CA  
source Location/Qualifiers  
1..54  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;  
Best Local Similarity 80.0%; Pred. No. 6.9e+05;  
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 2 AAATTAATACGACTCCTATAGGGAGCCACATTGTGCAATATCCCCAC 51  
|||||  
Db 2 AAATTAATACGACTCCTATAGGGAGCCACAGGGTGAACCTGGCGCAC 51  
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RESULT 58  
LOCUS AR594155 54 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 30 from patent US 6811985.  
ACCESSION AR594155  
VERSION AR594155.1 GI:56643660  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 54)  
AUTHORS Harvey,R.C. and Clark,T.J. Jr.  
TITLE Nucleic acid sequences for detecting genetic markers for cancer in a biological sample  
JOURNAL Patent: US 6811985-A 30 02-NOV-2004;  
FEATURES Gen-Probe Incorporated; San Diego, CA  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 54;  
Best Local Similarity 80.0%; Pred. No. 6.9e+05;  
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
Qy 2 AAATTAATACGACTCCTATAGGGAGCCACATTGTGCAATATCCCCAC 51  
|||||  
Db 2 AAATTAATACGACTCCTATAGGGAGCCACAGGGTGAACCTGGCGCAC 51  
|||||

RESULT 59

LOCUS AR344856 55 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 45 from patent US 6582920.  
ACCESSION AR344856  
VERSION AR344856.1 GI:33740937  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 45 24-JUN-2003;  
FEATURES Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 6.8e+05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATAGGACTCCTATAGGGAGACCACAT 34  
|||||  
Db 1 GAAATTAATAGGACTCCTATAGGGAGACCACAT 34  
|||||

RESULT 60

LOCUS AR720173 55 bp DNA linear PAT 07-OCT-2005  
DEFINITION Sequence 45 from patent US 6946254.  
ACCESSION AR720173  
VERSION AR720173.1 GI:77371238  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 55)  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 45 20-SEP-2005;  
FEATURES Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 63.0%; Score 34; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 6.8e+05;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATAGGACTCCTATAGGGAGACCACAT 34  
|||||  
Db 1 GAAATTAATAGGACTCCTATAGGGAGACCACAT 34  
|||||

RESULT 61

LOCUS AX397811 55 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 45 from Patent WO0220852.  
ACCESSION AX397811  
VERSION AX397811.1 GI:21260685  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

```

REFERENCE
AUTHORS      1 Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE        Amplification of hiv-1 sequences for detection of sequences
              associated with drug-resistance mutations
JOURNAL      Patent: WO 0220852-A 45 14-MAR-2002;
              Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
FEATURES     Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligonucleotide primer for Reverse Transcriptase
                target sequence"
              promoter
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ORIGIN
Query Match      63.0%; Score 34; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 6.8e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAAATTATACGACTCCTATAGGAGACCACAT 34
        |||||||
Db      1 GAAATTATACGACTCCTATAGGAGACCACAT 34

RESULT 62
CS072195 LOCUS      CS072195      61 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 2 from Patent WO2001044511.
ACCESSION CS072195
VERSION   CS072195.1 GI:63089420
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1 Brentano,S.T. and Lankford,R.L.
AUTHORS   Methods and compositions for detection of mycobacterium avium
TITLE     complex species
JOURNAL   Patent: WO 2001044511-A 2 21-JUN-2001;
          Gen-Probe Incorporated (US)
FEATURES  Location/Qualifiers
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            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: synthetic
            promoter-primer"
ORIGIN
Query Match      63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAAATTATACGACTCCTATAGGAGACCACAT 34
        |||||||
Db      1 GAAATTATACGACTCCTATAGGAGACCACAT 34

RESULT 63
CS072205/c LOCUS      CS072205      61 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 12 from Patent WO2001044511.
ACCESSION CS072205
VERSION   CS072205.1 GI:63089430
KEYWORDS  synthetic construct
SOURCE    synthetic construct
ORGANISM  other sequences; artificial sequences.
REFERENCE 1 Brentano,S.T. and Lankford,R.L.
AUTHORS   Methods and compositions for detection of mycobacterium avium
TITLE     complex species

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JOURNAL      Patent: WO 2001044511-A 12 21-JUN-2001;
FEATURES     Gen-Probe Incorporated (US)
              Location/Qualifiers
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                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Description of Artificial Sequence: synthetic
                probe"
ORIGIN
Query Match      63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAAATTATACGACTCCTATAGGAGACCACAT 34
        |||||||
Db      61 GAAATTATACGACTCCTATAGGAGACCACAT 28

RESULT 64
AR559010 LOCUS      AR559010      61 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 2 from patent US 6747141.
ACCESSION AR559010
VERSION   AR559010.1 GI:53966349
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 61)
AUTHORS   Brentano,S.T. and Lankford,R.L.
TITLE     Methods and compositions for detection of mycobacterium avium
          complex species
JOURNAL   Patent: US 6747141-A 2 08-JUN-2004;
          Gen-Probe Incorporated; San Diego, CA
FEATURES  Location/Qualifiers
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            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN
Query Match      63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAAATTATACGACTCCTATAGGAGACCACAT 34
        |||||||
Db      1 GAAATTATACGACTCCTATAGGAGACCACAT 34

RESULT 65
AR559020/c LOCUS      AR559020      61 bp      DNA      linear      PAT 08-OCT-2004
DEFINITION Sequence 12 from patent US 6747141.
ACCESSION AR559020
VERSION   AR559020.1 GI:53966359
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 61)
AUTHORS   Brentano,S.T. and Lankford,R.L.
TITLE     Methods and compositions for detection of mycobacterium avium
          complex species
JOURNAL   Patent: US 6747141-A 12 08-JUN-2004;
          Gen-Probe Incorporated; San Diego, CA
FEATURES  Location/Qualifiers
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            1..61
            /organism="unknown"
            /mol_type="genomic DNA"
ORIGIN

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Query Match          63.0%; Score 34; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 6.2e+05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
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Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 66
BD236961          52 bp DNA linear PAT 17-JUL-2003
LOCUS             Nucleic acid sequence for detecting genetic marker for cancer in
DEFINITION        biological samples.
ACCESSION         BD236961
VERSION           BD236961.1 GI:33046731
KEYWORDS          JP 2002535014-A/36.
SOURCE            synthetic construct
ORGANISM          other sequences; artificial sequences.
REFERENCE         1 (bases 1 to 52)
AUTHORS           Harvey,R.C. and Jr,T.J.C.
TITLE             Nucleic acid sequence for detecting genetic marker for cancer in
                  biological samples
JOURNAL           Patent: JP 2002535014-A 36 22-OCT-2002;
COMMENT           GEN PROBE INC
                  OS Artificial Sequence
                  PN JP 2002535014-A/36
                  PD 22-OCT-2002
                  PF 28-JAN-2000 JP 2000596180
                  PI 28-JAN-1999 US 60/117640
                  PR RICHARD C HARVEY, THOMAS J CLARK JR
                  PC C12N15/09,C12Q1/68,C12N15/00
                  CC Description of Artificial Sequence: synthetic construct FH
Key               Location/Qualifiers
FT               promoter
                  (i). .(28).
FEATURES         source
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                  /organism="synthetic construct"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:32630"
ORIGIN

Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38

RESULT 67
AR307447          52 bp DNA linear PAT 12-JUN-2003
LOCUS             Sequence 36 from patent US 6551778.
DEFINITION        AR307447
ACCESSION         AR307447
VERSION           AR307447.1 GI:31697986
KEYWORDS          .
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 52)
AUTHORS           Harvey,R.C. and Clark,T.J. Jr.
TITLE             Nucleic acid sequences for detecting genetic markers for cancer in
                  a biological sample
JOURNAL           Patent: US 6551778-A 36 22-APR-2003;
                  Gen-Probe Incorporated; San Diego, CA
FEATURES         source
                  1..52
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN

Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38

RESULT 69
AR647675          58 bp DNA linear PAT 20-APR-2005
LOCUS             Sequence 19 from patent US 6870045.
DEFINITION        AR647675
ACCESSION         AR647675
VERSION           AR647675.1 GI:62786794
KEYWORDS          .
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 58)
AUTHORS           Yang,Y.Y. and Burrell,T.A.
TITLE             Kits for detecting HIV-2
                  Patent: US 6870045-A 19 22-MAR-2005;
                  Gen-Probe Incorporated; San Diego, CA
FEATURES         source
                  1..58
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN

Query Match          61.5%; Score 33.2; DB 2; Length 58;
Best Local Similarity 92.1%; Pred. No. 8.3e+05;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACCCTG 38

RESULT 70
AX498431
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Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
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Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38
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RESULT 68
AR594161          52 bp DNA linear PAT 15-DEC-2004
LOCUS             Sequence 36 from patent US 6811985.
DEFINITION        AR594161
ACCESSION         AR594161
VERSION           AR594161.1 GI:56643666
KEYWORDS          .
SOURCE            Unknown.
ORGANISM          Unknown.
REFERENCE         1 (bases 1 to 52)
AUTHORS           Harvey,R.C. and Clark,T.J. Jr.
TITLE             Nucleic acid sequences for detecting genetic markers for cancer in
                  a biological sample
JOURNAL           Patent: US 6811985-A 36 02-NOV-2004;
                  Gen-Probe Incorporated; San Diego, CA
FEATURES         source
                  1..52
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN
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Query Match          62.6%; Score 33.8; DB 2; Length 52;
Best Local Similarity 94.6%; Pred. No. 7.5e+05;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTGTG 38
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Db 2 AAATTAATACGACTCACTATAGGAGACCATTCTG 38
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RESULT 69
AR647675          58 bp DNA linear PAT 20-APR-2005
LOCUS             Sequence 19 from patent US 6870045.
DEFINITION        AR647675
ACCESSION         AR647675
VERSION           AR647675.1 GI:62786794
KEYWORDS          .
SOURCE            Unknown.
ORGANISM          Unclassified.
REFERENCE         1 (bases 1 to 58)
AUTHORS           Yang,Y.Y. and Burrell,T.A.
TITLE             Kits for detecting HIV-2
                  Patent: US 6870045-A 19 22-MAR-2005;
                  Gen-Probe Incorporated; San Diego, CA
FEATURES         source
                  1..58
                  /organism="unknown"
                  /mol_type="genomic DNA"
ORIGIN
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Query Match          61.5%; Score 33.2; DB 2; Length 58;
Best Local Similarity 92.1%; Pred. No. 8.3e+05;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTGTG 38
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACCCTG 38

RESULT 70
AX498431
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LOCUS AX498431 58 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from Patent WO234951.
ACCESSION AX498431
VERSION AX498431.1 GI:23343309
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
AUTHORS Yang,Y.Y. and Burrell,T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
2 (hiv-2)
JOURNAL Patent: WO 0234951-A 19 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
source
1..58
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"
ORIGIN
Query Match 61.5%; Score 33.2; DB 2; Length 58;
Best Local Similarity 92.1%; Pred. No. 8.3e+05;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCCTATAGGAGACACCATTTGTG 38
|||||
Db 1 GAAATTAATACGACTCCTATAGGAGACACCATTTGTG 38
|||||
RESULT 71
AF521666 4356 bp DNA circular SYN 04-DEC-2002
LOCUS Cloning vector pLOI2065 complete sequence.
DEFINITION Cloning vector pLOI2065
ACCESSION AF521666
VERSION AF521666.1 GI:21780275
KEYWORDS Cloning vector pLOI2065
SOURCE Cloning vector pLOI2065
ORGANISM other sequences; artificial sequences; vectors.
REFERENCE 1 (bases 1 to 4356)
AUTHORS Underwood,S.A., Zhou,S., Causey,T.B., Yomano,L.P., Shanmugam,K.T.
and Ingram,L.O.
TITLE Genetic Changes To Optimize Carbon Partitioning between Ethanol and
Biosynthesis in Ethanologenic Escherichia coli
JOURNAL Appl. Environ. Microbiol. 68 (12), 6263-6272 (2002)
PUBMED 12450851
REFERENCE 2 (bases 1 to 4356)
AUTHORS Yomano,L.P. and Ingram,L.O.
TITLE Direct Submission
JOURNAL Submitted (13-JUN-2002) Microbiology & Cell Science, University of
Florida, POBox 110700, Museum Rd., Gainesville, FL 32611, USA
FEATURES
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/organism="Cloning vector pLOI2065"
/mol_type="genomic DNA"
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456..510
/bound_moiety="flipase"
complement(711..1901)
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/note="tetracycline resistance protein"
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/protein_id="AAW77666.1"
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/translation="MKSNNALIVILGTVTLDVAGIGLVMPVLPLGLLRDINVHSDSTASH
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gene
CDS
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YGVLLALYALMQFLCAPVLGALSDFRQRRPVLASLLGATIDYAIMATTPVWLILYAG
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LFIMQLGVOPPAALWLVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
KQALIAGMAADALGYLLAFATRCGWMAFPIMILLASGGIGMPALQAMLSLRQDDHOG
QLQGSALATSLTSLTITGFLIVTALYAAASTWNGLAMIYGAALYDLVCLPALRRGAWSR
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complement(3296..4156)
/gene="bla"
/note="ampicillin resistance protein"
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IELDNGSKILESFRPERPQMSTFEKLLGAVLSRIDAGQEQLGRIRHYSDNDLVE
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DRWEPELNEAIPNDERDITMPVAMATTLRLKLLTGELLTLASRQQLIDHWKADKVAQPL
LRSLAPAGWFIADKSGAGERSGIIAALGPDGKPSRIIVITTTGSAQTMDERNQIA
EIGASLIRKHW"
ORIGIN
Query Match 61.5%; Score 33.2; DB 8; Length 4356;
Best Local Similarity 75.9%; Pred. No. 2.8e+04;
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCCTATAGGAGACACCATTTGTGCAATATTCCCACTGC 54
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Db 2089 GAAATTAATACGACTCCTATAGGAGACCGGAATTCGTAATCATGTCATAGC 2142
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RESULT 72
AX202478 5731 bp DNA linear PAT 30-AUG-2001
LOCUS Sequence 66 from Patent WO0152620.
DEFINITION AX202478
ACCESSION AX202478
VERSION AX202478.1 GI:15392206
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Barbas,C.F., Stege,J.T., Guan,X. and Dalmia,B.
TITLE Methods and compositions to modulate expression in plants
JOURNAL Patent: WO 0152620-A 66 26-JUL-2001;
The Scripps Research Institute (US) ; SYNGENTA AGRICULTURAL
DISCOVERY, INC. (CA)
FEATURES
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1..5731
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="2C7-SID"
ORIGIN
Query Match 61.5%; Score 33.2; DB 2; Length 5731;
Best Local Similarity 75.9%; Pred. No. 2.3e+04;
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCCTATAGGAGACACCATTTGTGCAATATTCCCACTGC 54
|||||
Db 858 GAAATTAATACGACTCCTATAGGAGACCGGAATTCGTAATCATGTCATAGC 911
|||||
RESULT 73
CS072203
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LOCUS CS072203 33 bp DNA linear PAT 05-MAY-2005  
DEFINITION Sequence 10 from Patent WO2001044511.  
ACCESSION CS072203  
VERSION CS072203.1 GI:63089428  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Brentano,S.T. and Lankford,R.L.  
TITLE Methods and compositions for detection of mycobacterium avium  
JOURNAL complex species  
PATENT: WO 2001044511-A 10 21-JUN-2001;  
Gen-Probe Incorporated (US)  
FEATURES  
source Location/Qualifiers  
1..33  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="Description of Artificial Sequence: promoter"  
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Query Match 61.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
RESULT 74  
AR344815  
LOCUS AR344815 33 bp DNA linear PAT 17-AUG-2003  
DEFINITION Sequence 4 from patent US 6582920.  
ACCESSION AR344815  
VERSION AR344815.1 GI:33740896  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of HIV-1 RT sequences for detection of sequences  
associated with drug-resistance mutations  
JOURNAL Patent: US 6582920-A 4 24-JUN-2003;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
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Query Match 61.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
RESULT 75  
AR438668  
LOCUS AR438668 33 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 36 from patent US 6664081.  
ACCESSION AR438668  
VERSION AR438668.1 GI:42663592  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 33)

AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 36 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
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/organism="unknown"  
/mol\_type="genomic DNA"  
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Query Match 61.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
RESULT 76  
AR559018  
LOCUS AR559018 33 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 10 from patent US 6747141.  
ACCESSION AR559018  
VERSION AR559018.1 GI:53966357  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Brentano,S.T. and Lankford,R.L.  
TITLE Methods and compositions for detection of mycobacterium avium  
JOURNAL complex species  
PATENT: US 6747141-A 10 08-JUN-2004;  
Gen-Probe Incorporated; San Diego, CA  
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source Location/Qualifiers  
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/mol\_type="genomic DNA"  
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Query Match 61.1%; Score 33; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33  
|||||  
RESULT 77  
AR647685  
LOCUS AR647685 33 bp DNA linear PAT 20-APR-2005  
DEFINITION Sequence 29 from patent US 6870045.  
ACCESSION AR647685  
VERSION AR647685.1 GI:62786804  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Yang,Y.Y. and Burrell,T.A.  
TITLE Kits for detecting HIV-2  
JOURNAL Patent: US 6870045-A 29 22-MAR-2005;  
Gen-Probe Incorporated; San Diego, CA  
FEATURES  
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/mol\_type="genomic DNA"  
ORIGIN  
Query Match 61.1%; Score 33; DB 2; Length 33;



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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 78
LOCUS AR720132 33 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 4 from patent US 6946254.
ACCESSION AR720132
VERSION AR720132.1 GI:77371197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 33)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 4 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 79
LOCUS AX166870 33 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 36 from Patent WO0144510.
ACCESSION AX166870
VERSION AX166870.1 GI:14596472
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and
Rodrigue, M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 36 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES
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1..33
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="promoter"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 80
LOCUS AX397770 33 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 4 from Patent WO0220852.
ACCESSION AX397770
VERSION AX397770.1 GI:21260644
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 4 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US); Biomerieux S.A. (FR)
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter sequence"
1..33
promoter
ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 81
LOCUS AX498441 33 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 29 from Patent WO0234951.
ACCESSION AX498441
VERSION AX498441.1 GI:23343319
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORGANISM Human immunodeficiency virus 2
Viruses; Retro-transcribing viruses; Retroviridae;
Orthoretrovirinae; Lentivirus; Primate lentivirus group.
REFERENCE
1
AUTHORS Yang, Y.Y. and Burrell, T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
2 (hiv-2)
JOURNAL Patent: WO 0234951-A 29 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
source
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/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN
Query Match 61.1%; Score 33; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 82
LOCUS CS008909 41 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 6 from Patent WO2005007886.
ACCESSION CS008909
VERSION CS008909.1 GI:59669518
KEYWORDS

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SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Scott,C. and Walker,B.
TITLE       Patent: WO 2005007896-A 6 27-JAN-2005;
JOURNAL     The Queen's University of Belfast (GB)
FEATURES    Location/Qualifiers
             source
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               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Artificial sequence"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 83
AR193645
LOCUS       AR193645              41 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 15 from patent US 6348315.
ACCESSION  AR193645
VERSION     AR193645.1 GI:20240237
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 41)
AUTHORS    Pluckthun,A., Hanes,J. and Jermutus,L.
TITLE      Polysome display in the absence of functional ssrA-RNA
JOURNAL    Patent: US 6348315-A 15 19-FEB-2002;
FEATURES    Location/Qualifiers
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               /organism="unknown"
               /mol_type="unassigned DNA"

ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 84
AR352369
LOCUS       AR352369              41 bp      DNA      linear      PAT 17-AUG-2003
DEFINITION Sequence 15 from patent US 6589741.
ACCESSION  AR352369
VERSION     AR352369.1 GI:33757503
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 41)
AUTHORS    Pluckthun,A., Hanes,J. and Jermutus,L.
TITLE      Polysome display in the absence of functional ssrA-RNA
JOURNAL    Patent: US 6589741-A 15 08-JUL-2003;
            University of Zurich; Zurich;
            EPX;
FEATURES    Location/Qualifiers
             source
               1..41
               /organism="unknown"

SOURCE      synthetic construct
ORGANISM    synthetic construct
REFERENCE   1
AUTHORS     Scott,C. and Walker,B.
TITLE       Patent: WO 2005007896-A 6 27-JAN-2005;
JOURNAL     The Queen's University of Belfast (GB)
FEATURES    Location/Qualifiers
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               /note="Artificial sequence"

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Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 85
AX768001
LOCUS       AX768001              41 bp      DNA      linear      PAT 02-JUL-2003
DEFINITION Sequence 3 from Patent EP1316616.
ACCESSION  AX768001
VERSION     AX768001.1 GI:32436681
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Nemetz,C., Buchberger,B., Watzele,M., Mutter,W., Roeder,A. and
            Wessner,S.
TITLE      Method for producing linear dna fragments for the in vitro
            expression of proteins
JOURNAL    Patent: EP 1316616-A 3 04-JUN-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES    Location/Qualifiers
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               /db_xref="taxon:32644"
               /note="Primer"

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Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 86
AX768013
LOCUS       AX768013              41 bp      DNA      linear      PAT 02-JUL-2003
DEFINITION Sequence 15 from Patent EP1316616.
ACCESSION  AX768013
VERSION     AX768013.1 GI:32436693
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS    Nemetz,C., Buchberger,B., Watzele,M., Mutter,W., Roeder,A. and
            Wessner,S.
TITLE      Method for producing linear dna fragments for the in vitro
            expression of proteins
JOURNAL    Patent: EP 1316616-A 15 04-JUN-2003;
            Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)
FEATURES    Location/Qualifiers
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               /db_xref="taxon:32644"
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ORIGIN
Query Match      61.1%; Score 33; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

RESULT 87

AX299239

LOCUS AX299239

DEFINITION Sequence 2 from Patent WO0183734.

ACCESSION AX299239

VERSION AX299239.1 GI:17129110

KEYWORDS

SOURCE Enterobacteria phage T7

ORGANISM Enterobacteria phage T7

Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae; T7-like viruses.

REFERENCE 1

AUTHORS Nilsson, N.

TITLE Expression vector libraries

JOURNAL Patent: WO 0183734-A 2 08-NOV-2001; Bioinvent International AB (SE)

FEATURES

source 1. .49

/organism="Enterobacteria phage T7"

/mol\_type="unassigned DNA"

/db\_xref="taxon:10760"

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Best Local Similarity 100.0%; Pred. No. 1e+06;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

RESULT 88

BD080457

LOCUS BD080457

DEFINITION Methods for protein screening.

ACCESSION BD080457

VERSION BD080457.1 GI:22626060

KEYWORDS JP 2001514850-A/14.

SOURCE unidentified

ORGANISM unidentified

REFERENCE 1 (bases 1 to 50)

AUTHORS Carr, F.J., Carter, G., Hamilton, A.A., Adair, F.S. and Williams, S.

TITLE Methods for protein screening

JOURNAL Patent: JP 2001514850-A 14 18-SEP-2001; BIOVATION LTD

COMMENT OS Unidentified

PN JP 2001514850-A/14

PD 18-SEP-2001

PF 03-SEP-1998 JP 2000508788

PR 03-SEP-1997 GB 9718552.4 18-SEP-1997 GB 9719834.5 PR

24-SEP-1997 GB 9720184.2 29-SEP-1997 GB 9720522.3 PR

29-SEP-1997 GB 9720525.6 29-SEP-1997 GB 9720523.1 PR

29-SEP-1997 GB 9720524.9 30-DEC-1997 US 60/070063 PR

30-DEC-1997 US 60/070062, 30-DEC-1997 US 60/070037 PR

30-DEC-1997 US 60/070050, 22-JAN-1998 GB 9801255.2 PR

25-FEB-1998 GB 9803828.4, 14-APR-1998 GB 9807760.5 PR

23-MAY-1998 GB 9811130.5

PI FRANCIS JOSEPH CARR, GRAHAM CARTER, ANITA ANNE HAMILTON, FIONA PI SUZANNE ADAIR,

PI STEVEN WILLIAMS

PC C12N15/09, C07K17/00, C12N11/14, C12P21/00, C12Q1/68//C07K14/16,

PC C07K14/54, C12N15/00

PC C07K16/00, C12N15/00

CC Methods for protein screening

FEATURES

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Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:32644"

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Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

Db 15 GAAATTAAATACGACTCACTATAGGAGACCACA 47

RESULT 89

AR703437

LOCUS AR703437

DEFINITION Sequence 15 from patent US 6927025.

ACCESSION AR703437

VERSION AR703437.1 GI:75921308

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 50)

AUTHORS Carr, F.J., Carter, G., Hamilton, A.A., Adair, F.S. and Williams, S.

TITLE Methods for protein screening

JOURNAL Patent: US 6927025-A 15 09-AUG-2005; Biovation Limited; Aberdeen;

FEATURES

source 1. .50

Location/Qualifiers

/organism="unknown"

/mol\_type="genomic DNA"

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Query Match 61.1%; Score 33; DB 2; Length 50;

Best Local Similarity 100.0%; Pred. No. 9.9e+05;

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Qy 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33

Db 15 GAAATTAAATACGACTCACTATAGGAGACCACA 47

RESULT 90

AR344852

LOCUS AR344852

DEFINITION Sequence 41 from patent US 6582920.

ACCESSION AR344852

VERSION AR344852.1 GI:33740933

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 51)

AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.

TITLE Amplification of HIV-1 RT sequences for detection of sequences associated with drug-resistance mutations

JOURNAL Patent: US 6582920-A 41 24-JUN-2003; Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA

FEATURES

source 1. .51

Location/Qualifiers

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/mol\_type="genomic DNA"

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Query Match 61.1%; Score 33; DB 2; Length 51;

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Best Local Similarity 100.0%; Pred. No. 9.7e+05;
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 91
AR720169 AR720169 51 bp DNA linear PAT 07-OCT-2005
LOCUS Sequence 41 from patent US 6946254.
DEFINITION AR720169
ACCESSION AR720169
VERSION AR720169.1 GI:77371234
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 51)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 41 20-SEP-2005;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Best Local Similarity 100.0%; Pred. No. 9.7e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 92
AX397807 AX397807 51 bp DNA linear PAT 27-MAY-2002
LOCUS Sequence 41 from Patent WO0220852.
DEFINITION AX397807
ACCESSION AX397807
VERSION AX397807.1 GI:21260681
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 41 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
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Best Local Similarity 100.0%; Pred. No. 9.7e+05;
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Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

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RESULT 93
BD237698 BD237698 52 bp DNA linear PAT 17-JUL-2003
LOCUS Therapeutically active proteins in plants.
DEFINITION BD237698
ACCESSION BD237698
VERSION BD237698.1 GI:33047468
KEYWORDS JP 2002526116-A/27.
SOURCE synthetic construct
ORGANISM
REFERENCE
1 (bases 1 to 52)
AUTHORS Heifetz, P. B., Goff, S. A., Tuttle, A. B. and Wenk, M. E. G.
TITLE Therapeutically active proteins in plants
JOURNAL Patent: JP 2002526116-A 27 20-AUG-2002;
SYNGENTA PARTICIPATIONS AG
COMMENT OS Artificial Sequence
PN JP 2002526116-A/27
PD 20-AUG-2002
PF 05-OCT-1999 JP 2000574707
PR 07-OCT-1998 US 09/167362, 07-OCT-1998 US 09/168231 PI
PETER BERNARD HEIFETZ, STEPHEN ARTHUR GOFF, ANNMARIE BLOOM PI
TUTTLE,
PI MONIKA ELSE GRIOT WENK
PC A01H5/00, A23L1/30, A61K38/00, A61K38/16, A61K38/22, PC
A61K38/28
PC A61K38/43, A61K39/00, A61K39/35, A61P29/00, A61P37/00, A61P37/06,
PC A61P37/08,
PC C12N5/10, C12N15/09// (C12N5/10, C12R1:91), C12N15/00, C12N5/00, PC
A61K37/02,
PC A61K37/26, A61K37/48, A61K37/04, A61K37/24, (C12N5/00, C12R1:91) CC
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Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

RESULT 94
AR344850 AR344850 52 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 39 from patent US 6582920.
DEFINITION AR344850
ACCESSION AR344850
VERSION AR344850.1 GI:33740931
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 52)
AUTHORS Yang, Y. Y., Brentano, S. T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 39 24-JUN-2003;
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA
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Query Match      61.1%; Score 33; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 95
LOCUS AR720167 52 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 39 from patent US 6946254.
ACCESSION AR720167
VERSION AR720167.1 GI:77371232
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 52)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 gag sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6946254-A 39 20-SEP-2005;
FEATURES
Location/Qualifiers
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/organism="unknown"
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Query Match      61.1%; Score 33; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
LOCUS AX278216 52 bp DNA linear PAT 01-NOV-2001
DEFINITION Sequence 27 from Patent WO0177353.
ACCESSION AX278216
VERSION AX278216.1 GI:16605267
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Helfetz, P.B., Goff, S.A., Tuttle, A.B. and Griot-Wenk, M.E.
TITLE Expression of pollen allergens in plasmids
JOURNAL Patent: WO 0177353-A 27 18-OCT-2001;
SYNGENTA Participations AG (CH)
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
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Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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RESULT 97
Query Match      61.1%; Score 33; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 9.4e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 98
LOCUS AR344848 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 37 from patent US 6582920.
ACCESSION AR344848
VERSION AR344848.1 GI:33740929
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 53)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 37 24-JUN-2003;
GEN-PROBE Incorporated and Biomerieux S.A.; San Diego, CA
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RESULT 99
LOCUS AR720165 53 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 37 from patent US 6946254.
ACCESSION AR720165
VERSION AR720165.1 GI:77371230
KEYWORDS
SOURCE Unknown.

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AX397805
LOCUS AX397805 52 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 39 from Patent WO0220852.
ACCESSION AX397805
VERSION AX397805.1 GI:21260679
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE
1
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: WO 0220852-A 39 14-MAR-2002;
GEN-PROBE Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)
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Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Reverse Transcriptase
target sequence"
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promoter
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Query Match      61.1%; Score 33; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 9.6e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 98
LOCUS AR344848 53 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 37 from patent US 6582920.
ACCESSION AR344848
VERSION AR344848.1 GI:33740929
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 53)
AUTHORS Yang, Y.Y., Brentano, S.T., Babola, O., Tran, N. and Vernet, G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 37 24-JUN-2003;
GEN-PROBE Incorporated and Biomerieux S.A.; San Diego, CA
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Query Match      61.1%; Score 33; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 9.4e+05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
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RESULT 99
LOCUS AR720165 53 bp DNA linear PAT 07-OCT-2005
DEFINITION Sequence 37 from patent US 6946254.
ACCESSION AR720165
VERSION AR720165.1 GI:77371230
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.  
Unclassified  
REFERENCE 1 (bases 1 to 53)  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of HIV-1 gag sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: US 6946254-A 37 20-SEP-2005;  
Gen-Probe Incorporated and Biomerieux S.A.; San Diego, CA  
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
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RESULT 100  
AX397803  
LOCUS AX397803 53 bp DNA linear PAT 27-MAY-2002  
DEFINITION Sequence 37 from Patent WO0220852.  
ACCESSION AX397803  
VERSION AX397803.1 GI:21260677  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.  
1  
REFERENCE  
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.  
TITLE Amplification of hiv-1 sequences for detection of sequences associated with drug-resistance mutations  
JOURNAL Patent: WO 0220852-A 37 14-MAR-2002;  
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)  
FEATURES  
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Query Match 61.1%; Score 33; DB 2; Length 53;  
Best Local Similarity 100.0%; Pred.No. 9.4e+05;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
    |||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-10-665-708-11  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

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- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
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- 13: Geneseq2004bs:\*
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- 15: Geneseq2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	42	77.8	58 14 AEA08214 Aea08214 M. tuberc
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8	41	75.9	57 10 ADG88341 ADG88341 Mycobacte
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18	37	68.5	53 12 ADI18951 ADI18951 HIV-I pro

92	33	61.1	53	6	AAL45499	AAL45499 HIV-1 pol	165	33	61.1	166	10	ADP86215	Adf86215 DNA oligo
93	33	61.1	53	12	ADI18946	Adi18946 HIV-1 pol	166	33	61.1	167	10	ADP66629	Adf66629 Open read
94	33	61.1	55	2	AAQ50482	Aaq50482 Promoter-	167	33	61.1	167	10	ADP66630	Adf66630 Open read
95	33	61.1	55	2	AAQ85669	Aaq85669 Promoter	168	33	61.1	169	15	AEES92630	Aee92630 Expressio
96	33	61.1	55	3	AAA89910	Aaa89910 Primer #1	169	33	61.1	187	2	AAQ85293	Aaq85293 Portion o
97	33	61.1	55	6	ABK53144	Abk53144 HIV-1 rev	170	33	61.1	190	6	ABL56948	AbL56948 Galactose
98	33	61.1	55	6	AAAL45506	Aal45506 HIV-1 pol	171	33	61.1	193	8	AAL51539	Aal51539 Cell-free
99	33	61.1	55	12	ADI18953	Adi18953 HIV-1 pol	172	33	61.1	203	15	AEF92008	Aef92008 Expressio
100	33	61.1	56	3	AAA28796	Aaa28796 Plant pla	173	33	61.1	203	15	AEF92010	Aef92010 Expressio
101	33	61.1	56	5	AAAD21602	Aad21602 Phage RNA	174	33	61.1	203	15	AEF92009	Aef92009 Expressio
102	33	61.1	57	2	AAV00258	Aav00258 Cloned ps	175	33	61.1	204	3	AAC55484	Aac55484 Destinati
103	33	61.1	57	6	ABK93894	Abk93894 Human imm	176	33	61.1	216	8	ABZ70136	Abz70136 Oligonuc
104	33	61.1	58	10	ADH79429	Adh79429 PCR prime	177	33	61.1	216	8	ABZ80275	Abz80275 Peptide-1
105	33	61.1	59	4	ADL11021	Adl11021 Probe #1	178	33	61.1	216	8	ABZ80276	Abz80276 Peptide-1
106	33	61.1	59	4	ADL11011	Adl11011 Promoter-	179	33	61.1	217	10	ADP55564	Adp55564 Cell-free
107	33	61.1	60	10	ADD69693	Add69693 Nucleic a	180	33	61.1	217	10	ADJ66007	Adj66007 5' DNA fr
108	33	61.1	60	10	ADD69692	Add69692 T7 RNA pr	181	33	61.1	222	6	ABQ82240	Abq82240 Plasmid p
109	33	61.1	62	2	AAQ57040	Aaq57040 M. tuberc	182	33	61.1	222	6	ABQ82238	Abq82238 Plasmid p
110	33	61.1	63	2	AAV70233	Aav70233 scFv anti	183	33	61.1	222	6	ABQ82236	Abq82236 Plasmid p
111	33	61.1	66	8	ABA00556	Abao0556 Sense pri	184	33	61.1	227	12	ADK71959	Adk71959 PCR prime
112	33	61.1	66	10	ABV76279	Abv76279 Green flu	185	33	61.1	227	12	ADQ54850	Ado54850 PCR prime
113	33	61.1	67	2	AAAX25961	Aax25961 Capture d	186	33	61.1	227	13	ADS92548	Ads92548 PCR prime
114	33	61.1	71	6	ABN83684	Abn83684 T7 promot	187	33	61.1	227	14	AEC56031	Aec56031 BAG5 doma
115	33	61.1	74	12	ADL16931	Adl16931 Pseudomon	188	33	61.1	227	14	AEC56018	Aec56018 BAG3 doma
116	33	61.1	75	2	AAAX81449	Aax81449 PCR prime	189	33	61.1	228	12	ADM28957	Adm28957 PCR prime
117	33	61.1	75	8	ABQ77329	Abq77329 Bovine H-	190	33	61.1	244	10	ADP55565	Adp55565 Cell-free
118	33	61.1	75	8	AAAL50784	Aal50784 Exonuclea	191	33	61.1	244	10	ADJ66008	Adj66008 5' DNA fr
119	33	61.1	75	12	ADL16916	Adl16916 Pseudomon	192	33	61.1	254	14	ADZ39855	Adz39855 T7 P-Nhis
120	33	61.1	75	13	ADQ67875	Adq67875 HindIII r	193	33	61.1	254	14	ADZ02844	Adz02844 T7 P-Nhis
121	33	61.1	84	12	ADQ30930	Adq30930 Hairpin 1	194	33	61.1	258	2	AAQ41868	Aaq41868 T7 late g
122	33	61.1	85	10	ADF86217	Adf86217 PCR prime	195	33	61.1	287	15	AEF92004	Aef92004 Expressio
123	33	61.1	85	14	AEEO1636	Aee01636 Primer #3	196	33	61.1	287	15	ADL71887	Adl71887 Vector pE
124	33	61.1	88	3	AAA60713	Aaa60713 T7 promot	197	33	61.1	299	15	AEF92006	Aef92006 Expressio
125	33	61.1	88	4	AAF75873	Aaf75873 Oligonuc	198	33	61.1	303	12	ADU27300	Adl27300 Nucleotid
126	33	61.1	89	2	AAQ92012	Aaq92012 Oligomer	199	33	61.1	303	14	AEA51237	Aea51237 Human C4B
127	33	61.1	89	2	AAAT30154	Aat30154 Elements	200	33	61.1	350	9	ADB67799	Adb67799 DNA seque
128	33	61.1	89	2	AAV00260	Aav00260 Cloned T7	201	33	61.1	374	9	ADCB67796	Adcb67796 DNA seque
129	33	61.1	89	2	AAAX01917	Aax01917 Bacteriop	202	33	61.1	374	10	ADC64892	Adc64892 Polynucle
130	33	61.1	90	2	AAAX85755	Aax85755 Oligonuc	203	33	61.1	374	14	ADM64744	Adm64744 Transport
131	33	61.1	93	5	AAAF82145	Aaf82145 T7 promot	204	33	61.1	374	14	ADY75079	Ady75079 T7 RNA po
132	33	61.1	96	6	ABK88323	Abk88323 T4 RNA li	205	33	61.1	398	12	ADQ30980	Adq30980 Hairpin 1
133	33	61.1	96	6	ABK67969	Abk67969 Mutant DN	206	33	61.1	407	14	ADM64743	Adm64743 Transport
134	33	61.1	96	9	ADB67790	Adb67790 DNA seque	207	33	61.1	408	13	ADV34922	Adv34922 Recombina
135	33	61.1	96	10	ADC64886	Adc64886 T7 promot	208	33	61.1	412	2	AAV22974	Aav22974 Nucleic a
136	33	61.1	96	14	ADM64747	Adm64747 Transport	209	33	61.1	412	2	AAV70648	Aav70648 Human tau
137	33	61.1	96	14	ADX44479	Adx44479 pT7-FF re	210	33	61.1	424	12	ADQ17264	Adq17264 Human sof
138	33	61.1	102	3	AAAC55508	Aac55508 Destinati	211	33	61.1	424	12	ADQ22024	Adq22024 Human sof
139	33	61.1	102	3	AAAC55505	Aac55505 Destinati	212	33	61.1	431	12	ADQ30979	Adq30979 Hairpin 1
140	33	61.1	102	3	AAAC55511	Aac55511 Destinati	213	33	61.1	450	2	AAQ80820	Aaq80820 Gene X ci
141	33	61.1	104	1	AAAN70013	Aan70013 Sequence	214	33	61.1	495	14	AEEO1637	Aee01637 Undefined
142	33	61.1	104	2	AAQ46833	Aaq46833 GLO1 sequ	215	33	61.1	511	10	ADP55567	Adp55567 Cell-free
143	33	61.1	109	2	AAQ67092	Aaq67092 T7 promot	216	33	61.1	511	10	ADJ66010	Adj66010 5' DNA fr
144	33	61.1	110	6	AAAL50148	Aal50148 Protein 1	217	33	61.1	599	12	ADQ30982	Adq30982 Hairpin 1
145	33	61.1	110	8	ABZ22169	Abz22169 T7 promot	218	33	61.1	604	13	ADRI10590	Adri10590 Template
146	33	61.1	117	4	AAAF75879	Aaf75879 Oligonuc	219	33	61.1	632	12	ADQ30981	Adq30981 Hairpin 1
147	33	61.1	120	3	AAAC55482	Aac55482 Destinati	220	33	61.1	640	6	ABV99931	Abv99931 Leptin-re
148	33	61.1	124	12	ADK71953	Adk71953 PCR prime	221	33	61.1	644	5	AAI71848	Aai71848 Recombina
149	33	61.1	124	12	ADM6345	Adm6345 PCR prime	222	33	61.1	651	10	ADD69689	Add69689 Nucleic a
150	33	61.1	134	2	AAQ05915	Aaq05915 Upstream	223	33	61.1	651	10	ADP55566	Adp55566 Cell-free
151	33	61.1	135	2	AAV59148	Aav59148 Peptide 1	224	33	61.1	652	10	ADJ66009	Adj66009 5' DNA fr
152	33	61.1	136	8	AAAL51534	Aal51534 Cell-free	225	33	61.1	654	10	ADJ66960	Adj66960 Nucleic a
153	33	61.1	139	10	ADF86211	Adf86211 DNA oligo	226	33	61.1	670	13	ADRI10587	Adri10587 Template
154	33	61.1	143	9	ADB16304	Adb16304 Cleavase	227	33	61.1	701	15	AEF92014	Aef92014 Vector pi
155	33	61.1	144	2	AAV59151	Aav59151 Peptide 1	228	33	61.1	713	15	AEF92016	Aef92016 Vector pi
156	33	61.1	144	6	ADES3338	Ades3338 FEN-1 rel	229	33	61.1	728	2	AAQ55301	Aaq55301 Truncated
157	33	61.1	144	9	ADB16309	Adb16309 Vector pE	230	33	61.1	782	2	AAV60837	Aav60837 Partial s
158	33	61.1	144	10	ADC02516	Adc02516 Vector pE	231	33	61.1	821	15	AEF92035	Aef92035 Vector pi
159	33	61.1	144	10	ADD69702	Add69702 Nucleic a	232	33	61.1	844	10	ADP55563	Adp55563 Cell-free
160	33	61.1	146	2	AAAX85763	Aax85763 Nucleotid	233	33	61.1	844	10	ADJ66006	Adj66006 5' DNA fr
161	33	61.1	147	10	ADD69703	Add69703 Nucleic a	234	33	61.1	870	2	AAV58934	Aav58934 Humanised
162	33	61.1	153	3	AAAC5490	Aac5490 Destinati	235	33	61.1	905	12	ADQ30986	Adq30986 Hairpin 1
163	33	61.1	153	3	AAAC5487	Aac5487 Destinati	236	33	61.1	923	2	AAZ38850	Aaz38850 Human gra
164	33	61.1	160	10	ADF86213	Adf86213 DNA oligo	237	33	61.1	938	12	ADQ30985	Adq30985 Hairpin 1







PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
PT specific primers, and detecting the amplified nucleic acid.

XX Claim 1; Page 33; 44pp; English.

XX The invention relates to a method of detecting Mycobacterium species,  
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
CC comprising a polymerase, and at least two primers, and then detecting the  
CC amplified nucleic acid. The method is relatively simple and useful for  
CC detecting the presence of various Mycobacterium species in a biological  
CC sample, and thus important for diagnosis of infections resulting from  
CC them. The method is especially important for screening opportunistic  
CC infections caused by M. tuberculosis or a Mycobacterium other than  
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used  
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to  
CC standardise OS field)

XX Sequence 58 BP; 18 A; 16 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 77.8%; Score 42; DB 4; Length 58;  
Best Local Similarity 98.1%; Pred. No. 7.6e-07;  
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTTCCCACTGC 53

## RESULT 5

ADG88339  
ID ADG88339 standard; DNA; 58 BP.

XX

AC ADG88339;

XX 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #8.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium sp.

XX US2003165824-A1.

XX

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.

XX (JUCK/) JUCKER M T.

XX (DELG/) DELGADO F D.

XX (CLEU/) CLEUZIAZ P.

XX (RODR/) RODRIGUE M.

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SQ Sequence 58 BP; 18 A; 16 C; 10 G; 14 T; 0 U; 0 Other;

Query Match 77.8%; Score 42; DB 10; Length 58;

Best Local Similarity 98.1%; Pred. No. 7.6e-07;

Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTTCCCACTGC 54

|||||

Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTTCCCACTGC 53

## RESULT 6

AEA08214

ID AEA08214 standard; DNA; 58 BP.

XX

AC AEA08214;

XX

DT 14-JUL-2005 (first entry)

XX

DE M. tuberculosis 16S rRNA amplifying T7 promoter PCR primer, SEQ ID NO: 8.

XX

KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;

XX

KW PCR; primer; ss.

XX

OS Mycobacterium tuberculosis; ATCC 27294.

XX

OS Enterobacteria phage T7.

XX

PN US2005100915-A1.

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XX 12-MAY-2005.

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XX	DT	11-MAR-2004	(first entry)
XX	DE	Mycobacterium amplifying PCR primer #10.	
XX	KW	In vitro amplification; PCR; primer; ss.	
XX	OS	Mycobacterium sp.	
XX	PN	US2003165824-A1.	
XX	PD	04-SEP-2003.	
XX	PF	15-DEC-2000; 2000US-00738274.	
XX	PR	17-DEC-1999; 99US-0172190P.	
XX	PA	(BREN/) BRENTANO S T. (JUCK/) JUCKER M T. (DELG/) DELGADO F D. (CLEU/) CLEUZIAT P. (RODR/) RODRIGUE M.	
XX	PI	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;	
XX	DR	WPI; 2003-898044/82.	
XX	PT	Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present in a biological sample comprises performing in vitro nucleic acid amplification and detection of amplified products.	
XX	PS	Claim 1; SEQ ID NO 10; 20pp; English.	
XX	CC	The present invention relates to a method of detecting Mycobacterium species present in a biological sample comprising performing an in vitro amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and detecting the amplified Mycobacterium nucleic acid. The present sequence is Mycobacterium amplifying PCR primer.	
XX	SQ	Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;	
XX	Qy	Query Match 75.9%; Score 41; DB 10; Length 57; Best Local Similarity 94.7%; Pred. No. 1.9e-06; Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1	
XX	Db	1 GAAATTAAACGACTCACTATAGGGAGACCA---CATTTGTGCAATATTTCCCCTGC 54       1 GAAATTAAACGACTCACTATAGGGAGACCA---CATTTGTGCAATATTTCCCCTGC 57	
XX	RESULT 9		
XX	AEA08216		
XX	ID	AEA08216 standard; DNA; 57 BP.	
XX	AC	AEA08216;	
XX	DT	14-JUL-2005 (first entry)	
XX	DE	M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 10.	
XX	KW	Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA; PCR; primer; ss.	
XX	OS	Mycobacterium tuberculosis; ATCC 27294.	
XX	OS	Enterobacteria phage T7.	
XX	PN	US2005100915-A1.	
XX	PD	12-MAY-2005.	
XX	PF	18-SEP-2003; 2003US-00665708.	
XX	PR	17-DEC-1999; 99US-0172190P.	
XX	Qy	Query Match 75.9%; Score 41; DB 4; Length 57; Best Local Similarity 94.7%; Pred. No. 1.9e-06; Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;	
XX	Db	1 GAAATTAAACGACTCACTATAGGGAGACCA---CATTTGTGCAATATTTCCCCTGC 54       1 GAAATTAAACGACTCACTATAGGGAGACCA---CATTTGTGCAATATTTCCCCTGC 57	
XX	RESULT 8		
XX	ADG88341		
XX	ID	ADG88341 standard; DNA; 57 BP.	
XX	AC	ADG88341;	

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PR 15-DEC-2000; 2000US-00738274.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX Example 1; SEQ ID NO 10; 21pp; English.
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying T7
CC promoter PCR primer. This T7 promoter primer sequence include a T7
CC promoter sequence attached to the portion of the primer sequence that
CC binds to the target or its complement.
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ Query Match 75.9%; Score 41; DB 14; Length 57;
Best Local Similarity 94.7%; Pred. NO. 1.9e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 57

RESULT 10
AAD11259
ID AAD11259 standard; DNA; 59 BP.
XX AC AAD11259;
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #3.
DE Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
KW Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX Key Location/Qualifiers
FH promoter 1..33
FT /*tag= a
FT /label= T7_promoter
XX WO200144510-A2.
XX 21-JUN-2001.
XX 17-DEC-1999; 99WO-US030346.
XX 17-DEC-1999; 99WO-US030346.
XX (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX Claim 1; Page 34; 44pp; English.
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S RNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;
SQ Query Match 74.1%; Score 40; DB 4; Length 59;
Best Local Similarity 93.1%; Pred. No. 4.8e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58

RESULT 11
ADG88340
ID ADG88340 standard; DNA; 59 BP.
XX AC ADG88340;
XX 11-MAR-2004 (first entry)
DT Mycobacterium amplifying PCR primer #9.
DE Mycobacterium amplifying PCR primer #9.
XX In vitro amplification; PCR; primer; ss.
XX Mycobacterium sp.
OS US2003165824-A1.
PN 04-SEP-2003.
PD 15-DEC-2000; 2000US-00738274.
PF 17-DEC-1999; 99US-0172190P.
PR (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX Claim 1; SEQ ID NO 9; 20pp; English.
XX The present invention relates to a method of detecting Mycobacterium

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CC species present in a biological sample comprises performing an in vitro  
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
 CC is Mycobacterium amplifying PCR primer.

XX SQ Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 74.1%; Score 40; DB 10; Length 59;  
 Best Local Similarity 93.1%; Pred. No. 4.8e-06;  
 Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 54  
 Db 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 58

RESULT 12  
 AEA08215 ID AEA08215 standard; DNA; 59 BP.

XX AC AEA08215;

XX DT 14-JUL-2005 (first entry)

XX DE M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 9.

XX KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;  
 XX KW PCR; primer; ss.

XX OS Mycobacterium tuberculosis; ATCC 27294.  
 XX OS Enterobacteria phage T7.

XX PN US2005100915-A1.

XX PD 12-MAY-2005.

XX PF 18-SEP-2003; 2003US-00665708.

XX PR 17-DEC-1999; 99US-0172180P.

XX PR 15-DEC-2000; 2000US-00738274.

XX PA (BREN/) BRENTANO S T.

XX PA (JUCK/) JUCKER M T.

XX PA (DELG/) DELGADO F D.

XX PA (CLEU/) CLEUZIAT P.

XX PA (RODR/) RODRIGUE M.

XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX PS WPI; 2005-345392/35.

XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 XX PT in a biological sample, comprises using in vitro nucleic acid  
 XX PT amplification and detection of amplified products.

XX PS Example 1; SEQ ID NO 9; 21pp; English.

XX CC The present invention relates to a method of detecting Mycobacterium  
 XX CC species present in a biological sample. The method involves using in  
 XX CC vitro nucleic acid amplification and detection of amplified products. The  
 XX CC invention is useful for diagnostic detection of pathogenic bacteria such  
 XX CC as Mycobacterium species. The present sequence is the Mycobacterium  
 XX CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying T7  
 XX CC promoter PCR primer. This T7 promoter primer sequence include a T7  
 XX CC promoter sequence attached to the portion of the primer sequence that  
 XX CC binds to the target or its complement.

XX SQ Sequence 59 BP; 19 A; 17 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 74.1%; Score 40; DB 14; Length 59;  
 Best Local Similarity 93.1%; Pred. No. 4.8e-06;  
 Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 54  
 Db 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 58

RESULT 13

ABK53109

ID ABK53109 standard; DNA; 54 BP.

XX AC ABK53109;

XX DT 29-AUG-2003 (revised)

XX DT 12-AUG-2002 (first entry)

XX DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #12.

XX KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
 XX KW reverse transcriptase; infection; PCR.

XX OS Human immunodeficiency virus 1.

XX PN US2002055095-A1.

XX PD 09-MAY-2002.

XX PF 31-AUG-2001; 2001US-00944036.

XX PR 01-SEP-2000; 2000US-0229790P.

XX PA (YANG/) YANG Y Y.

XX PA (BREN/) BRENTANO S T.

XX PA (BABO/) BABOLA O.

XX PA (TRAN/) TRAN N.

XX PA (VERN/) VERNET G.

XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;

XX PS WPI; 2002-462902/49.

XX PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
 XX PT 1 and probes for detecting the amplified product are specific for gag and  
 XX PT pol regions and are useful to detect different subtypes of HIV-1.

XX PS Claim 1; Page 15; 37pp; English.

XX CC This invention relates to a series of nucleic acid oligomers for  
 XX CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
 XX CC virus type 1 (HIV-1). The invention also comprises a labeled  
 XX CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived  
 XX CC from gag or pol sequences, having one of the sequences fully defined in  
 XX CC the specification, and a method for detecting HIV-1 in a biological  
 XX CC sample, comprising mixing the sample with two or more of the  
 XX CC amplification oligomers that specifically amplify at least one HIV-1  
 XX CC target sequence within gag and a pol sequence which is a protease or  
 XX CC reverse transcriptase sequence, amplifying the target, and detecting the  
 XX CC amplified product. The oligonucleotides of the invention may be used to  
 XX CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
 XX CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection  
 XX CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 54 BP; 21 A; 9 C; 9 G; 15 T; 0 U; 0 Other;

Query Match 69.6%; Score 37.6; DB 6; Length 54;  
 Best Local Similarity 90.9%; Pred. No. 4.3e-05;  
 Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 44

Db 1 GAAATTAATACGACTACTATAGGAGACCA----CATTTGCAATATTCCTCCACTGC 44

RESULT 14  
 AAL45471







```
Db      1 GAAATTAATACGACTCACTATAGGAGGAGACACATCTTGATAATT 45
|||||
RESULT 19
AAD11023/c
ID      AAD11023 standard; DNA; 57 BP.
XX      AC
XX      AAD11023;
XX      DT
XX      24-SEP-2001 (first entry)
XX      DE Probe #3 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX      KW Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX      KW in vitro amplification; MAC infection; probe; ss.
XX      OS Mycobacterium sp.
XX      PN WO200144511-A2.
XX      PD 21-JUN-2001.
XX      PF 15-DEC-2000; 2000WO-US033872.
XX      PR 15-DEC-1999; 99US-0171202P.
XX      PA (GENP-) GEN-PROBE INC.
XX      PA (BREN/) BRENTANO S T.
XX      PA (LANK/) LANKFORD R L.
XX      PI Brentano ST, Lankford RL;
XX      DR WPI; 2001-398171/42.
XX      PT Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX      PT nucleic acid amplification with amplification oligonucleotides specific
XX      PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX      PS species.
XX      Claim 11; Page 26; 27pp; English.
XX      CC The present invention relates to a method for detecting Mycobacterium
XX      CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX      CC tuberculosis, M. paratuberculosis) present in a biological sample. The
XX      CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX      CC 16S rRNA obtained from a biological sample containing nucleic acid from a
XX      CC MAC species in an in vitro nucleic acid amplification mixture comprising
XX      CC a polymerase activity and a pair of primers to produce an amplified
XX      CC nucleic acid and detecting amplified nucleic acid. The method is useful
XX      CC for in vitro diagnostic detection of pathogenic bacteria, particularly
XX      CC detecting infections caused by MAC organisms, distinguished from other
XX      CC closely-related Mycobacterium species. The present sequence is a probe
XX      CC used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX      SQ Sequence 57 BP; 13 A; 9 C; 16 G; 19 T; 0 U; 0 Other;
Query Match      68.5%; Score 37; DB 4; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy      1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 52
Db      57 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 1
|||||
RESULT 20
AAD11013
ID      AAD11013 standard; DNA; 57 BP.
XX      AC
XX      AAD11013;
XX      DT 11-SEP-2003 (revised)
|||||
DT      24-SEP-2001 (first entry)
XX      DE Promoter-primer #3 used for in vitro amplification of MAC rRNA.
XX      KW Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
XX      KW in vitro amplification; MAC infection; promoter-primer; ss.
XX      OS Enterobacteria phage T7.
XX      OS Mycobacterium sp.
XX      OS Chimeric.
XX      FH Key Location/Qualifiers
XX      FT promoter 1..33
XX      FT /*tag= a
XX      FT /note= "T7 promoter"
XX      FT misc_feature 34..57
XX      FT /*tag= b
XX      FT /note= "PCR primer from Mycobacterium sp."
XX      PN WO200144511-A2.
XX      PD 21-JUN-2001.
XX      PF 15-DEC-2000; 2000WO-US033872.
XX      PR 15-DEC-1999; 99US-0171202P.
XX      PA (GENP-) GEN-PROBE INC.
XX      PA (BREN/) BRENTANO S T.
XX      PA (LANK/) LANKFORD R L.
XX      PI Brentano ST, Lankford RL;
XX      DR WPI; 2001-398171/42.
XX      PT Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX      PT nucleic acid amplification with amplification oligonucleotides specific
XX      PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX      PS species.
XX      Claim 1; Page 12; 27pp; English.
XX      CC The present invention relates to a method for detecting Mycobacterium
XX      CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
XX      CC tuberculosis, M. paratuberculosis) present in a biological sample. The
XX      CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
XX      CC 16S rRNA obtained from a biological sample containing nucleic acid from a
XX      CC MAC species in an in vitro nucleic acid amplification mixture comprising
XX      CC a polymerase activity and a pair of primers to produce an amplified
XX      CC nucleic acid and detecting amplified nucleic acid. The method is useful
XX      CC for in vitro diagnostic detection of pathogenic bacteria, particularly
XX      CC detecting infections caused by MAC organisms, distinguished from other
XX      CC closely-related Mycobacterium species. The present sequence is a promoter
XX      CC -primer from Bacteriophage T7 and Mycobacterium sp. Promoter-primer is
XX      CC used for in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to
XX      SQ standardise OS field)
Query Match      68.5%; Score 37; DB 4; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy      1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 52
Db      1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 57
|||||
RESULT 21
AAD11257
ID      AAD11257 standard; DNA; 57 BP.
XX      AC
XX      AAD11257;
XX      DT 11-SEP-2003 (revised)
```

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XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #1.
DE Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
XX Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX Key Location/Qualifiers
FT Promoter 1..33
FT /*tag= a
FT /label= T7_promoter
XX WO200144510-A2.
XX 21-JUN-2001.
XX 17-DEC-1999; 99WO-US030346.
XX 17-DEC-1999; 99WO-US030346.
XX (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX Claim 1; Page 33; 44pp; English.
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ Query Match 68.5%; Score 37; DB 4; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Oy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
Db 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 57
RESULT 22
ADG88338
ID ADG88338 standard; DNA; 57 BP.
XX AC ADG88338;
XX 11-MAR-2004 (first entry)
XX Mycobacterium amplifying PCR primer #7.
DE (JUCKER/) JUCKER M T.
PA (DELG/) DELGADO F D.
XX (BREN/) BRENTANO S T.
XX Mycobacterium tuberculosis; ATCC 27294.
OS Enterobacteria phage T7.
XX US2005100915-A1.
XX 12-MAY-2005.
XX 18-SEP-2003; 2003US-00665708.
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX (BREN/) BRENTANO S T.
PA (JUCKER/) JUCKER M T.
PA (DELG/) DELGADO F D.

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KW In vitro amplification; PCR; primer; ss.
XX Mycobacterium sp.
OS US2003165824-A1.
XX 04-SEP-2003.
XX 15-DEC-2000; 2000US-00738274.
XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
PA (JUCKER/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX Claim 1; SEQ ID NO 7; 20pp; English.
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;
SQ Query Match 68.5%; Score 37; DB 10; Length 57;
Best Local Similarity 91.2%; Pred. No. 7.6e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Oy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
Db 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 57
RESULT 23
AEA08213
ID AEA08213 standard; DNA; 57 BP.
XX AC AEA08213;
XX 14-JUL-2005 (first entry)
XX M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 7.
DE Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
XX PCR; primer; ss.
XX Mycobacterium tuberculosis; ATCC 27294.
OS Enterobacteria phage T7.
XX US2005100915-A1.
XX 12-MAY-2005.
XX 18-SEP-2003; 2003US-00665708.
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX (BREN/) BRENTANO S T.
PA (JUCKER/) JUCKER M T.
PA (DELG/) DELGADO F D.

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PA (CLEU/) CLEUZIAT P.  
XX (RODR/) RODRIGUE M.  
PI Brentano ST, Jucker MT, Delgado FD, CleuZIAT P, Rodrigue M;  
XX  
DR WPI; 2005-345392/35.  
XX  
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
PT in a biological sample, comprises using in vitro nucleic acid  
PT amplification and detection of amplified products.  
XX  
XX Example 1; SEQ ID NO 7; 21pp; English.  
XX  
CC The present invention relates to a method of detecting Mycobacterium  
CC species present in a biological sample. The method involves using in  
CC vitro nucleic acid amplification and detection of amplified products. The  
CC invention is useful for diagnostic detection of pathogenic bacteria such  
CC as Mycobacterium species. The present sequence is the Mycobacterium  
CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying T7  
CC promoter PCR primer. This T7 promoter primer sequence include a T7  
CC promoter sequence attached to the portion of the primer sequence that  
CC binds to the target or its complement.  
XX  
XX Sequence 57 BP; 19 A; 16 C; 9 G; 13 T; 0 U; 0 Other;  
XX  
Query Match 68.5%; Score 37; DB 14; Length 57;  
Best Local Similarity 91.2%; Pred. No. 7.6e-05;  
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 52  
DB 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTTGCAATATTTCCCACT 57  
XX  
RESULT 24  
ABK53102  
ID ABK53102 standard; DNA; 37 BP.  
XX  
AC ABK53102;  
XX  
DT 29-AUG-2003 (revised)  
DT 12-AUG-2002 (first entry)  
DE T7 promoter sequence #2.  
DE  
XX HIV; human immunodeficiency virus; ss; promoter; gag; pol; protease;  
KW reverse transcriptase; infection; T7.  
XX  
OS Enterobacteria phage T7.  
XX  
PN US2002055095-A1.  
XX  
XX 09-MAY-2002.  
XX  
PF 31-AUG-2001; 2001US-00944036.  
XX  
PR 01-SEP-2000; 2000US-0229790P.  
XX  
PA (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX  
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX  
DR WPI; 2002-462902/49.  
XX  
PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
PT 1 and probes for detecting the amplified product are specific for gag and  
PT pol regions and are useful to detect different subtypes of HIV-1.  
XX  
PS Disclosure; Page 13; 37pp; English.

XX This invention relates to a series of nucleic acid oligomers for  
CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
CC virus type 1 (HIV-1). The invention also comprises a labeled  
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived  
CC from gag or pol sequences, having one of the sequences fully defined in  
CC the specification, and a method for detecting HIV-1 in a biological  
CC sample, comprising mixing the sample with two or more of the  
CC amplification oligomers that specifically amplify at least one HIV-1  
CC target sequence within gag and a pol sequence which is a protease or  
CC reverse transcriptase sequence, amplifying the target, and detecting the  
CC amplified product. The oligonucleotides of the invention may be used to  
CC diagnose HIV-1 infection. The presents sequence represents a T7 promoter  
CC sequence used to produce transcripts from amplified target sequences  
CC produced using the oligonucleotide primers of the invention. (Updated on  
CC 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 37 BP; 15 A; 7 C; 7 G; 8 T; 0 U; 0 Other;  
XX  
Query Match 66.7%; Score 36; DB 6; Length 37;  
Best Local Similarity 100.0%; Pred. No. 0.00017;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
XX  
RESULT 25  
AAL45464  
ID AAL45464 standard; DNA; 37 BP.  
XX  
AC AAL45464;  
XX  
DT 29-AUG-2003 (revised)  
DT 06-JUN-2002 (first entry)  
XX  
DE Bacteriophage T7 promoter sequence SEQ ID NO: 2.  
XX  
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
KW promoter; ds.  
XX  
OS Enterobacteria phage T7.  
XX  
PN WO200220852-A1.  
XX  
PD 14-MAR-2002.  
XX  
PF 01-SEP-2000; 2000WO-US024117.  
XX  
PR 01-SEP-2000; 2000WO-US024117.  
XX  
PA (GENP-) GEN-PROBE INC.  
PA (INMR ) BIOMERIEUX SA.  
XX  
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX  
DR WPI; 2002-292273/33.  
XX  
PT New nucleic acid oligomer, useful for detecting selected regions of gag  
PT and pol genes of human immune deficiency virus, particularly for  
PT assessing drug resistance.  
XX  
PS Disclosure; Page 37; 82pp; English.  
XX  
CC The present invention provides a number of nucleic acid oligomers which  
CC can be used to amplify the gag and pol genes of human immunodeficiency  
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
CC genes, especially regions associated with drug resistance, and also for  
CC identifying genetic subtypes of the virus. The present sequence is a  
CC fragment of a bacteriophage T7 promoter described the invention. (Updated  
CC on 29-AUG-2003 to standardise OS field)  
XX

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SQ Sequence 37 BP; 15 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
  Query Match      66.7%; Score 36; DB 6; Length 37;
  Best Local Similarity 100.0%; Pred. No. 0.00017;
  Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
   |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 26
AD118911
ID AD118911 standard; DNA; 37 BP.
XX
AC AD118911;
XX
DT 22-APR-2004 (first entry)
XX
DE T7 promoter-primer #2.
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
OS Enterobacteria phage T7.
XX
PN US2003228574-A1.
XX
PD 11-DEC-2003.
XX
PP 28-APR-2003; 2003US-00425975.
XX
PR 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2004-060998/06.
XX
PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
PS Disclosure; SEQ ID NO 2; 39pp; English.
XX
CC The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is T7 promoter-
CC primer.
XX
SQ Sequence 37 BP; 15 A; 7 C; 7 G; 8 T; 0 U; 0 Other;
  Query Match      66.7%; Score 36; DB 12; Length 37;
  Best Local Similarity 100.0%; Pred. No. 0.00017;
  Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
   |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 27
ABK53106
ID ABK53106 standard; DNA; 54 BP.
XX
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```
XX AC ABK53106;
XX DT 29-AUG-2003 (revised)
XX DT 12-AUG-2002 (first entry)
XX DE HIV-1 Gag gene specific oligonucleotide primer #2.
XX KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
XX KW reverse transcriptase; infection; PCR.
XX OS Human immunodeficiency virus 1.
XX FH Key Location/Qualifiers
XX FT modified_base 46 /*tag= a
XX FT FT /mod_base= OTHER
XX FT FT /note= "OTHER= Nebularine"
XX PN US2002055095-A1.
XX PD 09-MAY-2002.
XX PF 31-AUG-2001; 2001US-00944036.
XX PR 01-SEP-2000; 2000US-0229790P.
XX PA (YANG/) YANG Y Y.
XX PA (BREN/) BRENTANO S T.
XX PA (BABO/) BABOLA O.
XX PA (TRAN/) TRAN N.
XX PA (VERN/) VERNET G.
XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX DR WPI; 2002-462902/49.
XX PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
XX PT 1 and probes for detecting the amplified product are specific for gag and
XX PT pol regions and are useful to detect different subtypes of HIV-1.
XX PS Claim 1; Page 14; 37pp; English.
XX CC This invention relates to a series of nucleic acid oligomers for
XX CC amplifying and detecting a nucleotide sequence of human immunodeficiency
XX CC virus type 1 (HIV-1). The invention also comprises a labeled
XX CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
XX CC from gag or pol sequences, having one of the sequences fully defined in
XX CC the specification, and a method for detecting HIV-1 in a biological
XX CC sample, comprising mixing the sample with two or more of the
XX CC amplification oligomers that specifically amplify at least one HIV-1
XX CC target sequence within gag and a pol sequence which is a protease or
XX CC reverse transcriptase sequence, amplifying the target, and detecting the
XX CC amplified product. The oligonucleotides of the invention may be used to
XX CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
XX CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
XX CC invention.. (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 54 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 1 Other;
  Query Match      66.7%; Score 36; DB 6; Length 54;
  Best Local Similarity 100.0%; Pred. No. 0.00019;
  Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
   |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36

RESULT 28
AAL45468
ID AAL45468 standard; DNA; 54 BP.
XX
```

AC	AA145468;	
XX		
XX	29-AUG-2003 (revised)	
DT	06-JUN-2002 (first entry)	
XX		
DE	HIV-1 gag amplification oligomer SEQ ID NO: 6.	
XX		
KW	HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;	
XX	probe; ss.	
XX		
OS	Human immunodeficiency virus 1.	
XX	Enterobacteria phage T7.	
XX		
Key	Location/Qualifiers	
FT	modified_base 46	
FT	/*tag= a	
FT	/mod_base= OTHER	
FT	/note= "nebularine"	
XX		
PN	WO200220852-A1.	
XX		
XX	14-MAR-2002.	
XX		
PF	01-SEP-2000; 2000WO-US024117.	
XX		
PR	01-SEP-2000; 2000WO-US024117.	
XX		
PA	(GENP-) GEN-PROBE INC.	
PA	(INMR ) BIOMERIEUX SA.	
XX		
XX	Yang YY, Brentano ST, Babola O, Tran N, Vernet G;	
PI	WPI; 2002-292273/33.	
XX		
DR		
XX		
PT	New nucleic acid oligomer, useful for detecting selected regions of gag	
PT	and pol genes of human immune deficiency virus, particularly for	
PT	assessing drug resistance.	
XX		
PS	Claim 1; Page 38; 82pp; English.	
XX		
CC	The present invention provides a number of nucleic acid oligomers which	
CC	can be used to amplify the gag and pol genes of human immunodeficiency	
CC	virus type I (HIV-1). These are used to detect regions of the gag and pol	
CC	genes, especially regions associated with drug resistance, and also for	
CC	identifying genetic subtypes of the virus. The present sequence is an	
CC	oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS	
CC	field)	
XX		
XX	Sequence 54 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 1 Other;	
Query Match	66.7%; Score 36; DB 6; Length 54;	
Best Local Similarity	100.0%; Pred. No. 0.00019;	
Matches	36; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36	
Db	1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36	
RESULT 29		
AD118915		
ID	AD118915 standard; DNA; 54 BP.	
XX		
XX	AD118915;	
AC		
XX		
XX	22-APR-2004 (first entry)	
DT		
XX		
DE	HIV-1 gag2 gene amplifying primer #1.	
XX		
KW	Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.	
OS	Human immunodeficiency virus 1.	
XX		

```

PR 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
PS
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GAAATTAATAGCACTCACTATAGGAGACACATGTGTC 39
Db 1 GAAATTAATAGCACTCACTATAGGAGACACATGTGTC 39
RESULT 31
ABK53134
ID ABK53134 standard; DNA; 53 BP.
AC ABK53134;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 Gag gene specific oligonucleotide primer #7.
DE
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX Key Location/Qualifiers
FH modified_base 45
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Nebularine"
XX
XX US2002050595-A1.
PN
XX 09-MAY-2002.
PD
XX 31-AUG-2001; 2001US-00944036.
PF
XX 01-SEP-2000; 2000US-0229790P.
PR

```

```

XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
PS
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 12 T; 0 U; 1 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GAAATTAATAGCACTCACTATAGGAGACACATGTGTC 39
Db 1 GAAATTAATAGCACTCACTATAGGAGACACATGTGTC 39
RESULT 32
AAL45496
ID AAL45496 standard; DNA; 53 BP.
XX
XX AAL45496;
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 gag amplification oligomer SEQ ID NO: 34.
DE
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX Enterobacteria phage T7.
XX
XX Key Location/Qualifiers
FH modified_base 45
FT /*tag= a
FT /mod_base= OTHER
FT /note= "nebularine"
XX
XX WO200220852-A1.
PN
XX 14-MAR-2002.
PD
XX 01-SEP-2000; 2000WO-US024117.
PF
XX 01-SEP-2000; 2000WO-US024117.
PR

```

```
XX (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
DR
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 58; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type I (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 12 T; 0 U; 1 Other;
SQ
Query Match 66.3%; Score 35.8; DB 6; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||
RESULT 34
AD118945
ID AD118945 standard; DNA; 53 BP.
XX
XX AD118945;
XX
XX 22-APR-2004 (first entry)
XX
XX HIV-1 gag2 gene amplifying primer #5.
XX
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
XX Human immunodeficiency virus 1.
XX
XX US2003228574-A1.
XX
XX 11-DEC-2003.
XX
XX 28-APR-2003; 2003US-00425975.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX
XX 31-AUG-2001; 2001US-00944036.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.
XX
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
XX Claim 1; SEQ ID NO 36; 39pp; English.
XX
XX The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 gag2 gene
CC amplifying primer.
XX
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
SQ
Query Match 66.3%; Score 35.8; DB 12; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00023;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||
XX
XX 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTC 39
|||
RESULT 33
AAL45498
ID AAL45498 standard; DNA; 53 BP.
XX
XX AAL45498;
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 gag amplification oligomer SEQ ID NO: 36.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 58; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
```

```
Db      1 GAAATTATACGACTCACTATAGGAGACCATGATGC 39
RESULT 35
AD118943
ID      AD118943 standard; DNA; 53 BP.
XX
XX      AC      AD118943;
XX
XX      DT      22-APR-2004 (first entry)
XX
XX      DE      HIV-1 gag2 gene amplifying primer #4.
XX
XX      KW      Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
XX      OS      Human immunodeficiency virus 1.
XX
XX      FH      Key      Location/Qualifiers
XX      modified_base 45
XX      FT      /*tag= a
XX      FT      /mod_base= OTHER
XX      FT      /note= "Nebularine"
XX
XX      FN      US2003228574-A1.
XX
XX      PD      11-DEC-2003.
XX
XX      PF      28-APR-2003; 2003US-00425975.
XX
XX      PR      01-SEP-2000; 2000US-0229790P.
XX      PR      31-AUG-2001; 2001US-00944036.
XX
XX      PA      (YANG/) YANG Y X.
XX      PA      (BREN/) BRENTANO S T.
XX      PA      (BABO/) BABOLA O.
XX      PA      (TRAN/) TRAN N.
XX      PA      (VERN/) VERNET G.
XX
XX      PI      Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX      WPI; 2004-060998/06.
XX
XX      New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
XX      sequences and in providing information about the infective agent, e.g.
XX      genetic subgroup or drug-resistance phenotype based on detectable
XX      sequence information.
XX
XX      PS      Claim 1; SEQ ID NO 34; 39pp; English.
XX
XX      The present invention relates to a nucleic acid oligomer for amplifying a
XX      nucleotide sequence of human immune deficiency virus (HIV)-1. The
XX      invention is useful in amplifying and detecting HIV-1 nucleic acid
XX      sequences and in providing additional information about the infective
XX      agent, such as its genetic subgroup or drug-resistance phenotype based on
XX      detectable sequence information. The present sequence is HIV-1 gag2 gene
XX      amplifying primer.
XX
XX      Sequence 53 BP; 17 A; 14 C; 9 G; 12 T; 0 U; 1 Other;
XX
XX      Query Match      66.3%; Score 35.8; DB 12; Length 53;
XX      Best Local Similarity 94.9%; Pred. No. 0.00023;
XX      Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX      QY      1 GAAATTATACGACTCACTATAGGAGACCATGATGC 39
XX      |||||
XX      DB      1 GAAATTATACGACTCACTATAGGAGACCATGATGC 39
XX
XX      RESULT 36
XX      ADH79436
XX      ID      ADH79436 standard; DNA; 53 BP.
XX
XX      AC      ADH79436;
XX
```

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```
XX      22-APR-2004 (first entry)
XX      DE      PCR primer of the invention SEQ ID NO:241.
XX      KW      RNA T7 polymerase; array; ss; PCR; primer.
XX      OS      Unidentified.
XX      FN      FR2834521-A1.
XX      PD      11-JUL-2003.
XX      PF      10-JAN-2002; 2002FR-00000265.
XX      PR      10-JAN-2002; 2002FR-00000265.
XX      (INMR ) BTO MERIEUX.
XX      Mabilat C, Desvarenne S, Babola O, Lacroix B;
XX      WPI; 2003-571829/54.
XX
XX      Determining origin of an animal sample, useful e.g. for detecting
XX      adulteration of food, by testing hybridization of sample DNA with set of
XX      species-specific reagents.
XX
XX      Example 5; SEQ ID NO 241; 98pp; French.
XX
XX      The invention relates to a novel method for determining the animal
XX      species that is the origin of a sample. The method is very general, quick
XX      and easy to do. It can detect material from a species even when present
XX      in small amounts in presence of materials from several other species, and
XX      the species being tested do not have to be known a priori. DNA was
XX      isolated from an animal sample and amplified by PCR using two primers.
XX      The amplicon, containing a promoter for RNA T7 polymerase (present in one
XX      of the primers) was transcribed with incorporation of a fluorescent
XX      ribonucleotide, then transcripts cleaved to fragments of 20 nucleotides.
XX      These were tested for hybridisation to a DNA chip carrying 17-mer capture
XX      probes, specific for different animal species. The present sequence is
XX      used in the exemplification of the invention.
XX
XX      Sequence 53 BP; 20 A; 11 C; 9 G; 13 T; 0 U; 0 Other;
XX
XX      Query Match      65.6%; Score 35.4; DB 10; Length 53;
XX      Best Local Similarity 86.7%; Pred. No. 0.00033;
XX      Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX
XX      QY      1 GAAATTATACGACTCACTATAGGAGACCATGTCATATT 45
XX      |||||
XX      DB      1 GAAATTATACGACTCACTATAGGAGACCATGATATT 45
XX
XX      RESULT 37
XX      AAA76220
XX      ID      AAA76220 standard; DNA; 54 BP.
XX
XX      AC      AAA76220;
XX
XX      DT      25-JAN-2001 (first entry)
XX
XX      DE      Human prostate-specific membrane antigen PCR primer SEQ ID NO: 49.
XX
XX      KW      Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
XX      KW      glandular kallikrein-2; HK2; prostate cancer; breast cancer; probe;
XX      KW      PCR primer; ss.
XX      OS      Homo sapiens.
XX      FN      WO200044940-A2.
XX      PD      03-AUG-2000.
XX
```



PF 28-JAN-2000; 2000WO-US002270.  
 XX  
 PR 28-JAN-1999; 99US-0117640P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Harvey RC, Clark TJ;  
 XX  
 XX WPI; 2000-505986/45.  
 DR  
 XX Detecting prostate-specific antigen (PSA), prostate specific membrane  
 PT antigen (PSMA) or human kallikrein 2 (hk2) nucleic acids in samples using  
 PT probe molecules, useful for the diagnosis of prostate and breast cancers.  
 XX  
 XX Claim 1; Page 14; 77pp; English.  
 XX  
 CC The present invention is concerned with the detection of nucleic acid  
 CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases  
 XX  
 SQ Sequence 54 BP; 17 A; 14 C; 8 G; 15 T; 0 U; 0 Other;  
 Query Match 65.6%; Score 35.4; DB 3; Length 54;  
 Best Local Similarity 79.2%; Pred. No. 0.00033;  
 Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 QY 2 AAATTAATACGACTCACTATAGGAGACCACCAATTTGTGCAATATCCCACTGC 54  
 |||||  
 DB 2 AAATTAATACGACTCACTATAGGAGACCACCAATTTCTTCGATCCAGCTTGC 54  
 |||||  
 RESULT 38  
 ABK53110  
 ID ABK53110 standard; DNA; 55 BP.  
 XX  
 AC ABK53110;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 12-AUG-2002 (first entry)  
 XX  
 XX HIV-1 reverse transcriptase gene specific oligonucleotide primer #3.  
 DE  
 KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
 KW reverse transcriptase; infection; PCR.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2002055095-A1.  
 XX  
 PD 09-MAY-2002.  
 XX  
 PF 31-AUG-2001; 2001US-00944036.  
 XX  
 PR 01-SEP-2000; 2000US-0229790P.  
 XX  
 XX (YANG/) YANG Y Y.  
 PA (BREN/) BRENTANO S T.  
 PA (BAGO/) BABOLA O.  
 PA (TRAN/) TRAN N.  
 PA (VERN/) VERNET G.  
 XX  
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX  
 DR WPI; 2002-462902/49.  
 XX  
 XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
 PT 1 and probes for detecting the amplified product are specific for gag and

PT pol regions and are useful to detect different subtypes of HIV-1.  
 XX  
 XX Claim 1; Page 15; 37pp; English.  
 XX  
 CC This invention relates to a series of nucleic acid oligomers for  
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
 CC virus type 1 (HIV-1). The invention also comprises a labeled  
 CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived  
 CC from gag or pol sequences, having one of the sequences fully defined in  
 CC the specification, and a method for detecting HIV-1 in a biological  
 CC sample, comprising mixing the sample with two or more of the  
 CC amplification oligomers that specifically amplify at least one HIV-1  
 CC target sequence within gag and a pol sequence which is a processase or  
 CC reverse transcriptase sequence, amplifying the target, and detecting the  
 CC amplified product. The oligonucleotides of the invention may be used to  
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection  
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;  
 Query Match 65.6%; Score 35.4; DB 6; Length 55;  
 Best Local Similarity 97.3%; Pred. No. 0.00033;  
 Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37  
 |||||  
 DB 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37  
 |||||  
 RESULT 39  
 AAL45472  
 ID AAL45472 standard; DNA; 55 BP.  
 XX  
 AC AAL45472;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 06-JUN-2002 (first entry)  
 XX  
 XX HIV-1 pol gene RT amplification oligomer SEQ ID NO: 10.  
 DE  
 KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 KW probe; ss.  
 XX  
 OS Human immunodeficiency virus 1.  
 OS Enterobacteria phage T7.  
 XX  
 PN WO200220852-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 01-SEP-2000; 2000WO-US024117.  
 XX  
 PR 01-SEP-2000; 2000WO-US024117.  
 XX  
 XX (GENP-) GEN-PROBE INC.  
 PA (INNR) BIOMERIEUX SA.  
 XX  
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX  
 DR WPI; 2002-292273/33.  
 XX  
 XX New nucleic acid oligomer, useful for detecting selected regions of gag  
 PT and pol genes of human immune deficiency virus, particularly for  
 PT assessing drug resistance.  
 XX  
 XX Claim 1; Page 40; 82pp; English.  
 XX  
 CC The present invention provides a number of nucleic acid oligomers which  
 CC can be used to amplify the gag and pol genes of human immunodeficiency  
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
 CC genes, especially regions associated with drug resistance, and also for  
 CC identifying genetic subtypes of the virus. The present sequence is an

```

CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;
    Query Match      65.6%; Score 35.4; DB 6; Length 55;
    Best Local Similarity 97.3%; Pred. No. 0.00033;
    Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCATGTGT 37
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTGT 37

RESULT 40
AD118919
ID AD118919 standard; DNA; 55 BP.
XX
AC AD118919;
XX
DT 22-APR-2004 (first entry)
XX
DE HIV-1 pol4 gene amplifying primer #1.
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
OS Human immunodeficiency virus 1.
XX
FN US2003228574-A1.
XX
PD 11-DEC-2003.
XX
PF 28-APR-2003; 2003US-00425975.
XX
PR 01-SEP-2000; 2000US-0229790P.
XX
PR 31-AUG-2001; 2001US-00944036.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
DR WPI; 2004-060998/06.
XX
New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
PS Claim 1; SEQ ID NO 10; 39pp; English.
XX
The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 pol4 gene
CC amplifying primer.
XX
SQ Sequence 55 BP; 18 A; 15 C; 9 G; 13 T; 0 U; 0 Other;
    Query Match      65.6%; Score 35.4; DB 12; Length 55;
    Best Local Similarity 97.3%; Pred. No. 0.00033;
    Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCATGTGT 37
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTGT 37

```

```

RESULT 41
AAD11262
ID AAD11262 standard; DNA; 52 BP.
XX
AC AAD11262;
XX
DT 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying T7 promoter-primer #6.
DE Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; T7 promoter; ss.
KW Enterobacteria phage T7.
XX OS Mycobacterium sp.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT promoter 1..33
FT /*tag= a
FT /label= T7_promoter
FN WO200144510-A2.
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Deigado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 34; 44pp; English.
XX
The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a T7 promoter-primer used
CC for amplifying Mycobacterium 16S rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;
    Query Match      64.8%; Score 35; DB 4; Length 52;
    Best Local Similarity 80.4%; Pred. No. 0.00047;
    Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCATGTGTGCAATATCCCCAC 51
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTGTGCGGCC 51
    |||||

RESULT 42
ABK53143
ID ABK53143 standard; DNA; 52 BP.
XX
AC ABK53143;

```

```
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #14.
DE HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
OS Human immunodeficiency virus 1.
XX US2002055095-A1.
XX 09-MAY-2002.
XX 31-AUG-2001; 2001US-00944036.
XX 01-SEP-2000; 2000US-0229790P.
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-462902/49.
XX
PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-1
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 26; 37pp; English.
XX
CC This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;

Query Match 64.8%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACACATT 35
DB 1 GAAATTATACGACTCACTATAGGAGACACATT 35

RESULT 43
AAL45505
ID AAL45505 standard; DNA; 52 BP.
XX
AC AAL45505;
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 43.
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
```

```
KW probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX (GENP-) GEN-PROBE INC.
PA (INNMR ) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
PT New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
PS Claim 1; Page 61; 82pp; English.
XX
CC The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;

Query Match 64.8%; Score 35; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.00047;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGAGACACATT 35
DB 1 GAAATTATACGACTCACTATAGGAGACACATT 35

RESULT 44
ADG88343
ID ADG88343 standard; DNA; 52 BP.
XX
AC ADG88343;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #12.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium sp.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
```

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 XX WPI; 2003-898044/82.  
 XX  
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 PT in a biological sample comprises performing in vitro nucleic acid  
 PT amplification and detection of amplified products.  
 XX  
 XX Claim 1; SEQ ID NO 12; 20pp; English.  
 PS  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample comprises performing an in vitro  
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
 CC is Mycobacterium amplifying PCR primer.  
 XX  
 XX Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 64.8%; Score 35; DB 10; Length 52;  
 Best Local Similarity 80.4%; Pred. No. 0.00047;  
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGCAATATTCGCCAC 51  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTCAGGCTTGGGCC 51  
 RESULT 45  
 AD118952  
 ID AD118952 standard; DNA; 52 BP.  
 XX  
 AC AD118952;  
 XX  
 XX 22-APR-2004 (first entry)  
 DT  
 DE HIV-1 pol3 gene amplifying primer #5.  
 XX  
 XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX US2003228574-A1.  
 PN  
 XX 11-DEC-2003.  
 PD  
 XX 28-APR-2003; 2003US-00425975.  
 PF  
 XX 01-SEP-2000; 2000US-0229790P.  
 PR 31-AUG-2001; 2001US-00944036.  
 XX  
 XX (YANG/) YANG Y Y.  
 PA (BREN/) BRENTANO S T.  
 PA (BABO/) BABOLA O.  
 PA (TRAN/) TRAN N.  
 PA (VERN/) VERNET G.  
 XX  
 PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX WPI; 2004-060998/06.  
 DR  
 XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
 PT sequences and in providing information about the infective agent, e.g.  
 PT genetic subgroup or drug-resistance phenotype based on detectable  
 PT sequence information.  
 XX  
 XX Claim 1; SEQ ID NO 43; 39pp; English.  
 PS  
 XX The present invention relates to a nucleic acid oligomer for amplifying a  
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
 CC sequences and in providing additional information about the infective  
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
 CC detectable sequence information. The present sequence is HIV-1 pol3 gene

CC amplifying primer.  
 XX  
 SQ Sequence 52 BP; 16 A; 10 C; 8 G; 18 T; 0 U; 0 Other;  
 Query Match 64.8%; Score 35; DB 12; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.00047;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTT 35  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTT 35  
 RESULT 46  
 AEA08218  
 ID AEA08218 standard; DNA; 52 BP.  
 XX  
 AC AEA08218;  
 XX  
 XX 14-JUL-2005 (first entry)  
 DT  
 XX M. tuberculosis 16SrRNA amplifying T7 promoter PCR primer, SEQ ID NO: 12.  
 DE  
 XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;  
 KW PCR; primer; ss.  
 KW  
 XX Mycobacterium tuberculosis; ATCC 27294.  
 OS  
 OS Enterobacteria phage T7.  
 XX  
 XX US2005100915-A1.  
 PN  
 XX 12-MAY-2005.  
 PD  
 XX 18-SEP-2003; 2003US-00665708.  
 PF  
 XX 17-DEC-1999; 99US-0172190P.  
 PR 15-DEC-2000; 2000US-00738274.  
 XX  
 XX (BREN/) BRENTANO S T.  
 PA (JUCK/) JUCKER M T.  
 PA (DELG/) DELGADO F D.  
 PA (CLEU/) CLEUZIA P.  
 PA (RODR/) RODRIGUE M.  
 XX  
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 XX WPI; 2005-345392/35.  
 DR  
 XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 PT in a biological sample, comprises using in vitro nucleic acid  
 PT amplification and detection of amplified products.  
 XX  
 XX Example 1; SEQ ID NO 12; 21pp; English.  
 PS  
 XX The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample. The method involves using in  
 CC vitro nucleic acid amplification and detection of amplified products. The  
 CC invention is useful for diagnostic detection of pathogenic bacteria such  
 CC as Mycobacterium species. The present sequence is the Mycobacterium  
 CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying T7  
 CC promoter PCR primer. This T7 promoter primer sequence include a T7  
 CC promoter sequence attached to the portion of the primer sequence that  
 CC binds to the target or its complement.  
 XX  
 XX Sequence 52 BP; 17 A; 14 C; 11 G; 10 T; 0 U; 0 Other;  
 SQ  
 Query Match 64.8%; Score 35; DB 14; Length 52;  
 Best Local Similarity 80.4%; Pred. No. 0.00047;  
 Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGCAATATTCGCCAC 51  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCATTCAGGCTTGGGCC 51

```
RESULT 47
ABK53335
ID ABK53135 standard; DNA; 53 BP.
XX
AC ABK53135;
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 gag gene specific oligonucleotide primer #8.
XX
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
XX
XX US2002055095-A1.
XX
XX 09-MAY-2002.
XX
XX 31-AUG-2001; 2001US-00944036.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABA/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 24; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 34.8; DB 6; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCGAATATTC 46
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCGAATATTC 46
RESULT 48
AAL45497
ID AAL45497 standard; DNA; 53 BP.
XX
XX AAL45497;
XX
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```
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 gag amplification oligomer SEQ ID NO: 35.
XX
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
XX WO200220852-A1.
XX
XX 14-MAR-2002.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX 01-SEP-2000; 2000WO-US024117.
XX
XX (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 58; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
XX Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
SQ
Query Match 64.4%; Score 34.8; DB 6; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCGAATATTC 46
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCGAATATTC 46
RESULT 49
AD118944
ID AD118944 standard; DNA; 53 BP.
XX
XX AD118944;
XX
XX 22-APR-2004 (first entry)
DT
XX
XX HIV-I gag1 gene amplifying primer #5.
DE
XX
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX US2003228574-A1.
XX
XX 11-DEC-2003.
XX
XX 28-APR-2003; 2003US-00425975.
XX
XX 01-SEP-2000; 2000US-0229790P.
```

```
PR 31-AUG-2001; 2001US-00944036.
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.
DR
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
PS Claim 1; SEQ ID NO 35; 39pp; English.
XX
CC The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 gag1 gene
CC amplifying primer.
XX
SQ Sequence 53 BP; 17 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
Query Match 64.4%; Score 34.8; DB 12; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00057;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTCGAATATTC 46
RESULT 50
ABKS3133
ID ABK53133 standard; DNA; 54 BP.
XX
XX ABK53133;
AC
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 Gag gene specific oligonucleotide primer #6.
DE
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX US200205095-A1.
PN
XX
XX 09-MAY-2002.
PD
XX
XX 31-AUG-2001; 2001US-00944036.
PF
XX
XX 01-SEP-2000; 2000US-0229790P.
PR
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-462902/49.
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT
```

```
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 24; 37pp; English.
XX
CC This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 Gag gene in the HIV detection method of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;
Query Match 63.7%; Score 34.4; DB 6; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00083;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTG 36
RESULT 51
AAL45495
ID AAL45495 standard; DNA; 54 BP.
XX
XX AAL45495;
AC
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 gag amplification oligomer SEQ ID NO: 33.
DE
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
XX Human immunodeficiency virus 1.
OS
XX Enterobacteria phage T7.
PN
XX WO200220852-A1.
XX
XX 14-MAR-2002.
PD
XX
XX 01-SEP-2000; 2000WO-US024117.
PF
XX
XX 01-SEP-2000; 2000WO-US024117.
PR (GENP-) GEN-PROBE INC.
PA (INWR ) BIOMERIEUX SA.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI WPI; 2002-292273/33.
XX
XX New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
XX Claim 1; Page 57; 82pp; English.
XX
XX The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
```

CC identifying genetic subtypes of the virus. The present sequence is an  
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
CC field)

XX SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;  
Query Match 63.7%; Score 34.4; DB 6; Length 54;  
Best Local Similarity 97.2%; Pred. No. 0.00083;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36  
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 52  
AD118942  
ID AD118942 standard; DNA; 54 BP.  
XX AC  
XX AD118942;  
XX 22-APR-2004 (first entry)  
XX HIV-I gagl gene amplifying primer #4.  
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
XX Human immunodeficiency virus 1.  
XX US2003228574-A1.  
XX 11-DEC-2003.  
XX 28-APR-2003; 2003US-00425975..  
XX 01-SEP-2000; 2000US-0229790P.  
XX 31-AUG-2001; 2001US-00944036.  
XX (YANG/) YANG Y Y.  
XX (BREN/) BRENTANO S T.  
XX (BABO/) BABOLA O.  
XX (TRAN/) TRAN N.  
XX (VERN/) VERNET G.  
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
XX WPT; 2004-060998/06.  
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
XX sequences and in providing information about the infective agent, e.g.  
XX genetic subgroup or drug-resistance phenotype based on detectable  
XX sequence information.

PS Claim 1; SEQ ID NO 33; 39pp; English.  
XX The present invention relates to a nucleic acid oligomer for amplifying a  
XX nucleotide sequence of human immune deficiency virus (HIV)-1. The  
XX invention is useful in amplifying and detecting HIV-1 nucleic acid  
XX sequences and in providing additional information about the infective  
XX agent, such as its genetic subgroup or drug-resistance phenotype based on  
XX detectable sequence information. The present sequence is HIV-I gagl gene  
XX amplifying primer.  
XX SQ Sequence 54 BP; 17 A; 12 C; 11 G; 14 T; 0 U; 0 Other;  
Query Match 63.7%; Score 34.4; DB 12; Length 54;  
Best Local Similarity 97.2%; Pred. No. 0.00083;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36  
Db 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36

RESULT 53  
AAD51759  
ID AAD51759 standard; DNA; 62 BP.  
XX AC  
XX AAD51759;  
XX 16-APR-2003 (first entry)  
XX Yeast intergenic region (YIR) 8 amplifying forward PCR primer #2.  
XX Yeast intergenic region; YIR; gene expression analysis; yeast; PCR;  
XX primer; ss.  
XX Saccharomyces cerevisiae.  
XX WO200290516-A2.  
XX 14-NOV-2002.  
XX 07-MAY-2002; 2002WO-US014575.  
XX 07-MAY-2001; 2001US-0289202P.  
XX 15-AUG-2001; 2001US-0312420P.  
XX (AMSH ) AMERSHAM BIOSCIENCES CORP.  
XX Samartzidou H, Turner L, Daniel S, Houts T;  
XX WPT; 2003-120541/11.

PT Producing at least one control useful as negative controls or calibrators  
PT in a gene expression analysis system, comprises selecting inter- or  
PT intragenic region of genomic DNA from a known sequence to be amplified  
PT and cloned into a vector.  
XX Disclosure; Page 15; 47pp; English.  
XX The invention relates to a method for producing at least one control  
XX useful as negative controls or calibrators in a gene expression analysis  
XX system, which involves selecting inter- or intragenic region of genomic  
XX DNA from a known sequence to be amplified and cloned into a vector. The  
XX method is useful for producing controls useful in gene expression  
XX analysis systems and which can be tested to ensure lack of hybridisation  
XX with mRNA from sources other than the control DNA itself. The controls  
XX are useful as negative controls or calibrators in a gene expression  
XX analysis system or in a two-colour gene expression analysis system. The  
XX present sequence is a PCR primer used for amplifying yeast intergenic  
XX region (YIR). This sequence is used to illustrate the method of the  
XX invention  
XX SQ Sequence 62 BP; 23 A; 13 C; 14 G; 12 T; 0 U; 0 Other;

Oy 1 GAAATTAATACGACTCACTATAGGAGACACCATTTG 36  
Db 15 GAAATTAATACGACTCACTATAGGAGACACCATTTG 50

RESULT 54  
ABK53138  
ID ABK53138 standard; DNA; 53 BP.  
XX AC  
XX ABK53138;  
XX 29-AUG-2003 (revised)  
XX 12-AUG-2002 (first entry)  
XX HIV-1 protease gene specific oligonucleotide primer #5.  
XX

KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
KW reverse transcriptase; infection; PCR.  
OS Human immunodeficiency virus 1.  
XX US2002055095-A1.  
XX 09-MAY-2002.  
XX 31-AUG-2001; 2001US-00944036.  
XX 01-SEP-2000; 2000US-0229790P.  
XX (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX WPI; 2002-462902/49.  
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
PT 1 and probes for detecting the amplified product are specific for gag and  
PT pol regions and are useful to detect different subtypes of HIV-1.  
XX Claim 1; Page 25; 37pp; English.  
XX This invention relates to a series of nucleic acid oligomers for  
XX amplifying and detecting a nucleotide sequence of human immunodeficiency  
CC virus type 1 (HIV-1). The invention also comprises a labeled  
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived  
CC from gag or pol sequences, having one of the sequences fully defined in  
CC the specification, and a method for detecting HIV-1 in a biological  
CC sample, comprising mixing the sample with two or more of the  
CC amplification oligomers that specifically amplify at least one HIV-1  
CC target sequence within gag and a pol sequence which is a protease or  
CC reverse transcriptase sequence, amplifying the target, and detecting the  
CC amplified product. The oligonucleotides of the invention may be used to  
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
CC used to amplify the HIV-1 protease gene in the HIV detection method of  
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;  
SQ Query Match 63.0%; Score 34; DB 6; Length 53;  
Best Local Similarity 88.1%; Pred. No. 0.0012;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCAT 42  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTCATT 42  
RESULT 55  
AAL45500  
ID AAL45500 standard; DNA; 53 BP.  
XX AAL45500;  
AC AAL45500;  
XX 29-AUG-2003 (revised)  
DT 06-JUN-2002 (first entry)  
XX HIV-1 pol gene protease amplification oligomer SEQ ID NO: 38.  
DE HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
XX probe; ss.  
KW Human immunodeficiency virus 1.  
XX Enterobacteria phage T7.  
OS WO200220852-A1.  
XX

XX 14-MAR-2002.  
PD 01-SEP-2000; 2000WO-US024117.  
XX 01-SEP-2000; 2000WO-US024117.  
XX (GENP-) GEN-PROBE INC.  
PA (INMR ) BIOMERIEUX SA.  
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX WPI; 2002-292273/33.  
XX New nucleic acid oligomer, useful for detecting selected regions of gag  
PT and pol genes of human immune deficiency virus, particularly for  
PT assessing drug resistance.  
XX Claim 1; Page 59; 82pp; English.  
XX The present invention provides a number of nucleic acid oligomers which  
CC can be used to amplify the gag and pol genes of human immunodeficiency  
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
CC genes, especially regions associated with drug resistance, and also for  
CC identifying genetic subtypes of the virus. The present sequence is an  
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
CC field)  
XX Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;  
SQ Query Match 63.0%; Score 34; DB 6; Length 53;  
Best Local Similarity 88.1%; Pred. No. 0.0012;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTCAT 42  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTCATT 42  
RESULT 56  
ADI18947  
ID ADI18947 standard; DNA; 53 BP.  
XX ADI18947;  
AC ADI18947;  
XX 22-APR-2004 (first entry)  
DT HIV-1 pol gene amplifying primer #5.  
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
DE Human immunodeficiency virus 1.  
XX US2003228574-A1.  
XX 11-DEC-2003.  
PD 28-APR-2003; 2003US-00425975.  
XX 01-SEP-2000; 2000US-0229790P.  
XX 31-AUG-2001; 2001US-00944036.  
XX (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
XX WPI; 2004-060998/06.  
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide



PT sequences and in providing information about the infective agent, e.g.  
PT genetic subgroup or drug-resistance phenotype based on detectable  
PT sequence information.  
XX  
PS Claim 1; SEQ ID NO 38; 39pp; English.  
XX  
CC The present invention relates to a nucleic acid oligomer for amplifying a  
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
CC sequences and in providing additional information about the infective  
CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
CC detectable sequence information. The present sequence is HIV-1 pol gene  
CC amplifying primer.  
XX  
SQ Sequence 53 BP; 18 A; 14 C; 8 G; 13 T; 0 U; 0 Other;  
  
Query Match 63.0%; Score 34; DB 12; Length 53;  
Best Local Similarity 88.1%; Pred. No. 0.0012;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAAT 42  
DB 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAAT 42  
  
RESULT 57  
AAAA76065  
ID AAA76065 standard; DNA; 54 BP.  
XX  
AC AAA76065;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Human prostate specific antigen PCR primer SEQ ID NO: 27.  
XX  
KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;  
KW glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;  
KW PCR primer; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200044940-A2.  
XX  
PD 03-AUG-2000.  
XX  
PF 28-JAN-2000; 2000WO-US002270.  
XX  
PR 28-JAN-1999; 99US-0117640P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Harvey RC, Clark TJ;  
XX  
DR WPI; 2000-505986/45.  
XX  
PT Detecting prostate-specific antigen (PSA), prostate specific membrane  
PT antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using  
PT probe molecules, useful for the diagnosis of prostate and breast cancers.  
XX  
PS Claim 1; Page 12; 77pp; English.  
XX  
CC The present invention is concerned with the detection of nucleic acid  
CC markers for prostate and breast cancer, and PCR primers and probes which  
CC are able to detect and quantify these markers. Prostate specific antigen  
CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
CC -2 (hK2) have all been linked to prostate and breast cancers, and the  
CC primers and probes of the invention are able to detect the abnormal  
CC presence of mRNA expressed by their coding sequences in tissues other  
CC than the prostate. This enables the presence of cancer to be perceived  
CC and aids in the detection of metastases  
XX  
SQ Sequence 54 BP; 19 A; 12 C; 13 G; 10 T; 0 U; 0 Other;

Query Match 63.0%; Score 34; DB 3; Length 54;  
Best Local Similarity 80.0%; Pred. No. 0.0012;  
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
QY 2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51  
DB 2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51  
  
RESULT 58  
ABK53145  
ID ABK53145 standard; DNA; 55 BP.  
XX  
AC ABK53145;  
XX  
DT 29-AUG-2003 (revised)  
DT 12-AUG-2002 (first entry)  
XX  
DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #16.  
XX  
KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
KW reverse transcriptase; infection; PCR.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN US200205095-A1.  
XX  
PD 09-MAY-2002.  
XX  
PF 31-AUG-2001; 2001US-00944036.  
XX  
PR 01-SEP-2000; 2000US-0229790P.  
XX  
PA (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX  
PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
XX  
DR WPI; 2002-462902/49.  
XX  
PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
PT 1 and probes for detecting the amplified product are specific for gag and  
PT pol regions and are useful to detect different subtypes of HIV-1.  
XX  
PS Claim 1; Page 26; 37pp; English.  
XX  
CC This invention relates to a series of nucleic acid oligomers for  
CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
CC virus type 1 (HIV-1). The invention also comprises a labeled  
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived  
CC from gag or pol sequences, having one of the sequences fully defined in  
CC the specification, and a method for detecting HIV-1 in a biological  
CC sample, comprising mixing the sample with two or more of the  
CC amplification oligomers that specifically amplify at least one HIV-1  
CC target sequence within gag and a pol sequence which is a protease or  
CC reverse transcriptase sequence, amplifying the target, and detecting the  
CC amplified product. The oligonucleotides of the invention may be used to  
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection  
CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 63.0%; Score 34; DB 6; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACT 34  
DB 1 GAAATTAATACGACTCACTATAGGAGACCACT 34

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RESULT 59
AAL45507
ID AAL45507 standard; DNA; 55 BP.
XX
AC AAL45507;
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 45.
XX
KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KW probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
XX
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR) BIOMERIEUX SA.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2002-292273/33.
XX
PT New nucleic acid oligomer, useful for detecting selected regions of gag
PT and pol genes of human immune deficiency virus, particularly for
PT assessing drug resistance.
XX
PS Claim 1; Page 62; 82pp; English.
XX
CC The present invention provides a number of nucleic acid oligomers which
CC can be used to amplify the gag and pol genes of human immunodeficiency
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
CC genes, especially regions associated with drug resistance, and also for
CC identifying genetic subtypes of the virus. The present sequence is an
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
CC field)
XX
SQ Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 63.0%; Score 34; DB 6; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAATTAATACGACTCACTATAGGAGGAGACCACAT 34
| | | | | | | | | | | | | | | | | | | | |
DB 1 GAAATTAATACGACTCACTATAGGAGGAGACCACAT 34
| | | | | | | | | | | | | | | | | | | | |

RESULT 60
ADI18954
ID ADI18954 standard; DNA; 55 BP.
XX
AC ADI18954;
XX
DT 22-APR-2004 (first entry)
XX
DE HIV-I pol4 gene amplifying primer #5.
XX
KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.
XX
OS Human immunodeficiency virus 1.
XX

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PN US2003228574-A1.
XX
PD 11-DEC-2003.
XX
PF 28-APR-2003; 2003US-00425975.
XX
PR 01-SEP-2000; 2000US-0229790P.
PR 31-AUG-2001; 2001US-00944036.
XX
PA (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX WPI; 2004-060998/06.
XX
PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
PT sequences and in providing information about the infective agent, e.g.
PT genetic subgroup or drug-resistance phenotype based on detectable
PT sequence information.
XX
PS Claim 1; SEQ ID NO 45; 39pp; English.
XX
CC The present invention relates to a nucleic acid oligomer for amplifying a
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
CC invention is useful in amplifying and detecting HIV-1 nucleic acid
CC sequences and in providing additional information about the infective
CC agent, such as its genetic subgroup or drug-resistance phenotype based on
CC detectable sequence information. The present sequence is HIV-1 pol4 gene
CC amplifying primer.
XX
SQ Sequence 55 BP; 17 A; 16 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 63.0%; Score 34; DB 12; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAATTAATACGACTCACTATAGGAGGAGACCACAT 34
| | | | | | | | | | | | | | | | | | | | |
DB 1 GAAATTAATACGACTCACTATAGGAGGAGACCACAT 34
| | | | | | | | | | | | | | | | | | | | |

RESULT 61
AAD11022/c
ID AAD11022 standard; DNA; 61 BP.
XX
AC AAD11022;
XX
DT 24-SEP-2001 (first entry)
XX
DE Probe #2 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
KW Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; probe; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144511-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-US033872.
XX
PR 15-DEC-1999; 99US-0171202P.
XX
PA (GENP-) GEN-PROBE INC.
PA (BREN/) BRENTANO S T.
PA (LANK/) LANKFORD R L.
XX
PI Brentano ST, Lankford RL;

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XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT nucleic acid amplification with amplification oligonucleotides specific
PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT species.
XX
XX Claim 11; Page 26; 27pp; English.
XX
XX The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a probe
CC used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX Sequence 61 BP; 13 A; 15 C; 16 G; 17 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
DB 61 GAAATTAATACGACTCACTATAGGAGACACAT 28

RESULT 62
AAAD11012
ID AAD11012 standard; DNA; 61 BP.
XX
XX AAD11012;
XX
XX 11-SEP-2003 (revised)
DT 24-SEP-2001 (first entry)
XX
XX Promoter-primer #2 used for in vitro amplification of MAC rRNA.
XX
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; promoter-primer; ss.
XX
XX Enterobacteria phage T7.
OS Mycobacterium sp.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT promoter 1..33
FT /*tag= a
FT /note= "T7 promoter"
FT misc_feature 34..61
FT /*tag= b
FT /note= "PCR primer from Mycobacterium sp."
XX
XX WO200144511-A2.
XX
XX 21-JUN-2001.
XX
XX 15-DEC-2000; 2000WO-US033872.
XX
XX 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
PA (BREN/) BRENTANO S T.
PA (LANK/) LANKFORD R L.
XX
XX Brentano ST, Lankford RL;
PI

```

```

XX WPI; 2001-398171/42.
XX
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT nucleic acid amplification with amplification oligonucleotides specific
PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT species.
XX
XX Claim 1; Page 14; 27pp; English.
XX
XX The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a promoter
CC -primer from Bacteriophage T7 and Mycobacterium sp. Promoter-primer is
CC used for in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
XX Sequence 61 BP; 17 A; 16 C; 15 G; 13 T; 0 U; 0 Other;
SQ
Query Match 63.0%; Score 34; DB 4; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACACAT 34
DB 1 GAAATTAATACGACTCACTATAGGAGACACAT 34

RESULT 63
AAA76204
ID AAA76204 standard; DNA; 52 BP.
XX
XX AAA76204;
XX
XX 25-JAN-2001 (first entry)
DT
XX
XX Human prostate specific antigen PCR primer SEQ ID NO: 33.
XX
XX Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
KW glandular kallikrein-2; HK2; prostate cancer; breast cancer; probe;
KW PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200044940-A2.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US002270.
XX
XX 28-JAN-1999; 99US-0117640P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Harvey RC, Clark TJ;
XX
XX WPI; 2000-505986/45.
XX
XX Detecting prostate-specific antigen (PSA), prostate specific membrane
PT antigen (PSMA) or human kallikrein 2 (HK2) nucleic acids in samples using
PT probe molecules, useful for the diagnosis of prostate and breast cancers.
XX
XX Claim 1; Page 13; 77pp; English.
XX
XX The present invention is concerned with the detection of nucleic acid
CC

```

CC markers for prostate and breast cancer, and PCR primers and probes which  
 CC are able to detect and quantify these markers. Prostate specific antigen  
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein  
 CC -2 (hk2) have all been linked to prostate and breast cancers, and the  
 CC primers and probes of the invention are able to detect the abnormal  
 CC presence of mRNA expressed by their coding sequences in tissues other  
 CC than the prostate. This enables the presence of cancer to be perceived  
 CC and aids in the detection of metastases

XX SQ Sequence 52 BP; 16 A; 11 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 62.6%; Score 33.8; DB 3; Length 52;

Best Local Similarity 94.6%; Pred. No. 0.0014; Length 52;  
 Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AAATTAATACGACTCACTATAGGGAGACCATTTGTG 38  
 |||||  
 Db 2 AAATTAATACGACTCACTATAGGGAGACCATTTGTG 38  
 |||||

#### RESULT 64

ID ABK93895  
 AC ABK93895 standard; DNA; 58 BP.

XX AC ABK93895;

XX DT 29-AUG-2003 (revised)

XX DT 26-AUG-2002 (first entry)

XX DE Human immunodeficiency virus type 2 detection probe #19.

XX KW Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;  
 KW hepatitis C virus; HCV; probe; ss.

XX OS Human immunodeficiency virus 2.

XX PN WO200234951-A2.

XX PD 02-MAY-2002.

XX PF 22-OCT-2001; 2001WO-US045396.

XX PR 23-OCT-2000; 2000US-0242620P.

XX PR 30-MAR-2001; 2001US-0280058P.

XX FA (GENP-) GEN-PROBE INC.

XX FI Yang YX, Burrell TA;

XX DR WPI; 2002-489953/52.

XX PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by  
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic  
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target  
 PT duplex.

XX PS Claim 11; Page 25; 58pp; English.

XX CC The invention relates to a method of detecting human immunodeficiency  
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with  
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
 CC base sequence, and detecting the amplified NA; or providing a  
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
 CC probe to form probe:target duplex, and detecting the duplex. The method  
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
 CC product such as plasma or serum, and also for detecting subtypes A, B, C  
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC in blood serum and also as components of multiplex amplification  
 CC reactions that synthesise amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABK93895 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 58 BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

Query Match 61.5%; Score 33.2; DB 6; Length 58;

Best Local Similarity 92.1%; Pred. No. 0.0026;  
 Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTG 38  
 |||||  
 Db 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTG 38  
 |||||

#### RESULT 65

ID ADZ15190 standard; DNA; 1246 BP.

XX AC ADZ15190;

XX DT 16-JUN-2005 (first entry)

XX DE Human glutamine synthetase (GS) DNA fragment from expression vector.

XX KW cell culture; artificial organ; liver disease; hepatotropic;  
 KW gastrointestinal disease; ds; glutamine synthetase;  
 KW glutamate-ammonia ligase.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN JP2003274963-A.

XX PD 30-SEP-2003.

XX PF 22-MAR-2002; 2002JP-00081344.

XX PR 22-MAR-2002; 2002JP-00081344.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX PA (KOKU-) KOKURITSU SEIKU IRYO CENT SOCHO.

XX DR WPI; 2003-869433/81.

XX PT New cell line transformed by a gene encoding an enzyme involved in drug  
 PT metabolism and by gene encoding an enzyme involved in ammonia metabolism,  
 PT useful in liver function supporting equipment for assessing liver  
 PT function.

XX PS Example 3; Page 11; 22pp; Japanese.

XX CC The invention relates to a novel cell line (HepG2) transformed by a gene  
 CC encoding an enzyme involved in drug metabolism, such as cytochrome P450  
 CC 3A4 (CYP3A4) and a gene encoding an enzyme involved in ammonia  
 CC metabolism, such as glutamine synthetase. The cell line of the invention  
 CC provides a hybrid artificial liver and facilitates cell procurement, and  
 CC thus may be useful in liver function studies. The current sequence is  
 CC that of the human glutamine synthetase (GS) DNA fragment of the invention  
 CC which was isolated from an expression vector.

XX SQ Sequence 1246 BP; 324 A; 325 C; 323 G; 274 T; 0 U; 0 Other;

Query Match 61.5%; Score 33.2; DB 11; Length 1246;

Best Local Similarity 75.9%; Pred. No. 0.0049;  
 Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGGAGACCATTTGTGCAATATATCCCACTGC 54  
 |||||

Db 39 GAAATTAATACGACTCACTATAGGGAGACCAAGCTTACCATGCCACCTCAGC 92  
 |||||

#### RESULT 66

ID AAD11615

XX AAD11615 standard; DNA; 5731 BP.

XX AC AAD11615;

XX 24-SEP-2001 (first entry)  
XX Six finger ZFP (2C7)-Sin3 interaction domain (SID) DNA.  
DE Zinc finger protein; ZFP; gene expression; metabolic pathway regulator;  
KW modulation; plant technology; agriculture; Sin3 interaction domain; SID;  
KW six finger ZFP; 2C7; ds.  
XX Unidentified.  
OS WO200152620-A2.  
XX 26-JUL-2001.  
PN 19-JAN-2001; 2001WO-US001817.  
XX 21-JAN-2000; 2000US-0177468P.  
PR 21-JUL-2000; 2000US-00620897.  
XX (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA AGRIC DISCOVERY INC.  
XX Barbas CF, Stege JT, Guan X, Dalmia B;  
PI WPI; 2001-465325/50.  
XX New zinc finger proteins, useful for modulating or regulating gene  
PT expression and metabolic pathways in plants, e.g. for treating in the  
PT plant cells a disorder that is associated with abnormal expression of the  
PT target gene.  
XX Disclosure; Page 153-156; 156pp; English.  
PS The patent discloses methods and compositions to modulate the expression  
CC of a target gene in plant cells. The method involves providing plant  
CC cells with a zinc finger protein (ZFP) which is capable of specifically  
CC binding to a target nucleotide sequence or its complementary strand  
CC within a target gene and allowing the ZFP binding to the target  
CC nucleotide sequence, where the expression of the target gene in the plant  
CC cells is modulated. The ZFP and fusions of the ZFP proteins are useful  
CC for modulating or regulating gene expression and metabolic pathways in  
CC plants. The ZFP, fusion proteins and methods are useful in plant and  
CC agricultural technology. The method is useful particularly for treating a  
CC disorder in the plant cells, where the disorder is associated with  
CC abnormal expression of the target gene. The present sequence is six  
CC finger ZFP (2C7)-Sin3 interaction domain (SID) DNA  
XX Sequence 5731 BP; 1340 A; 1515 C; 1463 G; 1413 T; 0 U; 0 Other;  
SQ Query Match 61.5%; Score 33.2; DB 4; Length 5731;  
Best Local Similarity 75.9%; Pred. No. 0.0068;  
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGCGCAATATTCCTCCACTGC 54  
DB 858 GAAATTAATACGACTCACTATAGGAGACCACTTGCGCTAGCATGGCGCTGC 911  
RESULT 67  
AADI1020  
ID AADI1020 standard; DNA; 33 BP.  
XX AADI1020;  
AC AADI1020;  
XX 11-SEP-2003 (revised)  
DT 24-SEP-2001 (first entry)  
XX Bacteriophage T7 promoter used to amplify MAC rRNA along with a primer.  
DE Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;  
KW Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;  
KW in vitro amplification; MAC infection; promoter; ds.  
XX

OS Enterobacteria phage T7.  
XX WO200144511-A2.  
PN 21-JUN-2001.  
XX 15-DEC-2000; 2000WO-US033872.  
XX 15-DEC-1999; 99US-0171202P.  
XX (GENP-) GEN-PROBE INC.  
PA (BREN/) BRENTANO S T.  
PA (LANK/) LANKFORD R L.  
XX Brentano ST, Lankford RL;  
PI WPI; 2001-398171/42.  
XX Detecting Mycobacterium avium complex organisms, comprises using in vitro  
PT nucleic acid amplification with amplification oligonucleotides specific  
PT for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial  
PT species.  
XX Disclosure; Page 26; 27pp; English.  
PS The present invention relates to a method for detecting Mycobacterium  
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.  
CC tuberculosis, M. paratuberculosis) present in a biological sample. The  
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding  
CC 16S rRNA obtained from a biological sample containing nucleic acid from a  
CC MAC species in an in vitro nucleic acid amplification mixture comprising  
CC a polymerase activity and a pair of primers to produce an amplified  
CC nucleic acid and detecting amplified nucleic acid. The method is useful  
CC for in vitro diagnostic detection of pathogenic bacteria, particularly  
CC detecting infections caused by MAC organisms, distinguished from other  
CC closely-related Mycobacterium species. The present sequence is  
CC Bacteriophage T7 promoter. This promoter along with a primer is used for  
CC in vitro amplification of MAC rRNA. (Updated on 11-SEP-2003 to  
CC standardise OS field)  
XX Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;  
SQ Query Match 61.1%; Score 33; DB 4; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0027;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGGAGACCA 33  
DB 1 GAAATTAATACGACTCACTATAGGAGACCA 33  
RESULT 68  
AADI1286  
ID AADI1286 standard; DNA; 33 BP.  
XX AADI1286;  
AC AADI1286;  
XX 11-SEP-2003 (revised)  
DT 24-SEP-2001 (first entry)  
XX Bacteriophage T7 promoter.  
DE Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
KW Mycobacterium other than tuberculosis; MOTT; T7 promoter; ds.  
XX Enterobacteria phage T7.  
OS WO200144510-A2.  
XX 21-JUN-2001.  
XX 17-DEC-1999; 99WO-US030346.  
XX



CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide  
 CC base sequence, and detecting the amplified NA; or providing a  
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the  
 CC probe to form probe:target duplex, and detecting the duplex. The method  
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood  
 CC product such as plasma or serum, and also for detecting subtypes A, B, C  
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA  
 CC in blood serum and also as components of multiplex amplification  
 CC reactions that synthesise amplicons corresponding to polynucleotides of  
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C  
 CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 71  
 AAL45466  
 ID AAL45466 standard; DNA; 33 BP.  
 XX  
 AC AAL45466;  
 XX  
 DT 29-AUG-2003 (revised)  
 DT 06-JUN-2002 (first entry)  
 XX  
 DE Bacteriophage T7 promoter sequence SEQ ID NO: 4.  
 XX  
 KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 KW promoter; ds.  
 XX  
 OS Enterobacteria phage T7.  
 XX  
 PN WO200220852-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 01-SEP-2000; 2000WO-US024117.  
 XX  
 PR 01-SEP-2000; 2000WO-US024117.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 PA (INNR) BIOMERIEUX SA.  
 XX  
 PI Yang YF, Brentano ST, Babola O, Tran N, Vernet G;  
 XX  
 DR WPI; 2002-292273/33.  
 XX  
 PT New nucleic acid oligomer, useful for detecting selected regions of gag  
 PT and pol genes of human immune deficiency virus, particularly for  
 PT assessing drug resistance.  
 XX  
 PS Disclosure; Page 37; 82pp; English.  
 XX  
 CC The present invention provides a number of nucleic acid oligomers which  
 CC can be used to amplify the gag and pol genes of human immunodeficiency  
 CC virus type I (HIV-1). These are used to detect regions of the gag and pol  
 CC genes, especially regions associated with drug resistance, and also for  
 CC identifying genetic subtypes of the virus. The present sequence is a  
 CC fragment of a bacteriophage T7 promoter described in the invention.  
 CC (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 6; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 72  
 ADG88367  
 ID ADG88367 standard; DNA; 33 BP.  
 XX  
 AC ADG88367;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE T7 promoter DNA.  
 XX  
 KW In vitro amplification; ds.  
 XX  
 OS Enterobacteria phage T7.  
 XX  
 PN US2003165824-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 15-DEC-2000; 2000US-00738274.  
 XX  
 PR 17-DEC-1999; 99US-0172190P.  
 XX  
 PA (BREN/) BRENTANO S T.  
 PA (JUCK/) JUCKER M T.  
 PA (DELG/) DELGADO F D.  
 PA (CLEU/) CLEUZIAT P.  
 PA (RODR/) RODRIGUE M.  
 XX  
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 XX  
 DR WPI; 2003-898044/82.  
 XX  
 PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 PT in a biological sample comprises performing in vitro nucleic acid  
 PT amplification and detection of amplified products.  
 XX  
 PS Disclosure; SEQ ID NO 36; 20pp; English.  
 XX  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample comprises performing an in vitro  
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
 CC is T7 promoter DNA.  
 XX  
 SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 10; Length 33;  
 Best Local Similarity 100.0%; Pred. No. 0.0027;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 73  
 ADI18913  
 ID ADI18913 standard; DNA; 33 BP.  
 XX  
 AC ADI18913;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE T7 promoter-primer #4.  
 XX  
 KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.

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XX OS Enterobacteria phage T7.
XX PA US2003228574-A1.
XX PN 11-DEC-2003.
XX PD
XX PF 28-APR-2003; 2003US-00425975.
XX PR 01-SEP-2000; 2000US-0229790P.
XX PR 31-AUG-2001; 2001US-00944036.
XX PA (YANG/) YANG Y Y.
XX PA (BREN/) BRENTANO S T.
XX PA (BABO/) BABOLA O.
XX PA (TRAN/) TRAN N.
XX PA (VERN/) VERNET G.
XX PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;
XX DR WPI; 2004-060998/06.
XX PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide
XX PT sequences and in providing information about the infective agent, e.g.
XX PT genetic subgroup or drug-resistance phenotype based on detectable
XX PT sequence information.
XX PS Disclosure; SEQ ID NO 4; 39pp; English.
XX CC The present invention relates to a nucleic acid oligomer for amplifying a
XX CC nucleotide sequence of human immune deficiency virus (HIV)-1. The
XX CC invention is useful in amplifying and detecting HIV-1 nucleic acid
XX CC sequences and in providing additional information about the infective
XX CC agent, such as its genetic subgroup or drug-resistance phenotype based on
XX CC detectable sequence information. The present sequence is T7 promoter-
XX CC primer.
XX SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 61.1%; Score 33; DB 12; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.0027;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 74
AEA08242
ID AEA08242 standard; DNA; 33 BP.
XX AC
XX AC AEA08242;
XX DT 14-JUL-2005 (first entry)
XX DE Bacteriophage T7 promoter DNA, SEQ ID NO: 36.
XX KW Microorganism detection; DNA amplification; promoter; ds.
XX OS Enterobacteria phage T7.
XX PA US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 98US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX CC Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX CC in a biological sample, comprises using in vitro nucleic acid
XX CC amplification and detection of amplified products.
XX PS Disclosure; SEQ ID NO 36; 21pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample. The method involves using in
XX CC vitro nucleic acid amplification and detection of amplified products. The
XX CC invention is useful for diagnostic detection of pathogenic bacteria such
XX CC as Mycobacterium species. The present sequence is the Bacteriophage T7
XX CC promoter DNA.
XX SQ Sequence 33 BP; 14 A; 7 C; 6 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 61.1%; Score 33; DB 14; Length 33;
XX Best Local Similarity 100.0%; Pred. No. 0.0027;
XX Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 75
ADM11857
ID ADM11857 standard; DNA; 39 BP.
XX AC ADM11857;
XX DT 01-JUL-2004 (first entry)
XX DE Peptide library RT-PCR primer.
XX KW ss: membrane interacting peptide; food putrefaction; infectious disease;
XX KW cancer; apoptosis; antibiotic; glioblastoma; leukaemia;
XX KW autoimmune disorder; viral infection; inflammation;
XX KW graft versus host disease; PCR; primer; RT-PCR;
XX KW reverse transcriptase PCR.
XX OS Synthetic.
XX PN US2004072992-A1.
XX PD 15-APR-2004.
XX PF 29-AUG-2003; 2003US-00651563.
XX PR 30-AUG-2002; 2002JP-00253169.
XX PR 29-JAN-2003; 2003JP-00021198.
XX PA (MACH/) MACHIDA S.
XX PA (TOKU/) TOKUYASU K.
XX PA (MATS/) MATSUNAGA S.
XX PA (SAKA/) SAKAKIBARA Y.
XX PA (KOB0/) KOBORI M.
XX PA (WENZ/) WEN Z.
XX PI Machida S, Tokuyasu K, Matsunaga S, Sakakibara Y, Kobori M;
XX PI Wen Z;
XX DR WPI; 2004-328618/30.
XX PT New peptide acting on a membrane of a microorganism, for preventing
XX PT putrefaction of food or industrial products and treating an infectious

```



PT disease, cancer, autoimmune disorders, inflammation and graft versus host  
 XX disease.

PS Example 6; SEQ ID NO 9; 58pp; English.

XX The invention relates to a peptide capable of specifically acting on a  
 CC membrane of a microorganism or an animal cell having an abnormality. The  
 CC peptide conforms to the formula given in claim 1 of the specification.  
 CC Exemplary sequences appear as ADMI1859-ADMI1965 (SEQ ID 110-113 and 119  
 CC are not indexed as being too short). Also included are a library  
 CC comprising nucleic acid sequences (each nucleic acid sequence comprising  
 CC (i) a first cassette comprising a base sequence encoding a first peptide,  
 CC (ii) a second cassette comprising a base sequence encoding a second  
 CC peptide, the base sequence having the same reading frame as that of the  
 CC base sequence encoding the first peptide, where the second peptide and  
 CC comprises a site allowing flexible movement of the first peptide and  
 CC (iii) a third cassette comprising a base sequence essentially required  
 CC for transcription and translation of the first and second cassette (e.g.  
 CC a T7 promoter), the third cassette being operatively linked to the first  
 CC and second cassette, where the number of the nucleic acid sequences in  
 CC the library whose first cassettes are different from another is at least  
 CC two), a vector comprising the library, a method for screening for a  
 CC nucleic acid encoding a peptide capable of acting on biological membrane,  
 CC a pharmaceutical composition for killing a microorganism (or preventing  
 CC putrefaction of food or industrial products, for treating an infectious  
 CC disease caused by a microorganism or a cancer and for suppressing  
 CC apoptosis), comprising the peptide, an antibiotic comprising the peptide,  
 CC a pharmaceutical delivery substance for delivering a drug to a site  
 CC infected with a microorganism (or to a cancer lesion site or to a site  
 CC undergoing apoptosis) comprising the peptide and a kit, for screening for  
 CC a nucleic acid encoding a peptide capable of acting on a biological  
 CC membrane. The peptides and compositions are useful in killing a  
 CC microorganism, preventing putrefaction of food or industrial products,  
 CC treating an infectious disease caused by a microorganism or a cancer,  
 CC e.g. bladder, stomach, breast, lung, prostate, large intestine, uterine,  
 CC ovarian or kidney cancer, glioblastoma, leukaemia, autoimmune disorders,  
 CC viral infections, inflammation and graft versus host disease and in  
 CC suppressing apoptosis. The present sequence is an RT-PCR (reverse  
 CC transcriptase PCR) primer used to recover mRNA expressing a membrane  
 CC interacting peptide of the invention.

XX Sequence 39 BP; 15 A; 9 C; 9 G; 6 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 12; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 0.0028;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33  
 DB 3 GAAATTAATACGACTCACTATAGGGAGACCACA 35

RESULT 76

AAV70242  
 ID AAV70242 standard; DNA; 41 BP.

AC AAV70242;

DT 04-FEB-1999 (first entry)

DE Polysome display library construction PCR primer T7B.

KW scFv antibody; identification; in vitro translation; PCR primer;  
 KW antisense oligonucleotide; tag-coding sequence; ssrA-RNA; polysome; ss.

OS Synthetic.

XX W09848008-A1.

PN 29-OCT-1998.

XX 23-APR-1998; 98WO-EF002420.

XX

PR 23-APR-1997; 97EP-00106753.

PA (PLUE/) PLUECKTHUN A.

PI Plueckthun A, Hanes J;

XX WPI; 1998-609984/51.

PT Method of identifying polypeptide binding target molecules - uses an in  
 CC vitro translation system with formation of polysomes.

XX Example 8; Page 27; 47pp; English.

XX A method has been developed of identifying a nucleic acid encoding a  
 CC (poly)peptide that interacts with a target molecule. The method  
 CC comprises: (i) translating a population of mRNA molecules lacking stop  
 CC codons, in the correct reading frame in an in vitro translation system,  
 CC where the system either comprises antisense oligonucleotides  
 CC complementary to the tag-coding sequence of ssrA-RNA or is free of ssrA-  
 CC RNA so that formation of polysomes is allowed; (ii) contacting the formed  
 CC polysomes with the target molecules so that the nascent (poly)peptide  
 CC encoded by the RNA and produced by the polysome, binds the target  
 CC molecule; (iii) separating polysomes where the nascent (poly)peptide  
 CC produced by the polysome is bound to the target molecule from those  
 CC polysomes not displaying novel (poly)peptides; and (iv) identifying the  
 CC nucleic acid sequence encoding the (poly)peptide binding the target  
 CC molecule. Optionally prior to the formation of polysomes, DNA molecules  
 CC devoid of stop codons are transcribed in the presence of a reducing  
 CC agent, either beta-mercaptoethanol or DTT, to produce the corresponding  
 CC RNA molecules, and the reducing agent is then removed from the RNA  
 CC molecule. The method is used to identify polypeptides that bind target  
 CC molecules. The present sequence represents a PCR primer used in an  
 CC example from the present invention for construction of a polysome display  
 CC library

XX Sequence 41 BP; 17 A; 9 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 2; Length 41;  
 Best Local Similarity 100.0%; Pred. No. 0.0028;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33  
 DB 5 GAAATTAATACGACTCACTATAGGGAGACCACA 37

RESULT 77

ACC70757  
 ID ACC70757 standard; DNA; 41 BP.

XX ACC70757;

DT 20-NOV-2003 (first entry)

DE Green fluorescent protein, GFP, PCR primer Md0 SS, SEQ ID 3.

KW PCR; primer; green fluorescent protein; GFP; ss.

OS Synthetic.

XX EPI316616-A1.

PN 04-JUN-2003.

PD 26-NOV-2002; 2002EP-00026225.

XX 30-NOV-2001; 2001DE-01058904.

PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.

PI Nemetz C, Buchberger B, Watzele M, Mutter W, Roeder A, Wessner S;

XX

```
DR WPI; 2003-543650/52.
XX
XX Producing linear DNA fragments for the in vitro expression of proteins,
PT comprises amplifying a linear DNA fragment containing control elements
PT and a protein-coding gene having two ends with complementary regions to
PT the linear DNA fragment.
XX
XX Example 1; Page 6; 26pp; English.
XX
XX The present invention relates to a method for producing linear DNA
CC fragments for the in vitro expression of proteins. The method comprises
CC amplifying a linear DNA fragment, which contains control elements and a
CC protein-coding gene having two ends with complementary regions to the two
CC ends of the linear DNA fragment, using a primer pair that binds upstream
CC and downstream of the expression control region on the linear DNA
CC fragment. The method is useful for producing a linear DNA fragment for
CC the in vitro expression of proteins. The linear DNA fragment is
CC particularly useful for the in vitro expression of a protein using a
CC lysate from bacterial strains or eukaryotic cells. The present sequence
CC is a PCR primer, which was used in an example from the invention
XX
XX Sequence 41 BP; 15 A; 9 C; 8 G; 9 T; 0 U; 0 Other;
SQ
Query Match 61.1%; Score 33; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
DB 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
RESULT 78
ADW95371
ID ADW95371 standard; DNA; 41 BP.
XX
XX AC ADW95371;
XX
XX 07-APR-2005 (first entry)
XX
XX PCR primer full T7 forward used to add T7 promoter.
XX
XX protease; T7 promoter; protein display; PCR; primer; ss.
XX
XX Synthetic.
XX
XX WO2005007886-A2.
XX
XX 27-JAN-2005.
XX
XX 12-JUL-2004; 2004WO-GB003055.
XX
XX 12-JUL-2003; 2003GB-00016314.
XX
XX (UYBE-) UNIV QUEENS BELFAST.
XX
XX Scott C, Walker B;
XX
XX WPI; 2005-122776/13.
XX
XX Displaying/selecting protease molecule, by incubating mRNA to enable its
PT translation to form complexes of ribosome, mRNA and encoded nascent
PT peptide, contacting complexes with protease binding ligand, selecting
PT complexes bound to ligand.
XX
XX Example 2; Page 41; 72pp; English.
XX
XX The specification describes a method for displaying and selecting
CC protease molecules. The method comprises incubating mRNA molecules
CC encoding a peptide under conditions suitable for translation of mRNA
CC molecules to form complexes comprising ribosome, mRNA and encoded nascent
CC peptide displayed on ribosome; contacting complexes with a protease
CC binding ligand; and selecting complexes which specifically bind protease
CC
CC binding ligand. The method is useful for displaying and selecting a
CC protease molecule; identifying one or more protease from a tissue sample;
CC identifying a protease with particular substrate specificity; identifying
CC protease binding ligand; displaying, characterizing and/or identifying
CC protease and modulators of protease activity; identifying new proteases
CC from library of peptides; and characterizing one or more tissues or
CC groups of tissues with respect to protease activity. The present PCR
CC primer was used to add the T7 promoter to mRNA constructs for display of
CC cathepsin S.
XX
XX Sequence 41 BP; 17 A; 9 C; 8 G; 7 T; 0 U; 0 Other;
SQ
Query Match 61.1%; Score 33; DB 14; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0028;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCTACTATAGGAGACCACA 33
DB 5 GAAATTAATACGACTCTACTATAGGAGACCACA 37
RESULT 79
AEE96336
ID AEE96336 standard; DNA; 42 BP.
XX
XX AC AEE96336;
XX
XX 23-FEB-2006 (first entry)
XX
XX T7 universal primer forward.
XX
XX ss; primer; toxin; DNA library; DNA detection; Mcal617;
XX restriction endonuclease.
XX
XX Enterobacteria phage T7.
XX
XX WO2005121946-A2.
XX
XX 22-DEC-2005.
XX
XX 01-JUN-2005; 2005WO-US019241.
XX
XX 02-JUN-2004; 2004US-0576196P.
XX
XX (NEWE ) NEW ENGLAND BIOLABS INC.
XX
XX Roberts RJ;
XX
XX WPI; 2006-067158/07.
XX
XX Identifying an open reading frame encoding toxic protein, involves
PT detecting gap in map of shotgun clones from shotgun library aligned on
PT target DNA sequence, corresponding to numerical deficiency in start sites
PT of shotgun clones.
XX
XX Example 1; SEQ ID NO 3; 34pp; English.
XX
XX This invention describes a novel method for identifying an open reading
CC frame encoding a toxic protein, which involves obtaining an in silico map
CC of several shotgun clones from a shotgun library aligned on target DNA
CC sequence, detecting a gap in the map corresponding to numerical
CC deficiency at the start sites of shotgun clones in a region such that
CC there is a statistically underrepresented number of clones spanning the
CC ORF, and determining whether the product of the ORF is a toxic protein.
CC The target DNA fragment is a genome chosen from a bacterial genome,
CC archaeal genome and viral genome. The toxic gene is mapped to an ORF
CC adjacent to a methylase. The step of identifying the gene expressing the
CC toxic protein from the ORF further involves expressing the ORF in vivo or
CC by in vitro translation. The method is useful for identifying ORF's
CC encoding toxic proteins e.g. restriction endonucleases and enables
CC efficient characterization of toxic genes. This sequence represents a T7
CC universal primer used with AEE96337 to identify the Methylococcus
CC capsulatus Mcal617 restriction endonuclease using the method of the
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CC invention.
XX SQ Sequence 42 BP; 15 A; 10 C; 8 G; 9 T; 0 U; 0 Other;
    Query Match 61.1%; Score 33; DB 15; Length 42;
    Best Local Similarity 100.0%; Pred. No. 0.0029;
    Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
    |||||
DB 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
    |||||

RESULT 80
ABL53868
ID ABL53868 standard; DNA; 49 BP.
XX AC ABL53868;
XX 29-AUG-2003 (revised)
DT 24-JUN-2002 (first entry)
XX DE Phase T7 promoter.
XX KW Phase T7; promoter; phase display; library; ss.
XX OS Enterobacteria phage T7.
XX FH Key Location/Qualifiers
FT misc_feature 23
FT /tag= a
FT /note= "site of initiation of transcription"
XX WO200183734-A2.
XX PD 08-NOV-2001.
XX PF 03-MAY-2001; 2001WO-EP005016.
XX PR 03-MAY-2000; 2000GB-00010543.
XX PA (BIOI-) BIOINVENT INT AB.
XX PI Nilsson N;
XX WPI; 2002-062123/08.
XX DR Expression vector library, especially a phage display library comprises
XX PT several nucleic acid sequences whose expression is under regulatory
XX PT control of T7 promoter and encode antibodies or their fragments.
XX PS Claim 4; Page 43; 54pp; English.
XX CC The present sequence is a T7 promoter sequence preferred for use in
XX CC claimed expression vector libraries of the invention. These expression
XX CC vector libraries, preferably phage display libraries, comprise nucleic
XX CC acid sequences whose expression is under the regulatory control of a T7
XX CC promoter, and which encode antibodies or antibody fragments. The strong
XX CC repression of the T7 promoter increases the possibility of finding larger
XX CC variability in the pool of antibody fragments due to the low frequency of
XX CC deletion of undesirable, to the bacterial host, gene fragments. The high
XX CC efficiency of T7 RNA polymerase allows induction, by infection, at late
XX CC stages of the cell cycle, increasing the number of host cells and
XX CC limiting unwanted effects on the bacterial cells. (Updated on 29-AUG-2003
XX CC to standardise OS field)
XX SQ Sequence 49 BP; 22 A; 8 C; 10 G; 9 T; 0 U; 0 Other;
    Query Match 61.1%; Score 33; DB 6; Length 49;
    Best Local Similarity 100.0%; Pred. No. 0.003;
    Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
    |||||
DB 1 GAAATTAAATACGACTCACTATAGGAGACCACA 33
    |||||

RESULT 81
AAAX25962
ID AAAX25962 standard; DNA; 50 BP.
XX AC AAAX25962;
XX 08-JUN-1999 (first entry)
DT Capture domain primer T7loop.
XX DE
XX KW Capture domain; screening; gene library; selection; phenotype; isolation;
XX KW cell survival; microorganism; bacterium; bacteriophage; liposome; primer;
XX KW PCR; amplification; ss.
XX OS Synthetic.
XX PN WO9911777-A1.
XX PD 11-MAR-1999.
XX PF 03-SEP-1998; 98WO-GB002649.
XX PR 03-SEP-1997; 97GB-00018552.
XX PR 18-SEP-1997; 97GB-00019834.
XX PR 24-SEP-1997; 97GB-00020184.
XX PR 29-SEP-1997; 97GB-00020522.
XX PR 29-SEP-1997; 97GB-00020523.
XX PR 29-SEP-1997; 97GB-00020524.
XX PR 29-SEP-1997; 97GB-00020525.
XX PR 30-DEC-1997; 97US-0070037P.
XX PR 30-DEC-1997; 97US-0070050P.
XX PR 30-DEC-1997; 97US-0070062P.
XX PR 30-DEC-1997; 97US-0070063P.
XX PR 22-JAN-1998; 98GB-00001255.
XX PR 25-FEB-1998; 98GB-00003828.
XX PR 14-APR-1998; 98GB-00007760.
XX PR 23-MAY-1998; 98GB-00011130.
XX PA (BIOV-) BIOVATION LTD.
XX PI Carr FJ, Carter G, Hamilton A, Adair F, Williams S;
XX WPI; 1999-205184/17.
XX DR Screening proteins or polypeptides by generating a gene library and
XX PT synthesizing proteins - useful for direct selection of a biological
XX PT phenotype.
XX PS Example 10; Page 69; 118pp; English.
XX CC This sequence corresponds to a PCR primer used to amplify a capture
XX CC domain sequence used in a method of screening proteins or polypeptides,
XX CC involving the generation of a gene library and the synthesis of proteins.
XX CC The methods permit direct selection of a biological phenotype, involving
XX CC contacting displayed proteins or polypeptides with target cells to enable
XX CC binding to the cell. The resulting alteration in the target cell permits
XX CC isolation of the cell and recovery of genes encoding the displayed
XX CC protein or polypeptide. Binding also results in the production or
XX CC cessation of production of molecules from the target cell, which also
XX CC permits the recovery of genes encoding the displayed protein or
XX CC polypeptide. Molecules produced are needed for cell survival when the
XX CC cell is a microorganism (especially a bacteria or bacteriophage). Release
XX CC of a molecule is needed for release of other molecules from liposomes.
XX CC Alteration also results in appearance or disappearance of a cell surface
XX CC marker on a cell
XX SQ Sequence 50 BP; 20 A; 10 C; 9 G; 11 T; 0 U; 0 Other;
    Query Match 61.1%; Score 33; DB 2; Length 50;
```

```

Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 15 GAAATTAATACGACTCACTATAGGAGACCACA 47

RESULT 82
AAX85760
ID AAX85760 standard; DNA; 51 BP.
AC AAX85760;
XX
XX
DT 07-SEP-1999 (first entry)
XX
XX
XX PCR primer used to amplify a polysome library.
XX
XX Polysome library; nascent peptide display; PCR primer;
KW affinity interaction screening; multiple binding specificity;
KW single chain antibody; ss.
XX
XX Synthetic.
XX
XX US5922545-A.
PN
XX
XX 13-JUL-1999.
PD
XX
XX 29-JUL-1997; 97US-00902623.
XX
XX 29-OCT-1993; 93US-00144775.
PR
XX 02-SEP-1994; 94US-00300262.
PR
XX 25-OCT-1994; 94WO-US012206.
PR
XX 17-JAN-1996; 96US-00586176.
XX
XX (APFY-) APFYMAX TECHNOLOGIES NV.
XX
XX Mattheakis LC, Dower WJ;
XX
XX WPI; 1999-417975/35.
DR
XX
XX In vitro peptide and antibody display libraries for identifying multiple
XX binding specificities of single chain antibodies.
XX
XX Example 1; Col 46; 50pp; English.
XX
XX The specification describes a method for generating libraries of
XX polysomes displaying nascent peptides suitable for affinity interaction
XX screening. The method can be used to identify multiple binding
XX specificities of single chain antibodies, and comprises contacting
XX antigens with a polysome library displaying nascent peptides having a
XX single chain antibody segment, separating polysomes bound to the antigen
XX species from polysomes not bound to the antigen species, and synthesizing
XX cDNA from the separated bound polysomes to identify single chain
XX antibodies which bind to at least one of the antigen species present. The
XX method for generating libraries of polysomes displaying nascent peptides
XX is useful for affinity interaction screening. PCR primers AAX85760-61
XX were used in the course of the invention
XX
XX Sequence 51 BP; 16 A; 14 C; 8 G; 13 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 83
ABK53141
ID ABK53141 standard; DNA; 51 BP.

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XX ABK53141;
AC
XX
XX 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
XX HIV-1 reverse transcriptase gene specific oligonucleotide primer #12.
DE
XX HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KW reverse transcriptase; infection; PCR.
XX
XX Human immunodeficiency virus 1.
OS
XX
XX US200205095-A1.
PN
XX
XX 09-MAY-2002.
PD
XX
XX 31-AUG-2001; 2001US-00944036.
PF
XX
XX 01-SEP-2000; 2000US-0229790P.
PR
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
PI
XX
XX WPI; 2002-462902/49.
DR
XX
XX New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
XX Claim 1; Page 26; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
XX amplifying and detecting a nucleotide sequence of human immunodeficiency
XX virus type 1 (HIV-1). The invention also comprises a labeled
XX oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
XX from gag or pol sequences, having one of the sequences fully defined in
XX the specification, and a method for detecting HIV-1 in a biological
XX sample, comprising mixing the sample with two or more of the
XX amplification oligomers that specifically amplify at least one HIV-1
XX target sequence within gag and a pol sequence which is a protease or
XX reverse transcriptase sequence, amplifying the target, and detecting the
XX amplified product. The oligonucleotides of the invention may be used to
XX diagnose HIV-1 infection. The presents sequence represents a PCR primer
XX used to amplify the HIV-1 reverse transcriptase gene in the HIV detection
XX method of the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
XX Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;
Query Match 61.1%; Score 33; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 84
AAL45503
ID AAL45503 standard; DNA; 51 BP.
XX
XX AAL45503;
AC
XX
XX 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
XX HIV-1 pol gene RT amplification oligomer SEQ ID NO: 41.
DE

```

XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 KW probe; ss.  
 XX OS Human immunodeficiency virus 1.  
 OS Enterobacteria phage T7.  
 XX PN WO200220852-A1.  
 XX PD 14-MAR-2002.  
 XX PF 01-SEP-2000; 2000WO-US024117.  
 XX PR 01-SEP-2000; 2000WO-US024117.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PA (INMR ) BIOMERIEUX SA.  
 XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX WPI; 2002-292273/33.  
 XX New nucleic acid oligomer, useful for detecting selected regions of gag  
 PT and pol genes of human immune deficiency virus, particularly for  
 PT assessing drug resistance.  
 XX PS Claim 1; Page 60; 82pp; English.  
 XX CC The present invention provides a number of nucleic acid oligomers which  
 CC can be used to amplify the gag and pol genes of human immunodeficiency  
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
 CC genes, especially regions associated with drug resistance, and also for  
 CC identifying genetic subtypes of the virus. The present sequence is an  
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX SQ Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 6; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 85  
 ADI18950  
 ID ADI18950 standard; DNA; 51 BP.  
 XX AC ADI18950;  
 XX DT 22-APR-2004 (first entry)  
 XX DE HIV-1 pol2 gene amplifying primer #6.  
 XX KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
 XX OS Human immunodeficiency virus 1.  
 XX PN US2003228574-A1.  
 XX PD 11-DEC-2003.  
 XX PF 28-APR-2003; 2003US-00425975.  
 XX PR 01-SEP-2000; 2000US-0229790P.  
 XX PR 31-AUG-2001; 2001US-00944036.  
 XX PA (YANG/) YANG Y Y.  
 XX PA (BREN/) BRENTANO S T.  
 XX PA (BABO/) BABOLA O.

PA (TRAN/) TRAN N.  
 PA (VERN/) VERNET G.  
 XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX WPI; 2004-060998/06.  
 XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
 PT sequences and in providing information about the infective agent, e.g.  
 PT genetic subgroup or drug-resistance phenotype based on detectable  
 PT sequence information.  
 XX PS Claim 1; SEQ ID NO 41; 39pp; English.  
 XX CC The present invention relates to a nucleic acid oligomer for amplifying a  
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
 CC sequences and in providing additional information about the infective  
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
 CC detectable sequence information. The present sequence is HIV-1 pol2 gene  
 CC amplifying primer.  
 XX SQ Sequence 51 BP; 17 A; 12 C; 9 G; 13 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 12; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 86  
 AAA29795  
 ID AAA29795 standard; DNA; 52 BP.  
 XX AC AAA29795;  
 XX DT 06-AUG-2003 (revised)  
 XX DT 17-AUG-2000 (first entry)  
 XX DE Plant plastid expressing human BPI gene construction oligonucleotide #3.  
 XX KW Plant; transgenic; therapeutically active protein; plastid genome;  
 KW vacuole; allergen; vaccine; antiinflammatory; immunosuppressant; allergy;  
 KW autoimmune disease; transplant rejection; ss.  
 XX OS Homo sapiens.  
 XX OS Viridiplantae.  
 XX OS Synthetic.  
 XX PN WO200020612-A2.  
 XX PD 13-APR-2000.  
 XX PF 05-OCT-1999; 99WO-EP007414.  
 XX PR 07-OCT-1998; 98US-00167362.  
 XX PR 07-OCT-1998; 98US-00168231.  
 XX PA (NOVS ) NOVARTIS AG.  
 XX PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX PI Heifetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;  
 XX WPI; 2000-328938/28.  
 XX Novel transgenic plants expressing therapeutically active proteins form  
 PT their plastid genome, useful for producing allergens for vaccines.  
 XX PS Example 30; Page 58; 99pp; English.

CC The present invention describes plants (I) comprising a DNA molecule (II)  
 CC encoding a protein that is therapeutically active when administered to a  
 CC host, in its plastid genome. The transgenic plants are used to express  
 CC therapeutically active proteins, such as antigens, allergens, and  
 CC autoantigens. The therapeutically active proteins are used to treat or  
 CC prevent diseases, e.g. allergies, autoimmune diseases or transplant  
 CC rejection. The invention allows the production of large and inexpensive  
 CC supplies of protein-based medications. The plants are able to express  
 CC large amounts of proteins in a cost effective manner, and, as the  
 CC proteins are packaged in plastids, they can be isolated easily. The  
 CC present sequence represents an oligonucleotide used in the construction  
 CC of plant plastids which express the human BPI gene, which is used in an  
 CC example from the present invention. (Updated on 06-AUG-2003 to correct OS  
 CC field.)  
 XX

SQ Sequence 52 BP; 16 A; 16 C; 10 G; 10 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 3; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||  
 Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

## RESULT 87

AAAD21601  
 ID AAAD21601 standard; DNA; 52 BP.

XX  
 AC AAD21601;

XX  
 DT 28-JAN-2002 (first entry)

XX  
 DE Phage RNA polymerase-human BPI chimeric gene constructing T73a\_U oligo.

XX  
 KW Transgenic plant; antibacterial; immunosuppressive; virucide; therapy;  
 KW antiparasitic; allergy; autoimmune disease; immune response; PCR primer;  
 KW transplantation; ss.

OS Unidentified.

XX WO200177353-A2.

XX  
 PD 18-OCT-2001.

XX  
 PF 03-APR-2001; 2001WO-EP003788.

XX  
 PR 05-APR-2000; 2000US-00543619.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX  
 PI Heifetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;

XX  
 DR WPI; 2001-657175/75.

XX  
 PT Novel plant useful for treating or preventing allergy, comprising a DNA  
 PT molecule encoding a mature ragweed pollen allergen in its plastid genome  
 PT and capable of expressing the pollen allergen.

XX  
 PS Example 30; Page 59; 99pp; English.

XX  
 CC The invention relates to a transgenic plant comprising in its plastid  
 CC genome a DNA molecule encoding a mature ragweed pollen allergen, which is  
 CC capable of expressing the pollen allergen. The plant or plant matter  
 CC derived from the transgenic plant such as tobacco, tomato, soybean, rice  
 CC or maize is useful for treating or preventing an allergy. The plant is  
 CC also useful as a pharmaceutical and as a medical food. The plant is  
 CC useful for suppressing and reducing undesired immune response, and  
 CC production of an antigen for determination of immunological activity. The  
 CC plant is useful for treating and preventing bacterial, parasitic and  
 CC viral diseases, allergies, autoimmune diseases and transplantations. The  
 CC present sequence is an oligonucleotide used for constructing a chimeric

CC gene containing human BPI gene under control of a promoter element  
 CC responsive to the bacteriophage T7 RNA polymerase

XX  
 SQ Sequence 52 BP; 16 A; 16 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 5; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||  
 Db 10 GAAATTAATACGACTCACTATAGGAGACCACA 42

## RESULT 88

ABK53139  
 ID ABK53139 standard; DNA; 52 BP.

XX  
 AC ABK53139;

XX  
 DT 29-AUG-2003 (revised)

XX  
 DT 12-AUG-2002 (first entry)

XX  
 DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #10.

XX  
 KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
 KW reverse transcriptase; infection; PCR.

OS Human immunodeficiency virus 1.

XX US2002055095-A1.

XX  
 PD 09-MAY-2002.

XX  
 PF 31-AUG-2001; 2001US-00944036.

XX  
 PR 01-SEP-2000; 2000US-0229790P.

XX (YANG/) YANG Y. Y.

XX (BREN/) BRENTANO S T.

XX (BABO/) BABOLA O.

XX (TRAN/) TRAN N.

XX (VERN/) VERNET G.

XX  
 PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;

XX  
 DR WPI; 2002-462902/49.

XX  
 PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
 PT 1 and probes for detecting the amplified product are specific for gag and  
 PT pol regions and are useful to detect different subtypes of HIV-1.

XX  
 PS Claim 1; Page 25; 37pp; English.

XX  
 CC This invention relates to a series of nucleic acid oligomers for  
 CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
 CC virus type 1 (HIV-1). The invention also comprises a labeled  
 CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived  
 CC from gag or pol sequences, having one of the sequences fully defined in  
 CC the specification, and a method for detecting HIV-1 in a biological  
 CC sample, comprising mixing the sample with two or more of the  
 CC amplification oligomers that specifically amplify at least one HIV-1  
 CC target sequence within gag and a pol sequence which is a protease or  
 CC reverse transcriptase sequence, amplifying the target, and detecting the  
 CC amplified product. The oligonucleotides of the invention may be used to  
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection  
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX  
 SQ Sequence 52 BP; 17 A; 13 C; 9 G; 13 T; 0 U; 0 Other;

Query Match 61.1%; Score 33; DB 6; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.003;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 89  
 AAL45501  
 ID AAL45501 standard; DNA; 52 BP.  
 XX AAL45501;  
 AC AAL45501;  
 XX 29-AUG-2003 (revised)  
 DT 06-JUN-2002 (first entry)  
 XX HIV-1 pol gene RT amplification oligomer SEQ ID NO: 39.  
 DE HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 KW probe; ss.  
 XX Human immunodeficiency virus 1.  
 OS Enterobacteria phage T7.  
 XX WO200220852-A1.  
 XX 14-MAR-2002.  
 XX 01-SEP-2000; 2000WO-US024117.  
 XX 01-SEP-2000; 2000WO-US024117.  
 XX (GENP-) GEN-PROBE INC.  
 PA (INNR) BIOMERIEUX SA.  
 XX Yang YX, Brentano ST, Babola O, Tran N, Vernet G;  
 PI WPI; 2002-292273/33.  
 DR New nucleic acid oligomer, useful for detecting selected regions of gag  
 PT and pol genes of human immune deficiency virus, particularly for  
 PT assessing drug resistance.  
 XX Claim 1; Page 60; 82pp; English.  
 CC The present invention provides a number of nucleic acid oligomers which  
 CC can be used to amplify the gag and pol genes of human immunodeficiency  
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
 CC genes, especially regions associated with drug resistance, and also for  
 CC identifying genetic subtypes of the virus. The present sequence is an  
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
 CC field)  
 XX Sequence 52 BP; 17 A; 13 C; 9 G; 13 T; 0 U; 0 Other;  
 SQ Query Match 61.1%; Score 33; DB 6; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 90  
 ADI18948  
 ID ADI18948 standard; DNA; 52 BP.  
 XX ADI18948;  
 AC ADI18948;  
 XX 22-APR-2004 (first entry)  
 DT HIV-1 pol2 gene amplifying primer #4.  
 DE HIV-1 pol2 gene amplifying primer #4.

XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
 KW Human immunodeficiency virus 1.  
 OS US2003228574-A1.  
 XX 11-DEC-2003.  
 XX 28-APR-2003; 2003US-00425975.  
 PF 01-SEP-2000; 2000US-0229790P.  
 PR 31-AUG-2001; 2001US-00944036.  
 XX (YANG/) YANG Y X.  
 PA (BREN/) BRENTANO S T.  
 PA (BABO/) BABOLA O.  
 PA (TRAN/) TRAN N.  
 PA (VERN/) VERNET G.  
 XX Yang YX, Brentano ST, Babola O, Tran N, Vernet G;  
 PI WPI; 2004-060998/06.  
 DR New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
 PT sequences and in providing information about the infective agent, e.g.  
 PT genetic subgroup or drug-resistance phenotype based on detectable  
 PT sequence information.  
 XX Claim 1; SEQ ID NO 39; 39pp; English.  
 XX The present invention relates to a nucleic acid oligomer for amplifying a  
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
 CC sequences and in providing additional information about the infective  
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
 CC detectable sequence information. The present sequence is HIV-1 pol2 gene  
 CC amplifying primer.  
 XX Sequence 52 BP; 17 A; 13 C; 9 G; 13 T; 0 U; 0 Other;  
 SQ Query Match 61.1%; Score 33; DB 12; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
 Db 1 GAAATTATACGACTCACTATAGGAGACCACA 33

RESULT 91  
 ABK53137  
 ID ABK53137 standard; DNA; 53 BP.  
 XX ABK53137;  
 XX 29-AUG-2003 (revised)  
 DT 12-AUG-2002 (first entry)  
 XX HIV-1 protease gene specific oligonucleotide primer #4.  
 DE HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
 KW reverse transcriptase; infection; PCR.  
 XX Human immunodeficiency virus 1.  
 OS US200205095-A1.  
 XX 09-MAY-2002.  
 PD 31-AUG-2001; 2001US-00944036.  
 PF 01-SEP-2000; 2000US-0229790P.

XX (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
XX WPI; 2002-462902/49.  
DR New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
XX 1 and probes for detecting the amplified product are specific for gag and  
PT pol regions and are useful to detect different subtypes of HIV-1.  
XX  
PS Claim 1; Page 25; 37pp; English.  
XX  
XX This invention relates to a series of nucleic acid oligomers for  
CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
CC virus type 1 (HIV-1). The invention also comprises a labeled  
CC oligonucleotide that specifically hybridises to an HIV-1 sequence derived  
CC from gag or pol sequences, having one of the sequences fully defined in  
CC the specification, and a method for detecting HIV-1 in a biological  
CC sample, comprising mixing the sample with two or more of the  
CC amplification oligomers that specifically amplify at least one HIV-1  
CC target sequence within gag and a pol sequence which is a protease or  
CC reverse transcriptase sequence, amplifying the target, and detecting the  
CC amplified product. The oligonucleotides of the invention may be used to  
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
CC used to amplify the HIV-1 protease gene in the HIV detection method of  
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)  
XX  
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;  
SQ  
Query Match 61.1%; Score 33; DB 6; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
RESULT 92  
ID AAL45499 standard; DNA; 53 BP.  
XX  
XX AAL45499;  
AC  
DT 29-AUG-2003 (revised)  
DT 06-JUN-2002 (first entry)  
XX  
DE HIV-1 pol gene protease amplification oligomer SEQ ID NO: 37.  
XX  
XX HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
KW probe; ss.  
XX  
XX Human immunodeficiency virus 1.  
OS Enterobacteria phage T7.  
XX  
XX WO200220852-A1.  
XX  
XX 14-MAR-2002.  
XX  
XX 01-SEP-2000; 2000WO-US024117.  
XX  
XX 01-SEP-2000; 2000WO-US024117.  
XX  
XX (GENP-) GEN-PROBE INC.  
PA (INMR ) BIOMERIEUX SA.  
XX  
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
PI  
XX

DR WPI; 2002-292273/33.  
XX  
XX New nucleic acid oligomer, useful for detecting selected regions of gag  
PT and pol genes of human immune deficiency virus, particularly for  
PT assessing drug resistance.  
XX  
PS Claim 1; Page 59; 82pp; English.  
XX  
XX The present invention provides a number of nucleic acid oligomers which  
CC can be used to amplify the gag and pol genes of human immunodeficiency  
CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
CC genes, especially regions associated with drug resistance, and also for  
CC identifying genetic subtypes of the virus. The present sequence is an  
CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
CC field)  
XX  
XX Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;  
SQ  
Query Match 61.1%; Score 33; DB 6; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.003;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
RESULT 93  
ID ADI18946  
ID ADI18946 standard; DNA; 53 BP.  
XX  
XX ADI18946;  
AC  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE HIV-1 pol gene amplifying primer #4.  
XX  
XX Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
KW  
XX  
OS Human immunodeficiency virus 1.  
XX  
XX US2003228574-A1.  
XX  
XX 11-DEC-2003.  
PD  
XX  
XX 28-APR-2003; 2003US-00425975.  
PF  
XX  
XX 01-SEP-2000; 2000US-0229790P.  
PR  
XX 31-AUG-2001; 2001US-00944036.  
XX  
XX (YANG/) YANG Y Y.  
PA (BREN/) BRENTANO S T.  
PA (BABO/) BABOLA O.  
PA (TRAN/) TRAN N.  
PA (VERN/) VERNET G.  
XX  
XX Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
XX  
XX WPI; 2004-060998/06.  
DR  
XX  
XX New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
PT sequences and in providing information about the infective agent, e.g.  
PT genetic subgroup or drug-resistance phenotype based on detectable  
PT sequence information.  
XX  
XX Claim 1; SEQ ID NO 37; 39pp; English.  
PS  
XX  
XX The present invention relates to a nucleic acid oligomer for amplifying a  
CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
CC sequences and in providing additional information about the infective  
CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
CC detectable sequence information. The present sequence is HIV-1 pol gene



```

CC amplifying primer.
XX
SQ Sequence 53 BP; 17 A; 14 C; 9 G; 13 T; 0 U; 0 Other;
    Query Match      61.1%; Score 33; DB 12; Length 53;
    Best Local Similarity 100.0%; Pred. No. 0.003;
    Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 94
AAQ50482
ID AAQ50482 standard; DNA; 55 BP.
XX
AC AAQ50482;
XX
DT 25-MAR-2003 (revised)
DT 20-MAY-1994 (first entry)
XX
DE Promoter-primer.
XX
KW Mycobacterium tuberculosis; 16S rRNA; promoter-primer; hybridisation;
KW amplification; RNA polymerase; reverse transcriptase; probe;
KW helper probe; ss.
OS Synthetic.
XX
PN WO9322461-Al.
XX
PD 11-NOV-1993.
XX
PF 29-APR-1993; 93WO-US004015.
XX
PR 06-MAY-1992; 92US-00879686.
XX
PA (GENP-) GEN PROBE INC.
XX
PI Kacian DL, Mcallister DL, McDonough SH, Dattagupta N;
XX
DR WPI; 1993-368818/46.
XX
NT Nucleic acid sequence amplification method - utilises RNA polymerase and
PT reverse transcriptase under stable conditions.
XX
PS Claim 56; Page 34; 51pp; English.
XX
CC Promoter-primers with a sequence complementary to the 16S rRNA of
CC Mycobacterium tuberculosis (AAQ50482) were synthesised, either modified
CC with cordycepin or unmodified. These promoter-primers were used to
CC amplify Mycobacterium tuberculosis rRNA. The reaction was assayed with
CC probes (AAQ50483) and helper probes (AAQ50484-85). A mixt. of modified
CC and unmodified promoter primer worked better than completely modified
CC promoter primer. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;
    Query Match      61.1%; Score 33; DB 2; Length 55;
    Best Local Similarity 100.0%; Pred. No. 0.003;
    Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
AAQ89910
ID AAQ89910 standard; DNA; 55 BP.
XX
AC AAQ89910;
XX
DT 18-DEC-2000 (first entry)
XX
DE Primer #1 used to generate M.avium rRNA amplicon.
XX
KW Oligonucleotide; probe; nucleic acid detection; ss.
XX
OS Mycobacterium avium.
XX
PN WO200047777-Al.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US003525.
XX
PR 12-FEB-1999; 99US-0120019P.
XX
PA (GENP-) GEN-PROBE INC.

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AC AAQ85669;
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1995 (first entry)
XX
DE Promoter primer for Mycobacterium avium rRNA.
XX
KW Mycobacterium avium; promoter primer; ss.
OS Synthetic.
XX
PN WO9506755-Al.
XX
PD 09-MAR-1995.
XX
PF 01-SEP-1994; 94WO-US009902.
XX
PR 03-SEP-1993; 93US-00116984.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Hammond PW;
XX
DR WPI; 1995-115467/15.
XX
NT Hybridisation probes for detection and quantification of Mycobacterium
NT avium complex organism - comprise nucleic acid sequences derived from M.
NT avium ribosomal RNA, and distinguish M. avium from other Mycobacterium
NT species.
XX
PS Example; Page 27; 43pp; English.
XX
CC rRNA from a clinical isolate of an organism biochemically classified as
CC mycobacterium avium complex (MAC) but not reactive with AccProbe M. avium
CC or M. intracellulare species- specific probes, was amplified by
CC incubating at 42 degrees C for two hours in 100 microl of a soln. contg.
CC 0.15 microm of a promoter-primer (AAQ85669), and 0.15 microm of a primer
CC (AAQ85970). (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;
    Query Match      61.1%; Score 33; DB 2; Length 55;
    Best Local Similarity 100.0%; Pred. No. 0.003;
    Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
AAQ89910
ID AAQ89910 standard; DNA; 55 BP.
XX
AC AAQ89910;
XX
DT 18-DEC-2000 (first entry)
XX
DE Primer #1 used to generate M.avium rRNA amplicon.
XX
KW Oligonucleotide; probe; nucleic acid detection; ss.
XX
OS Mycobacterium avium.
XX
PN WO200047777-Al.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-US003525.
XX
PR 12-FEB-1999; 99US-0120019P.
XX
PA (GENP-) GEN-PROBE INC.

```

XX PI Brentano ST, Mcdonough SH, Nelson NC;  
 XX DR WPI; 2000-524543/47.  
 XX PT Protective compositions for stabilizing signaling labels on  
 XX PT oligonucleotide probes used in nucleic acid amplification reactions.  
 XX PS Example 4; Page 29; 6lpp; English.  
 XX CC The present invention relates to oligonucleotide probes for detecting the  
 XX CC presence of nucleic acids in samples. The method involves compositions  
 XX CC made up of detection probe, containing a label susceptible to chemical or  
 XX CC enzymatic alteration, and a protection probe. The protection probe  
 XX CC protects the label from alteration and/or enhances nucleic acid  
 XX CC amplification. The present sequence is a primer used to generate a  
 XX CC Mycobacterium avium rRNA amplicon used in an example of the invention  
 XX SQ Sequence 55 BP; 20 A; 18 C; 9 G; 8 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 3; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 97  
 ABK53144  
 ID ABK53144 standard; DNA; 55 BP.  
 XX AC ABK53144;  
 XX DT 29-AUG-2003 (revised)  
 XX DT 12-AUG-2002 (first entry)  
 XX DE HIV-1 reverse transcriptase gene specific oligonucleotide primer #15.  
 XX KW HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;  
 XX KW reverse transcriptase; infection; PCR.  
 XX OS Human immunodeficiency virus 1.  
 XX US2002055095-A1.  
 XX PD 09-MAY-2002.  
 XX PF 31-AUG-2001; 2001US-00944036.  
 XX PR 01-SEP-2000; 2000US-0229790P.  
 XX PA (YANG/) YANG Y Y.  
 XX PA (BREN/) BRENTANO S T.  
 XX PA (BABO/) BABOLA O.  
 XX PA (TRAN/) TRAN N.  
 XX PA (VERN/) VERNET G.  
 XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX WPI; 2002-462902/49.  
 XX PT New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-  
 XX PT 1 and probes for detecting the amplified product are specific for gag and  
 XX PT pol regions and are useful to detect different subtypes of HIV-1.  
 XX PS Claim 1; Page 26; 37pp; English.  
 XX CC This invention relates to a series of nucleic acid oligomers for  
 XX CC amplifying and detecting a nucleotide sequence of human immunodeficiency  
 XX CC virus type 1 (HIV-1). The invention also comprises a labeled  
 XX CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived

CC from gag or pol sequences, having one of the sequences fully defined in  
 CC the specification, and a method for detecting HIV-1 in a biological  
 CC sample, comprising mixing the sample with two or more of the  
 CC amplification oligomers that specifically amplify at least one HIV-1  
 CC target sequence within gag and a pol sequence which is a protease or  
 CC reverse transcriptase sequence, amplifying the target, and detecting the  
 CC amplified product. The oligonucleotides of the invention may be used to  
 CC diagnose HIV-1 infection. The presents sequence represents a PCR primer  
 CC used to amplify the HIV-1 reverse transcriptase gene in the HIV detection  
 CC method of the invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 6; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 RESULT 98  
 AAL45506  
 ID AAL45506 standard; DNA; 55 BP.  
 XX AC AAL45506;  
 XX DT 29-AUG-2003 (revised)  
 XX DT 06-JUN-2002 (first entry)  
 XX DE HIV-1 pol gene RT amplification oligomer SEQ ID NO: 44.  
 XX KW HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;  
 XX KW probe; ss.  
 XX OS Human immunodeficiency virus 1.  
 XX OS Enterobacteria phage T7.  
 XX WO200220852-A1.  
 XX PD 14-MAR-2002.  
 XX PF 01-SEP-2000; 2000WO-US024117.  
 XX PR 01-SEP-2000; 2000WO-US024117.  
 XX PA (GENP-) GEN-PROBE INC.  
 XX PA (INMR) BIOMERIEUX SA.  
 XX PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;  
 XX WPI; 2002-292273/33.  
 XX PT New nucleic acid oligomer, useful for detecting selected regions of gag  
 XX PT and pol genes of human immune deficiency virus, particularly for  
 XX PT assessing drug resistance.  
 XX PS Claim 1; Page 61; 82pp; English.  
 XX CC The present invention provides a number of nucleic acid oligomers which  
 XX CC can be used to amplify the gag and pol genes of human immunodeficiency  
 XX CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol  
 XX CC genes, especially regions associated with drug resistance, and also for  
 XX CC identifying genetic subtypes of the virus. The present sequence is an  
 XX CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS  
 XX CC field)  
 XX SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;  
 Query Match 61.1%; Score 33; DB 6; Length 55;  
 Best Local Similarity 100.0%; Pred. No. 0.003;  
 Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||

RESULT 99  
 ADI18953  
 ID ADI18953 standard; DNA; 55 BP.  
 XX  
 AC ADI18953;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX  
 DE HIV-1 pol4 gene amplifying primer #4.  
 XX  
 KW Human immune deficiency virus; HIV-1; drug-resistance; primer; ss.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN US2003228574-A1.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 28-APR-2003; 2003US-00425975.  
 XX  
 PR 01-SEP-2000; 2000US-0229790P.  
 PR 31-AUG-2001; 2001US-00944036.  
 XX  
 PA (YANG/) YANG Y. Y.  
 PA (BREN/) BRENTANO S T.  
 PA (BABO/) BABOLA O.  
 PA (TRAN/) TRAN N.  
 PA (VERN/) VERNET G.  
 XX  
 PI Yang YV, Brentano ST, Babola O, Tran N, Vernet G;  
 XX  
 DR WPI; 2004-060998/06.  
 XX  
 PT New nucleic acid oligomer for amplifying and detecting HIV-1 nucleotide  
 PT sequences and in providing information about the infective agent, e.g.  
 PT genetic subgroup or drug-resistance phenotype based on detectable  
 PT sequence information.  
 XX  
 PS Claim 1; SEQ ID NO 44; 39pp; English.  
 XX  
 CC The present invention relates to a nucleic acid oligomer for amplifying a  
 CC nucleotide sequence of human immune deficiency virus (HIV)-1. The  
 CC invention is useful in amplifying and detecting HIV-1 nucleic acid  
 CC sequences and in providing additional information about the infective  
 CC agent, such as its genetic subgroup or drug-resistance phenotype based on  
 CC detectable sequence information. The present sequence is HIV-1 pol4 gene  
 CC amplifying primer.  
 XX  
 SQ Sequence 55 BP; 18 A; 16 C; 9 G; 12 T; 0 U; 0 Other;  
 CC  
 CC Query Match 61.1%; Score 33; DB 12; Length 55;  
 CC Best Local Similarity 100.0%; Pred. No. 0.003;  
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||  
 Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||

RESULT 100  
 AAA29796/c  
 ID AAA29796 standard; DNA; 56 BP.  
 XX  
 AC AAA29796;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 17-AUG-2000 (first entry)

XX Plant plasmid expressing human BPI gene construction oligonucleotide #4.  
 DE Plant; transgenic; therapeutically active protein; plasmid genome;  
 KW vacuole; allergen; vaccine; antiinflammatory; immunosuppressant; allergy;  
 KW autoimmune disease; transplant rejection; ss.  
 XX  
 OS Homo sapiens.  
 OS Viridiplantae.  
 OS Synthetic.  
 XX  
 PN WO200020612-A2.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 05-OCT-1999; 99WO-EP007414.  
 XX  
 PR 07-OCT-1998; 98US-00167362.  
 PR 07-OCT-1998; 98US-00168231.  
 XX  
 PA (NOVS ) NOVARTIS AG.  
 PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX  
 PI Helfetz PB, Goff SA, Tuttle AB, Griot-Wenk ME;  
 XX  
 DR WPI; 2000-328938/28.  
 XX  
 PT Novel transgenic plants expressing therapeutically active proteins form  
 PT their plasmid genome, useful for producing allergens for vaccines.  
 XX  
 PS Example 30; Page 58; 99pp; English.  
 XX  
 CC The present invention describes plants (I) comprising a DNA molecule (II)  
 CC encoding a protein that is therapeutically active when administered to a  
 CC host, in its plasmid genome. The transgenic plants are used to express  
 CC therapeutically active proteins, such as antigens, allergens, and  
 CC autoantigens. The therapeutically active proteins are used to treat or  
 CC prevent diseases, e.g. allergies, autoimmune diseases or transplant  
 CC rejection. The invention allows the production of large and inexpensive  
 CC supplies of protein-based medications. The plants are able to express  
 CC large amounts of proteins in a cost effective manner, and, as the  
 CC proteins are packaged in plasmids, they can be isolated easily. The  
 CC present sequence represents an oligonucleotide used in the construction  
 CC of plant plasmids which express the human BPI gene, which is used in an  
 CC example from the present invention. (Updated on 06-AUG-2003 to correct OS  
 CC field.)  
 XX  
 SQ Sequence 56 BP; 12 A; 10 C; 17 G; 17 T; 0 U; 0 Other;  
 CC  
 CC Query Match 61.1%; Score 33; DB 3; Length 56;  
 CC Best Local Similarity 100.0%; Pred. No. 0.003;  
 CC Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
 |||||  
 Db 47 GAAATTAATACGACTCACTATAGGAGACCACA 15  
 |||||

Search completed: May 19, 2006, 04:19:07  
 Job time : 642.615 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 3611.49 Seconds  
(without alignments)  
836.120 Million cell updates/sec

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Perfect score: 54  
Sequence: 1 gaataataacgactacta.....tgtgaattatcccaactgc 54

Scoring table: IDENTITY\_NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

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2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hic:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	33.2	61.5	701	7	BE749125
C 2	32	59.3	864	8	CV775907
C 3	31.8	58.9	203	2	BF974085
C 4	31	57.4	188	2	BF974085
C 5	30.8	57.0	681	14	AG002474
C 6	30.8	57.0	687	14	AG002475
C 7	30.8	57.0	688	14	AG002477
C 8	30.4	56.3	815	7	BE278087
C 9	30.2	55.9	143	3	BQ102727
C 10	30.2	55.9	267	3	BQ102748
C 11	30.2	55.9	310	3	BQ102753
C 12	30.2	55.9	329	3	BQ102753
C 13	30.2	55.9	348	3	BQ102721
C 14	30.2	55.9	389	3	BQ102690
C 15	30.2	55.9	393	3	BQ102723
C 16	30.2	55.9	395	3	BQ102707
C 17	30.2	55.9	401	3	BQ102746
C 18	30.2	55.9	427	3	BQ102731
C 19	30.2	55.9	452	3	BQ102670



c 239	26.4	48.9	413	3	BP998412	BP998412 BP998412
240	26.4	48.9	461	11	AQ171228	AQ171228 HS_3070_B
241	26.4	48.9	505	5	CD631050	CD631050 55140629H
c 242	26.4	48.9	595	13	CL704198	CL704198 SP_BB001
243	26.4	48.9	723	14	AG379777	AG379777 Mus muscu
244	26.4	48.9	735	14	AG435050	AG435050 Mus muscu
c 245	26.4	48.9	757	11	AQ858630	AQ858630 nb60002E
246	26.4	48.9	792	14	AG367837	AG367837 Mus muscu
c 247	26.4	48.9	892	13	CW942745	CW942745 TcB24_2_D
c 248	26.4	48.9	905	13	C2715694	C2715694 OC_Ba003
c 249	26.4	48.9	1300	14	AG324440	AG324440 Mus muscu
c 250	26.2	48.5	130	13	CW958757	CW958757 TcB54.3_H
c 251	26.2	48.5	167	2	BM186956	BM186956 fV80b08.Y
c 252	26.2	48.5	410	2	BM005515	BM005515 LF223SP6
c 253	26.2	48.5	420	10	H55771	H55771 YG94e03.s1
254	26.2	48.5	488	11	A2926197	A2926197 476.dio46
255	26.2	48.5	495	11	A2301942	A2301942 UP_517-2C
256	26.2	48.5	560	1	AA563566	AA563566 SWMFC255
257	26.2	48.5	583	5	CD607374	CD607374 55060996H
258	26.2	48.5	666	14	AG090508	AG090508 Pan trogl
c 259	26.2	48.5	701	12	CG401344	CG401344 ZMMBB023
260	26.2	48.5	709	14	AG394908	AG394908 Mus muscu
261	26.2	48.5	718	14	AG359933	AG359933 Mus muscu
262	26.2	48.5	725	14	AG385033	AG385033 Mus muscu
263	26.2	48.5	735	14	AG359851	AG359851 Mus muscu
264	26.2	48.5	735	14	AG400808	AG400808 Mus muscu
265	26.2	48.5	735	14	AG406173	AG406173 Mus muscu
266	26.2	48.5	745	14	AG376726	AG376726 Mus muscu
267	26.2	48.5	748	14	AG423394	AG423394 Mus muscu
268	26.2	48.5	757	14	AG417058	AG417058 Mus muscu
269	26.2	48.5	758	14	AG408324	AG408324 Mus muscu
270	26.2	48.5	760	14	AG386670	AG386670 Mus muscu
271	26.2	48.5	768	14	AG410770	AG410770 Mus muscu
c 272	26.2	48.5	883	13	CW951415	CW951415 TcB36.4_F
c 273	26.2	48.5	909	13	CW953575	CW953575 TcB39.3_H
c 274	26.2	48.5	255	2	BI500972	BI500972 kx26d03.Y
c 275	26.2	48.5	443	12	CG768183	CG768183 TcB51.2_C
c 276	26.2	48.5	482	1	AA694637	AA694637 BT2223 Tr
c 277	26.2	48.5	537	11	AQ310216	AQ310216 CITHI-E1-
278	26.2	48.5	569	5	CD635331	CD635331 56011036J
c 279	26.2	48.5	693	14	DU499213	DU499213 109842111
280	26.2	48.5	699	5	CD607454	CD607454 55136570H
c 281	26.2	48.5	702	14	DU528222	DU528222 1098600991
282	26.2	48.5	710	5	CD635028	CD635028 55121053H
c 283	26.2	48.5	782	3	BM674823	BM674823 UI-B-EJ0-
c 284	26.2	48.5	853	3	BM677847	BM677847 UI-B-EJ0-
c 285	26.2	48.5	866	13	CW938257	CW938257 TcB18.1_A
c 286	26.2	48.5	895	13	CW940903	CW940903 TcB21.4_H
287	26.2	48.5	924	14	AG400158	AG400158 Mus muscu
c 288	25.8	47.8	297	7	BE991294	BE991294 UI-M-B21-
c 289	25.8	47.8	321	3	BM936027	BM936027 UI-M-B21-
c 290	25.8	47.8	527	14	CT187225	CT187225 Sus scrof
c 291	25.8	47.8	550	9	DB297418	DB297418 DB297418
292	25.8	47.8	694	14	AG409090	AG409090 Mus muscu
293	25.8	47.8	703	14	AG038946	AG038946 Pan trogl
294	25.8	47.8	703	14	AG326720	AG326720 Mus muscu
295	25.8	47.8	704	14	AG381409	AG381409 Mus muscu
296	25.8	47.8	706	14	AG292046	AG292046 Mus muscu
297	25.8	47.8	706	14	AG377165	AG377165 Mus muscu
298	25.8	47.8	708	14	AG369869	AG369869 Mus muscu
299	25.8	47.8	708	14	AG397557	AG397557 Mus muscu
300	25.8	47.8	710	14	AG393687	AG393687 Mus muscu

## ALIGNMENTS

RESULT 1	BE749125/c	BE749125	701 bp	mRNA	linear	EST 15-SEP-2000
LOCUS	601123221F1	NTIH_MGC_5	Homo sapiens	cDNA	clone IMAGE:3348173 5'	
DEFINITION		mRNA sequence.				
ACCESSION	BE749125					

VERSION	BE749125.1	GI:10163117
KEYWORDS	EST.	
SOURCE	Homo sapiens	(human)
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/.	
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCW140 row: i column: 06 High quality sequence start: 2 High quality sequence stop: 205. Location/Qualifiers 1..701 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3348173" /tissue_type="carcinoma cell line" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 5" /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."	
FEATURES	source	
ORIGIN	Query Match 61.5%; Score 33.2; DB 7; Length 701; Best Local Similarity 75.9%; Pred. No. 0.098; Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	
QY	1 GAATTATATACACTCACTATAGGAGACACATTGTCATATATCCCATGCG 54	
DB	58 GAAATTAATACGACTCACTATAGGAGACCGCAGATCTGATATTCATCGCGC 5	
RESULT 2	CV775907/c	
LOCUS	CV775907	864 bp mRNA linear EST 10-NOV-2004
DEFINITION	FGAS070311 Triticum aestivum FGAS: Library 2 Gate 3 Triticum aestivum cDNA, mRNA sequence.	
ACCESSION	CV775907	
VERSION	CV775907.1	GI:55680847
KEYWORDS	EST.	
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade; Poideae; Triticeae; Triticum.	
AUTHORS	1. (bases 1 to 864) Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilsson, D., Penniket, C., Roach, J.L. and Sarhan, F.	
TITLE	Functional Genomics of Abiotic Stress In Wheat and Canola Crops	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Wm L Crosby Bioinformatics University of Saskatchewan, Department of Computer Science	

1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033

Email: fgas\_est@cs.usask.ca

This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [95,663].

Plate: WEF085 row: K column: 23.

Location/Qualifiers

#### FEATURES

source

1..864

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="caxon:4565"

/clone\_lib="Triticum aestivum FGAS: Library 2 Gate 3"  
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Aerial  
parts (crown and leaf) of wheat cultivar Norstar from  
control and long exposure times to low temperature. 4 mRNA  
populations were combined before constructing the library;  
7 days non-acclimated plants and 1, 23, and 53 days  
cold-acclimated at 4C. Non-acclimated and cold-acclimated  
plants were grown in vermiculite This is the only library  
that was done according to the Invitrogen manual, and  
therefore, a percentage of clones will not have the 3  
prime end because of NotI digestion within the cDNA."

#### ORIGIN

Query Match 59.3%; Score 32; DB 8; Length 864;

Best Local Similarity 87.5%; Pred. No. 0.29;

Matches 35; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 ATTAATACGACTCACTATAGGAGACCAATGTGCAATA 43

|||||

Db 821 AATAATACGACTCACTATAGGGGACCCTTTGTACAAGA 782

#### RESULT 3

BF974085/c

LOCUS

DEFINITION BF974085 203 bp mRNA linear EST 22-JAN-2001  
602240343F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4328843 5',  
mRNA sequence.

ACCESSION BF974085

VERSION BF974085.1 GI:12341300

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 203)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1189 row: f column: 12

High quality sequence start: 59

High quality sequence stop: 155.

Location/Qualifiers

#### FEATURES

source

1..203

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4328843"

/tissue\_type="leiomyosarcoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_46"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Size-selected >500bp for average insert size

1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)

using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC

Library."

#### ORIGIN

Query Match 58.9%; Score 31.8; DB 2; Length 203;

Best Local Similarity 94.3%; Pred. No. 0.29;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACCAATT 35

|||||

Db 131 GAAATTAATACGACTCACTATAGGAGACCAATT 97

#### RESULT 4

BG475075/c

LOCUS

DEFINITION BG475075 188 bp mRNA linear EST 21-MAR-2001  
602491094F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4620071 5',  
mRNA sequence.

ACCESSION BG475075

VERSION BG475075.1 GI:13407352

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 188)

NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCPD/Drp

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1380 row: 1 column: 24

High quality sequence stop: 100.

Location/Qualifiers

#### FEATURES

source

1..188

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4620071"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_20"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCAGCAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match

Best Local Similarity 57.4%; Score 31; DB 2; Length 188;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 1 GAAATTAATACGACTCACTATAGGAGACCA 31
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Db 67 GAAATTAATACGACTCACTATAGGAGACCA 37

RESULT 5
AG002474/c
LOCUS Homo sapiens genomic DNA, 681 bp DNA linear GSS 16-FEB-2005
DEFINITION survey sequence.
ACCESSION AG002474
VERSION AG002474.2 GI:55786605
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 681)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1997) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsic.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT On Nov 16, 2004 this sequence version replaced gi:2641771.
FEATURES
            Location/Qualifiers
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            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="21"
            /map="21q22.1"
            /clone="Q82F5A16"

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Query Match 57.0%; Score 30.8; DB 14; Length 681;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCCA 50
    |||||
Db 218 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGGACA 169

RESULT 6
AG002475/c
LOCUS Homo sapiens genomic DNA, 687 bp DNA linear GSS 16-FEB-2005
DEFINITION survey sequence.
ACCESSION AG002475
VERSION AG002475.2 GI:55786606
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 687)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1997) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion

```

```

Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsic.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
COMMENT On Nov 16, 2004 this sequence version replaced gi:2641772.
FEATURES
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            /chromosome="21"
            /map="21q22.1"
            /clone="Q82F5A16"

ORIGIN
Query Match 57.0%; Score 30.8; DB 14; Length 687;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCCA 50
    |||||
Db 216 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGGACA 167

RESULT 7
AG002477/c
LOCUS Homo sapiens genomic DNA, 688 bp DNA linear GSS 16-FEB-2005
DEFINITION survey sequence.
ACCESSION AG002477
VERSION AG002477.1 GI:2641774
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1997)
REFERENCE 2 (bases 1 to 688)
AUTHORS Hattori,M., Ishii,K., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (21-NOV-1997) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gsic.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)
FEATURES
            Location/Qualifiers
            source
            1..688
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="21"
            /map="21q22.1"
            /clone="Q82F5A16"

ORIGIN
Query Match 57.0%; Score 30.8; DB 14; Length 688;
Best Local Similarity 76.0%; Pred. No. 0.82;
Matches 38; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTCCCA 50
    |||||
Db 217 GAAATTAATACGACTCACTATAGGAGACCAAGCTTAGGATCTTGGACA 168

RESULT 8
BE278087/c
LOCUS BE278087
DEFINITION 601179624F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546485 5',
            mRNA sequence.
ACCESSION BE278087

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VERSION BE278087.1 GI:9153063
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 815)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM244 row: P column: 06
High quality sequence stop: 99.
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        /db_xref="taxon:9606"
        /clone="IMAGE:3546485"
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        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH MGC 21"
        /note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
        Site 2: EcoRI. cDNA made by oligo-dT priming.
        Directionally cloned into EcoRI/XhoI sites using the
        following 5' adaptor: GGACGAG(G). Size-selected >500bp
        for average insert size 1.8kb. Library constructed by
        Ling Hong in the laboratory of Gerald M. Rubin (University
        of California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
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ORIGIN
Query Match 56.3%; Score 30.4; DB 7; Length 815;
Best Local Similarity 96.9%; Pred. No. 1.2;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCAC 32
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Db 63 GAAATTATACGACTCACTATAGGAGACCAC 32
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RESULT 9
LOCUS BQ102727/c 143 bp mRNA linear EST 12-APR-2002
DEFINITION UGC0111 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102727
VERSION BQ102727.1 GI:20144210
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 143)
REFERENCE Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
```

```

Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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    1..143
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        /db_xref="taxon:7227"
        /dev_stage="embryonic 8-12 hr post-fertilization"
        /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
        /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
        F.C. (1988) Functional cDNA libraries from Drosophila
        embryos. J. Mol Biol. 203, 425-37."
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ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 143;
Best Local Similarity 91.4%; Pred. No. 1.1;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATT 35
|||||
Db 48 GAAATTATACGACTCACTATAGGAGACCGGAAT 14
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RESULT 10
LOCUS BQ102748/c 267 bp mRNA linear EST 12-APR-2002
DEFINITION UGC0132 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102748
VERSION BQ102748.1 GI:20144231
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 267)
REFERENCE Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
AUTHORS Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:7227"
        /dev_stage="embryonic 8-12 hr post-fertilization"
        /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
        /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
        F.C. (1988) Functional cDNA libraries from Drosophila
        embryos. J. Mol Biol. 203, 425-37."
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ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 267;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACATT 35
|||||
Db 57 GAAATTATACGACTCACTATAGGAGACCGGAAT 23

RESULT 11
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BQ102753/c
LOCUS      BQ102753      310 bp      mRNA      linear      EST 12-APR-2002
DEFINITION UUGC0137 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION  BQ102753
VERSION    BQ102753.1  GI:20144236
KEYWORDS   EST.
ORGANISM   Drosophila melanogaster (fruit fly)
SOURCE     Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 310)
AUTHORS   Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
           Metherall,J.E. and Letsou,A.
TITLE     An automated screen for spatially restricted transcripts in
JOURNAL   Drosophila embryogenesis
COMMENT   Genome Res. (2002) In press
           Contact: Letsou, A.
           Department of Human Genetics
           Eccles Institute of Human Genetics, University of Utah
           15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
           Tel: 801 581-4422
           Fax: 801 581-7796
           Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
  1..310
   /organism="Drosophila melanogaster"
   /mol_type="mRNA"
   /db_xref="taxon:7227"
   /dev_stages="embryonic 8-12 hr post-fertilization"
   /clone_lib="Drosophila 8-12 hr embryonic cDNA library"
   /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match      55.9%; Score 30.2; DB 3; Length 310;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GAAATTAATACGACTCACTATAGGAGACCACATT 35
      |||||||
Db   43 GAAATTAATACGACTCACTATAGGAGACCGGAAT 9

RESULT 12
BQ102710/c
LOCUS      BQ102710      329 bp      mRNA      linear      EST 12-APR-2002
DEFINITION UUGC0094 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION  BQ102710
VERSION    BQ102710.1  GI:20144193
KEYWORDS   EST.
ORGANISM   Drosophila melanogaster (fruit fly)
SOURCE     Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 329)
AUTHORS   Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
           Metherall,J.E. and Letsou,A.
TITLE     An automated screen for spatially restricted transcripts in
JOURNAL   Drosophila embryogenesis
COMMENT   Genome Res. (2002) In press
           Contact: Letsou, A.
           Department of Human Genetics
           Eccles Institute of Human Genetics, University of Utah
           15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
           Tel: 801 581-4422
           Fax: 801 581-7796
           Email: aletsou@genetics.utah.edu

ORIGIN
Query Match      55.9%; Score 30.2; DB 3; Length 310;
Best Local Similarity 91.4%; Pred. No. 1.2;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GAAATTAATACGACTCACTATAGGAGACCACATT 35
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Db   43 GAAATTAATACGACTCACTATAGGAGACCGGAAT 9

RESULT 13
BQ102721/c
LOCUS      BQ102721      348 bp      mRNA      linear      EST 12-APR-2002
DEFINITION UUGC0105 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION  BQ102721
VERSION    BQ102721.1  GI:20144204
KEYWORDS   EST.
ORGANISM   Drosophila melanogaster (fruit fly)
SOURCE     Drosophila melanogaster
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 348)
AUTHORS   Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
           Metherall,J.E. and Letsou,A.
TITLE     An automated screen for spatially restricted transcripts in
JOURNAL   Drosophila embryogenesis
COMMENT   Genome Res. (2002) In press
           Contact: Letsou, A.
           Department of Human Genetics
           Eccles Institute of Human Genetics, University of Utah
           15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
           Tel: 801 581-4422
           Fax: 801 581-7796
           Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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   /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."

ORIGIN
Query Match      55.9%; Score 30.2; DB 3; Length 348;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GAAATTAATACGACTCACTATAGGAGACCACATT 35
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Db   48 GAAATTAATACGACTCACTATAGGAGACCGGAAT 14

RESULT 14
BQ102690/c
LOCUS      BQ102690      389 bp      mRNA      linear      EST 12-APR-2002

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DEFINITION UUGC0071 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102690
VERSION BQ102690.1 GI:20144173
SOURCE EST.
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 389)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 389;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 53 GAAATTAATACGACTCACTATAGGAGACCACTT 19
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RESULT 15
BQ102723/c
LOCUS BQ102723
DEFINITION UUGC0107 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102723
VERSION BQ102723.1 GI:20144206
SOURCE EST.
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 393)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
FEATURES
source
393 bp mRNA linear EST 12-APR-2002
UUGC0107 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
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Db 53 GAAATTAATACGACTCACTATAGGAGACCACTT 19
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RESULT 16
BQ102707/c
LOCUS BQ102707
DEFINITION UUGC0091 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102707
VERSION BQ102707.1 GI:20144190
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 395)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 395;
Best Local Similarity 91.4%; Pred. No. 1.3;
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RESULT 17
BQ102746/c
LOCUS BQ102746
DEFINITION UUGC0130 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102746
VERSION BQ102746.1 GI:20144206
SOURCE EST.
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 393)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
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15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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UUGC0130 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.

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/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
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Query Match 55.9%; Score 30.2; DB 3; Length 393;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
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Db 43 GAAATTAATACGACTCACTATAGGAGACCGGAAT 9
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RESULT 16
BQ102707/c
LOCUS BQ102707
DEFINITION UUGC0091 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102707
VERSION BQ102707.1 GI:20144190
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 395)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
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15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
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F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
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Query Match 55.9%; Score 30.2; DB 3; Length 395;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Db 46 GAAATTAATACGACTCACTATAGGAGACCGGAAT 12
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RESULT 17
BQ102746/c
LOCUS BQ102746
DEFINITION UUGC0130 Drosophila 8-12 hr embryonic cDNA library Drosophila
ACCESSION BQ102746
VERSION BQ102746.1 GI:20144206
SOURCE EST.
ORGANISM Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 393)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
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Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
FEATURES
source
401 bp mRNA linear EST 12-APR-2002
UUGC0130 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.

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ACCESSION BQ102746
VERSION BQ102746.1 GI:20144229
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 401)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
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F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
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Best Local Similarity 91.4%; Pred. No. 1.3;
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QY 1 GAAATTAATACGACTCACTATAGGAGACACCAT 35
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Db 56 GAAATTAATACGACTCACTATAGGAGACCGGAAT 22
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RESULT 18
BQ102731/c
LOCUS BQ102731.1 GI:20144214
DEFINITION UUGC0115 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102731
VERSION BQ102731.1 GI:20144214
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 427)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
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/mol_type="mRNA"
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F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 55.9%; Score 30.2; DB 3; Length 427;
Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACACCAT 35
|||||
Db 48 GAAATTAATACGACTCACTATAGGAGACCGGAAT 14
|||||

RESULT 19
BQ102670/c
LOCUS BQ102670.1 GI:20144153
DEFINITION UUGC0050 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102670
VERSION BQ102670.1 GI:20144153
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 452)
AUTHORS Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Metherall,J.E. and Letsou,A.
TITLE An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL Genome Res. (2002) In press
COMMENT Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: aletsou@genetics.utah.edu
Seq primer: SP6.
FEATURES
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F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
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Best Local Similarity 91.4%; Pred. No. 1.3;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GAAATTAATACGACTCACTATAGGAGACACCAT 35
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RESULT 20
BQ102693/c
LOCUS BQ102693.1 GI:20144176
DEFINITION UUGC0074 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION BQ102693
VERSION BQ102693.1 GI:20144176

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[illegible]

**SOURCE ORGANISM**  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
**REFERENCE AUTHORS TITLE**  
1 (bases 1 to 739)  
Liang, Z. and Biggin, M.D.  
Eve and ftz regulate a wide array of genes in blastoderm embryos:  
the selector homeoproteins directly or indirectly regulate most  
genes in Drosophila  
**JOURNAL PUBMED COMMENT**  
Development 125 (22), 4471-4482 (1998)  
9778506  
Contact: Biggin, M. D.  
Department of Molecular Biophysics and Biochemistry  
Yale University  
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA  
Tel: 203 432 6178  
Fax: 203 432 5791  
Email: mark.biggin@yale.edu  
pair-rule, strong segmentally repeated patterns  
Seq primer: SP6  
High quality sequence stop: 739.

**FEATURES source**  
Location/Qualifiers  
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/clone\_lib="Drosophila 8-12 hr embryonic cDNA library"  
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,  
F.C. (1988) Functional cDNA libraries from Drosophila  
embryos. J. Mol Biol. 203, 425-37."  
**ORIGIN**  
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**RESULT 24**  
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**LOCUS** 748 bp mRNA linear EST 28-SEP-1999  
**DEFINITION** 1.53 Drosophila 8-12 hr embryonic cDNA library Drosophila  
melanogaster cDNA 5', mRNA sequence.  
**ACCESSION** A1124281  
**VERSION** A1124281.1 GI:3540022  
**KEYWORDS** EST.  
**SOURCE ORGANISM**  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
**REFERENCE AUTHORS TITLE**  
1 (bases 1 to 748)  
Liang, Z. and Biggin, M.D.  
Eve and ftz regulate a wide array of genes in blastoderm embryos:  
the selector homeoproteins directly or indirectly regulate most  
genes in Drosophila  
**JOURNAL PUBMED COMMENT**  
Development 125 (22), 4471-4482 (1998)  
9778506  
Contact: Biggin, M. D.  
Department of Molecular Biophysics and Biochemistry  
Yale University  
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA  
Tel: 203 432 6178  
Fax: 203 432 5791  
Email: mark.biggin@yale.edu  
strong segmentally repeated patterns  
Seq primer: SP6  
High quality sequence stop: 748.

**FEATURES source**  
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/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,  
F.C. (1988) Functional cDNA libraries from Drosophila  
embryos. J. Mol Biol. 203, 425-37."  
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Query Match 55.9%; Score 30.2; DB 1; Length 748;  
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Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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**Db** 66 GAAATTAATACGACTCACTATAGGAGACCGGAAT 32  
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**RESULT 25**  
A1124257/c  
**LOCUS** 753 bp mRNA linear EST 28-SEP-1999  
**DEFINITION** 1.17 Drosophila 8-12 hr embryonic cDNA library Drosophila  
melanogaster cDNA 5', similar to EF-1-alpha F, mRNA sequence.  
**ACCESSION** A1124257  
**VERSION** A1124257.1 GI:3539998  
**KEYWORDS** EST.  
**SOURCE ORGANISM**  
Drosophila melanogaster (fruit fly)  
Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
**REFERENCE AUTHORS TITLE**  
1 (bases 1 to 753)  
Liang, Z. and Biggin, M.D.  
Eve and ftz regulate a wide array of genes in blastoderm embryos:  
the selector homeoproteins directly or indirectly regulate most  
genes in Drosophila  
**JOURNAL PUBMED COMMENT**  
Development 125 (22), 4471-4482 (1998)  
9778506  
Contact: Biggin, M. D.  
Department of Molecular Biophysics and Biochemistry  
Yale University  
P.O. Box 208114 266 Whitney Ave, New Haven, CT 06520-208114, USA  
Tel: 203 432 6178  
Fax: 203 432 5791  
Email: mark.biggin@yale.edu  
weak segmentally repeated patterns  
Seq primer: SP6  
High quality sequence stop: 753.  
**FEATURES source**  
Location/Qualifiers  
1..753  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/dev\_stage="embryonic 8-12 hr post-fertilization"  
/clone\_lib="Drosophila 8-12 hr embryonic cDNA library"  
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,  
F.C. (1988) Functional cDNA libraries from Drosophila  
embryos. J. Mol Biol. 203, 425-37."  
**ORIGIN**  
Query Match 55.9%; Score 30.2; DB 1; Length 753;  
Best Local Similarity 91.4%; Pred. No. 1.4;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
**QY** 1 GAAATTAATACGACTCACTATAGGAGACACATT 35  
|||||  
**Db** 343 GAAATTAATACGACTCACTATAGGAGACCGGAAT 309  
|||||  
**RESULT 26**

BE391582/c  
LOCUS BE391582 181 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601282148F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3604090 5',  
mRNA sequence.  
ACCESSION BE391582  
VERSION BE391582.1 GI:9336947  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 181)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM249 row: P column: 11  
High quality sequence start: 70  
High quality sequence stop: 178.  
Location/Qualifiers  
1..181  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3604090"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 44"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
FEATURES  
source  
Query Match 55.6%; Score 30; DB 7; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 143 GAAATTAATACGACTCACTATAGGAGACC 114  
|||||  
ORIGIN  
Query Match 55.6%; Score 30; DB 7; Length 181;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 143 GAAATTAATACGACTCACTATAGGAGACC 114  
|||||  
RESULT 27  
BE262878/c  
LOCUS BE262878 182 bp mRNA linear EST 26-OCT-2000  
DEFINITION 601148014F1 NIH\_MGC\_19 Homo sapiens CDNA clone IMAGE:3163514 5',  
mRNA sequence.  
ACCESSION BE262878  
VERSION BE262878.1 GI:9136277  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 182)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LLCM124 row: k column: 03  
High quality sequence start: 66  
High quality sequence stop: 131.  
Location/Qualifiers  
1..182  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3163514"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Note: this is a NIH\_MGC Library."  
ORIGIN  
Query Match 55.6%; Score 30; DB 7; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 96 GAAATTAATACGACTCACTATAGGAGACC 67  
|||||  
RESULT 28  
BF976190/c  
LOCUS BF976190 183 bp mRNA linear EST 22-JAN-2001  
DEFINITION 602245057F1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4336023 5',  
mRNA sequence.  
ACCESSION BF976190  
VERSION BF976190.1 GI:12343405  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 183)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1208 row: a column: 16  
High quality sequence start: 14  
High quality sequence stop: 106.  
Location/Qualifiers  
1..183  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4336023"  
FEATURES  
source  
Query Match 55.6%; Score 30; DB 7; Length 182;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 96 GAAATTAATACGACTCACTATAGGAGACC 67  
|||||  
RESULT 28  
BF976190/c  
LOCUS BF976190 183 bp mRNA linear EST 22-JAN-2001  
DEFINITION 602245057F1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4336023 5',  
mRNA sequence.  
ACCESSION BF976190  
VERSION BF976190.1 GI:12343405  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 183)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1208 row: a column: 16  
High quality sequence start: 14  
High quality sequence stop: 106.  
Location/Qualifiers  
1..183  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4336023"  
FEATURES  
source



/tissue\_type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dt priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 183;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 DB 77 GAAATTAATACGACTCACTATAGGAGACC 48

## RESULT 29

BE314661/c  
 LOCUS BE314661 185 bp mRNA linear EST 26-OCT-2000  
 DEFINITION 60114677F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3161970 5',  
 mRNA sequence.

ACCESSION BE314661  
 VERSION BE314661.1 GI:9136063  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

## REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLCM120 row: j column: 19  
 High quality sequence start: 60  
 High quality sequence stop: 122.

## FEATURES

## source

1..185

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3161970"  
 /tissue\_type="neuroblastoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_19"

/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 DB 89 GAAATTAATACGACTCACTATAGGAGACC 60

## RESULT 30

BE397962/c  
 LOCUS BE397962 195 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601290494F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3620903 5',  
 mRNA sequence.

ACCESSION BE397962  
 VERSION BE397962.1 GI:9343327  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo.

1 (bases 1 to 195)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLCM293 row: 1 column: 24  
 High quality sequence start: 5  
 High quality sequence stop: 143.

Location/Qualifiers

1..195

## FEATURES

## source

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3620903"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_8"

/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dt priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 195;

Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 DB 109 GAAATTAATACGACTCACTATAGGAGACC 80

## RESULT 31

BE410828/c  
 LOCUS BE410828 204 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601301490F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3636046 5',  
 mRNA sequence.

ACCESSION BE410828  
 VERSION BE410828.1 GI:9347278  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 204)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM333 row: c column: 23
High quality sequence start: 53
High quality sequence stop: 177.
FEATURES
    source
        Location/Qualifiers
            1..204
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3636046"
                /tissue_type="choriocarcinoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_21"
                /note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;
                Site 2: EcoRI; cDNA made by oligo-dT priming.
                Directionally cloned into EcoRI/XhoI sites using the
                following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                for average insert size 1.8kb. Library constructed by
                Ling Hong in the laboratory of Gerald M. Rubin (University
                of California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
    Query Match      55.6%; Score 30; DB 7; Length 204;
    Best Local Similarity 100.0%; Pred. No. 1.4;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    ||||||||||||||||||||||||||||
Db 144 GAAATTAATACGACTCACTATAGGAGACC 115

RESULT 32
BE398063/c
LOCUS      BE398063      206 bp      mRNA      linear      EST 21-JUL-2000
DEFINITION      601290252F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620772 5',
                mRNA sequence.
ACCESSION      BE398063
VERSION        BE398063.1 GI:9343428
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 206)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM293 row: g column: 13
High quality sequence start: 33
High quality sequence stop: 160.

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```

FEATURES
    source
        Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3620772"
                /tissue_type="Burkitt lymphoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_8"
                /note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN
    Query Match      55.6%; Score 30; DB 7; Length 206;
    Best Local Similarity 100.0%; Pred. No. 1.4;
    Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    ||||||||||||||||||||||||||||
Db 126 GAAATTAATACGACTCACTATAGGAGACC 97

RESULT 33
BF027436/c
LOCUS      BF027436      227 bp      mRNA      linear      EST 10-OCT-2000
DEFINITION      601672556F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955452 5',
                mRNA sequence.
ACCESSION      BF027436
VERSION        BF027436.1 GI:10735148
KEYWORDS
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 227)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DrP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM829 row: p column: 13
High quality sequence start: 13
High quality sequence stop: 161.
FEATURES
    source
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3955452"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_20"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."

```

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 |||  
 Db 128 GAAATTAATACGACTCACTATAGGAGACC 99

## RESULT 34

BE391744/c  
 LOCUS BE391744.1 272 bp mRNA linear EST 21-JUL-2000  
 DEFINITION 601282029F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3603943 5',  
 mRNA sequence.

ACCESSION BE391744

VERSION BE391744.1 GI:9337109

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

## REFERENCE

1 (bases 1 to 272)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

UNPUBLISHED (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L12M249 row: j column: 08

High quality sequence start: 102

High quality sequence stop: 217.

## FEATURES

source

1..272

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3603943"

/tissue\_type="endometrium, adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC\_44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Library constructed by Ling Hong

in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 272;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 |||  
 Db 194 GAAATTAATACGACTCACTATAGGAGACC 165

## RESULT 35

BG425691/c  
 LOCUS BG425691.1 334 bp mRNA linear EST 14-MAR-2001  
 DEFINITION 602448292F1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4586926 5',  
 mRNA sequence.

## ACCESSION

BG425691

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

## REFERENCE

1 (bases 1 to 334)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

## JOURNAL

## COMMENT

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L12M1316 row: g column: 23

High quality sequence start: 22

High quality sequence stop: 82.

## FEATURES

source

1..334

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4586926"

/tissue\_type="renal cell adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 14"

/note="Organ: kidney; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM1928 row: h column: 19  
High quality sequence stop: 93.  
Location/Qualifiers  
1. 347  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5446338"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

FEATURES  
source

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 347;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 58 GAAATTAATACGACTCACTATAGGAGACC 29  
|||||

RESULT 37  
BM041853/c  
LOCUS  
DEFINITION 603614347F1 NIH\_MGC\_108 Homo sapiens cDNA clone IMAGE:5420363 5', mRNA sequence.  
ACCESSION BM041853  
VERSION BM041853.1 GI:16771120  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 349)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM1874 row: n column: 12  
High quality sequence start: 34  
High quality sequence stop: 157.  
Location/Qualifiers  
1. 349  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5420363"  
/tissue\_type="Wilms' tumor, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_108"  
/note="Organ: kidney; Vector: pOTB7; Site\_1: XhoI; Site\_2:

FEATURES  
source

Query Match 55.6%; Score 30; DB 2; Length 351;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 349;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 125 GAAATTAATACGACTCACTATAGGAGACC 96  
|||||

RESULT 38

BF974094/c

LOCUS  
DEFINITION 602242718F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4331093 5', mRNA sequence.  
ACCESSION BF974094  
VERSION BF974094.1 GI:12341309  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 351)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM195 row: d column: 06  
High quality sequence start: 93  
High quality sequence stop: 210.  
Location/Qualifiers  
1. 351  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4331093"  
/tissue\_type="leiomyosarcoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_46"  
/note="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 351;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 175 GAAATTAATACGACTCCTATAGGAGACC 146

RESULT 39  
BE391553/c  
LOCUS  
DEFINITION  
601283214F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3605139 5',  
mRNA sequence.  
ACCESSION  
BE391553  
VERSION  
BE391553.1 GI:9336918  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 394)  
AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM252 row: 1 column: 04  
High quality sequence start: 81  
High quality sequence stop: 182.  
Location/Qualifiers  
1..394  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3605139"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source  
1..394  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3605139"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGACGAG(G). Library constructed by Ling Hong  
in the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
Query Match 55.6%; Score 30; DB 7; Length 394;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCCTATAGGAGACC 30  
|||||  
Db 172 GAAATTAATACGACTCCTATAGGAGACC 143  
|||||

RESULT 40  
W91597/c  
LOCUS  
DEFINITION  
W91597 MTA.G05.077.A MTA adult mouse thymus library Mus musculus cDNA  
clone MTA.G05.077 3' end similar to CT repeat, mRNA sequence.  
ACCESSION  
W91597  
VERSION  
W91597.1 GI:1408023  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 418)

AUTHORS  
Nguyen, C., Rocha, D., Granjeaud, S., Bernard, K., Naquet, P. and  
Jordan, B.R.  
Gene expression in different cell types of the mouse thymus  
Unpublished (1996)  
COMMENT  
Contact: Jordan BR  
Genome Structure and Immune Functions  
Centre d'Immunologie INSERM/CNRS  
Case 906, 13288 MARSEILLE Cedex 9, FRANCE  
Tel: 330491269496  
Fax: 330491269430  
Email: [jordan@ciml.univ-mrs.fr](mailto:jordan@ciml.univ-mrs.fr)  
This sequence was determined at Engelhardt Institute of Molecular  
Biology, Moscow, Russia (V Zakhariev)  
Seq primer: SP6.  
Location/Qualifiers  
1..418  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="MTA.G05.077"  
/lab\_host="MC1061 p3"  
/clone\_lib="MTA adult mouse thymus library"  
/note="Vector: pCDNAL; Site:1: NotI; Site:2: EcoRI; The  
cDNA library was constructed from poly(A)+ RNA of an adult  
mouse thymus by oligo-dT primed reverse transcription.  
cDNA was selected on gel for size above 800 nucleotides  
after second strand synthesis, then directionally cloned  
after adaptor ligation and restriction enzyme cleavage  
into the pCDNAL vector (Not I on polyA side, EcoR I on the  
5'side)."

ORIGIN  
Query Match 55.6%; Score 30; DB 10; Length 418;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCCTATAGGAGACC 30  
|||||  
Db 371 GAAATTAATACGACTCCTATAGGAGACC 342  
|||||

RESULT 41  
BG398598/c  
LOCUS  
DEFINITION  
6024339706F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4565904 5',  
mRNA sequence.  
ACCESSION  
BG398598  
VERSION  
BG398598.1 GI:13292046  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 426)  
AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1283 row: 1 column: 01  
High quality sequence start: 17  
High quality sequence stop: 421.  
Location/Qualifiers  
1..426

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4565904"  
 /tissue\_type="primary B-cells from tonsils (cell line)"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_48"  
 /note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI;  
 Site:2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by Ling  
 Hong in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 426;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 |||||||  
 Db 157 GAAATTAATACGACTCACTATAGGAGACC 128

## RESULT 42

BE562252/c  
 LOCUS BE562252  
 DEFINITION 601344666F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3677512 5',  
 mRNA sequence.

ACCESSION BE562252  
 VERSION BE562252.1 GI:9805972

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 485)  
 NIH-MGC http://mgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM353 row: c column: 17

High quality sequence start: 12

High quality sequence stop: 480.

## FEATURES

Location/Qualifiers

1. 485

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3677512"

/tissue\_type="Burkitt lymphoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 485;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 |||||||  
 Db 143 GAAATTAATACGACTCACTATAGGAGACC 114

## RESULT 43

BE398001/c  
 LOCUS BE398001  
 DEFINITION 601290550F1 NIH\_MGC\_8 Homo sapiens cDNA clone IMAGE:3620700 5',  
 mRNA sequence.

ACCESSION BE398001

VERSION BE398001.1 GI:9343366

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

1 (bases 1 to 511)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM293 row: d column: 13

High quality sequence start: 2

High quality sequence stop: 506.

## FEATURES

Location/Qualifiers

1. 511

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3620700"

/tissue\_type="Burkitt lymphoma"

/lab\_host="NIH\_MGC\_8"

/clone\_lib="NIH\_MGC\_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Location/Qualifiers

1. 511

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3620700"

/tissue\_type="Burkitt lymphoma"

/lab\_host="NIH\_MGC\_8"

/clone\_lib="NIH\_MGC\_8"

/note="Organ: lymph; Vector: pOTB7; Site:1: XhoI; Site:2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 530)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM159 row: a column: 23  
High quality sequence start: 35  
High quality sequence stop: 490.  
Location/Qualifiers  
1..530  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4300318"  
/tissue\_type="epitheloid carcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_42"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library. |"

FEATURES source  
Query Match 55.6%; Score 30; DB 7; Length 530;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 456 GAAATTAATACGACTCACTATAGGAGACC 427  
|||||

RESULT 45  
BE410907/c  
LOCUS BE410907 550 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601303550F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3637957 5', mRNA sequence.

ACCESSION BE410907  
VERSION BE410907.1 GI:9347357  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 550)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM338 row: c column: 14  
High quality sequence start: 95  
High quality sequence stop: 217.  
Location/Qualifiers  
1..550  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3637957"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES source  
Query Match 55.6%; Score 30; DB 7; Length 550;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 183 GAAATTAATACGACTCACTATAGGAGACC 154  
|||||

RESULT 46  
BE281606/c  
LOCUS BE281606 561 bp mRNA linear EST 13-JUL-2000  
DEFINITION 601154965F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3138329 5', mRNA sequence.

ACCESSION BE281606  
VERSION BE281606.1 GI:9156628  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 561)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM103 row: a column: 18  
High quality sequence start: 6  
High quality sequence stop: 560.  
Location/Qualifiers  
1..561  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3138329"  
/tissue\_type="choriocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 561;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 124 GAAATTAATACGACTCACTATAGGAGACC 95

## RESULT 47

BG491845/c

LOCUS 60253593271 NIH\_MGC\_41 Homo sapiens CDNA clone IMAGE:4685046 3',  
DEFINITION mRNA sequence.

ACCESSION BG491845

VERSION BG491845.1 GI:13453357

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1 (bases 1 to 578)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTP/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L10M1493 row: p column: 07

High quality sequence stop: 569.

## FEATURES

source

1..578

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4685046"

/tissue\_type="amelanotic melanoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_41"

/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.6%; Score 30; DB 2; Length 578;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 543 GAAATTAATACGACTCACTATAGGAGACC 514

## RESULT 48

BE737047/c

LOCUS

DEFINITION 601304208F1 NIH\_MGC\_39 Homo sapiens CDNA clone IMAGE:3639000 5',  
mRNA sequence.

ACCESSION BE737047

VERSION BE737047.1 GI:10151039

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 579)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L10M340 row: o column: 01

High quality sequence stop: 502.

## FEATURES

source

1..579

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3639000"

/tissue\_type="adenocarcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_39"

/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin

(University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

Db 96 GAAATTAATACGACTCACTATAGGAGACC 67

## RESULT 49

BE728141/c

LOCUS

DEFINITION 601563696F1 NIH\_MGC\_20 Homo sapiens CDNA clone IMAGE:3833351 5',  
mRNA sequence.

ACCESSION BE728141

VERSION BE728141.1 GI:10142133

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 587)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

COMMENT

Unpublished (1999)



```

COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: ATCC/DCTD/DTT
              cDNA Library Preparation: Ling Hong/Rubin Laboratory
              cDNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
              Plate: LLCW511 row: p column: 24
              High quality sequence stop: 587.
              Location/Qualifiers
                1..587
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3833351"
                /tissue_type="melanotic melanoma"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_20"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

```

Query Match      55.6%; Score 30; DB 7; Length 587;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||||||||||||||||||||||||||||
Db 121 GAAATTAATACGACTCACTATAGGAGACC 92

RESULT 50
BM007071/c
LOCUS      BM007071 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5421543 3',
DEFINITION mRNA sequence.
ACCESSION  BM007071.1 GI:16521425
VERSION     EST.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 617)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: DCTD/DTT
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCW1877 row: o column: 16
            High quality sequence start: 26
            High quality sequence stop: 611.
            Location/Qualifiers
                1..617
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:5421543"

FEATURES             source
    source
    /tissue_type="ductal carcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_110"
    /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
    Site 2: EcoRI; cDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGCACGAG(G). Library constructed by
    Ling Hong in the laboratory of Gerald M. Rubin (University
    of California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library."
```

ORIGIN

```

Query Match      55.6%; Score 30; DB 2; Length 617;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||||||||||||||||||||||||||||
Db 579 GAAATTAATACGACTCACTATAGGAGACC 550

RESULT 51
BG491861/c
LOCUS      BG491861 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:4684860 3',
DEFINITION mRNA sequence.
ACCESSION  BG491861.1 GI:13453373
VERSION     EST.
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 634)
            NIH-MGC http://mgs.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: DCTD/DTT
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1493 row: h column: 13
            High quality sequence stop: 624.
            Location/Qualifiers
                1..634
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:4684860"
                /tissue_type="amelanotic melanoma, cell line"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH_MGC_41"
                /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
                EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCACGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NIH_MGC Library."
```

ORIGIN

```

Query Match      55.6%; Score 30; DB 2; Length 634;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES             source
    source
    /tissue_type="ductal carcinoma, cell line"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_110"
    /note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
    Site 2: EcoRI; cDNA made by oligo-dT priming.
    Directionally cloned into EcoRI/XhoI sites using the
    following 5' adaptor: GGCACGAG(G). Library constructed by
    Ling Hong in the laboratory of Gerald M. Rubin (University
    of California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies).
    Note: this is a NIH_MGC Library."
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Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 596 GAAATTAATACGACTCACTATAGGAGACC 567

RESULT 52
BF973256/c
LOCUS
DEFINITION 602241528F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4330039 5',
mRNA sequence.
ACCESSION BF973256
VERSION BF973256.1 GI:12340382
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 694)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10C1192 row: h column: 08
High quality sequence stop: 417.
FEATURES
Location/Qualifiers
1..694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4330039"
/tissue_type="leiomyosarcoma cell line"
/lab_hosts="DH10B (phage-resistant)"
/clone_libs="NIH_MGC_46"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 55.6%; Score 30; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 38 GAAATTAATACGACTCACTATAGGAGACC 9

RESULT 53
BE398149/c
LOCUS
DEFINITION 601290392F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620783 5',
mRNA sequence.
ACCESSION BE398149
VERSION BE398149.1 GI:9343514
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 746)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10C1293 row: g column: 24
High quality sequence start: 2
High quality sequence stop: 567.
FEATURES
Location/Qualifiers
1..746
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3620783"
/tissue_type="Burkitt lymphoma"
/lab_hosts="DH10B (phage-resistant)"
/clone_libs="NIH_MGC_8"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 55.6%; Score 30; DB 7; Length 746;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 120 GAAATTAATACGACTCACTATAGGAGACC 91

RESULT 54
BG767227/c
LOCUS
DEFINITION 602740245F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869995 5',
mRNA sequence.
ACCESSION BG767227
VERSION BG767227.1 GI:14077880
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10C1742 row: j column: 12
High quality sequence start: 2

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High quality sequence stop: 77.
Location/Qualifiers
1. .747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:486995"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 49"
/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library. ]"

ORIGIN
Query Match 55.6%; Score 30; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 44 GAAATTAATACGACTCACTATAGGAGACC 15
|||||

RESULT 55
BE397784/c
LOCUS 747 bp mRNA linear EST 21-JUL-2000
DEFINITION 601289549F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619861 5',
mRNA sequence.
ACCESSION BE397784
VERSION BE397784.1 GI:9343149
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 747)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC291 row: a column: 14
High quality sequence stop: 7
High quality sequence start: 7
Location/Qualifiers
1. .747
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3619861"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 8"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACCAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of

FEATURES
source
Query Match 55.6%; Score 30; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 127 GAAATTAATACGACTCACTATAGGAGACC 98
|||||

RESULT 57
BE397868/c
LOCUS 775 bp mRNA linear EST 21-JUL-2000
DEFINITION 601290989F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3621046 5',
mRNA sequence.
ACCESSION BE397868
VERSION BE397868.1 GI:10148706
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 774)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLC535 row: f column: 13
High quality sequence start: 2
High quality sequence stop: 160.
Location/Qualifiers
1. .774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3842316"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

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California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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mRNA sequence..
ACCESSION BE397868
VERSION BE397868.1 GI:9343233
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL Hominidae; Homo.
COMMENT 1 (bases 1 to 775)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM294 row: b column: 23
High quality sequence start: 16
High quality sequence stop: 513.
Location/Qualifiers
FEATURES
source
1..775
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3621046"
/tissue_type="Burkitt lymphoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_8"
/notes="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 55.6%; Score 30; DB 7; Length 775;  
Best Local Similarity 100.0%; Pred. No. 1.7; Length 775;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 111 GAAATTAATACGACTCACTATAGGAGACC 82

RESULT 58  
CK199881/c  
LOCUS CK199881.1  
DEFINITION FGAS008388 Triticum aestivum FGAS: Library 3 Gate 6 Triticum  
aestivum CDNA, mRNA sequence.  
ACCESSION CK199881  
VERSION CK199881.1 GI:39562271  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
JOURNAL clade; Pooidae; Triticeae; Triticum.  
COMMENT 1 (bases 1 to 793)  
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,  
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,  
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,  
Penniket, C., Roach, J.L. and Sarhan, F.  
Functional Genomics of Abiotic Stress in Wheat and Canola Crops  
Unpublished (2003)  
Contact: Wm L Crosby

Query Match 55.6%; Score 30; DB 5; Length 793;  
Best Local Similarity 86.8%; Pred. No. 1.7;  
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACATTGTGCAATA 43  
|||||  
Db 747 TAATACGACTCACTATAGGAGACCATTGTGCAAGA 710

RESULT 59  
BE391895/c  
LOCUS BE391895.1  
DEFINITION 601283033F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3604880 5',  
mRNA sequence.  
ACCESSION BE391895  
VERSION BE391895.1 GI:9337260  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
JOURNAL Hominidae; Homo.  
COMMENT 1 (bases 1 to 793)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1CM252 row: a column: 09  
High quality sequence start: 65  
High quality sequence stop: 189.  
Location/Qualifiers
FEATURES
source
1..793
/organism="Homo sapiens"

Bioinformatics  
University of Saskatchewan, Department of Computer Science  
1C101 Engineering Building, 57 Campus Drive, Saskatoon,  
Saskatchewan, S7N 5A9, Canada  
Tel: 306 966 1769  
Fax: 306 966 2033  
Email: fgas\_esta@cs.usask.ca  
This sequence is the direct result of the Base calling software  
Phred (default parameters). It is the raw base calls. To aid in the  
identification of the high quality insert the software Lucy  
(default parameters) has been run on this sequence. Lucy identified  
the region [102,627].  
Plate: L3C111 row: G column: 09.  
Location/Qualifiers
FEATURES
source
1..793
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone\_lib="Triticum aestivum FGAS: Library 3 Gate 6"  
/notes="Organ: Root; Vector: pCMV.SPORT6; Root tissue from  
control, cold-acclimated and salt stressed wheat cultivar  
Norstar. 7 mRNA populations were combined before  
constructing the library; 7 day non-acclimated roots, 1,  
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3  
hours and 6 hours treated roots with 200mM NaCl.  
Non-acclimated and cold-acclimated plants were grown in  
vermiculite while salt stressed plant were grown  
hydroponically. First strand synthesis in this library was  
done in the presence of methylated dCTP thereby protecting  
from internal cleavage with NotI."

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3604880"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match          55.6%; Score 30; DB 7; Length 793;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 157 GAAATTAATACGACTCACTATAGGAGACC 128

RESULT 60
LOCUS BE387643/c
DEFINITION 601275036F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616160 5',
mRNA sequence.
ACCESSION BE387643
VERSION BE387643.1 GI:9333008
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTp
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM281 row: g column: 09
High quality sequence start: 7
High quality sequence stop: 192.
Location/Qualifiers
1. .803
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3616160"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match          55.6%; Score 30; DB 7; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 73 GAAATTAATACGACTCACTATAGGAGACC 102

RESULT 62
LOCUS BE737520/c
DEFINITION 60130689F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640990 5',
mRNA sequence.
ACCESSION BE737520
VERSION BE737520.1 GI:10151512
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTp
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM281 row: g column: 09
High quality sequence start: 7
High quality sequence stop: 192.
Location/Qualifiers
1. .803
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/mol_type="mRNA"
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/clone="IMAGE:3616160"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 127 GAAATTAATACGACTCACTATAGGAGACC 98

RESULT 61
LOCUS BE899343
DEFINITION 601681168F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951401 5',
mRNA sequence.
ACCESSION BE899343
VERSION BE899343.1 GI:10366945
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 830)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTp
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM819 row: g column: 18
High quality sequence start: 30
High quality sequence stop: 228.
Location/Qualifiers
1. .830
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951401"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match          55.6%; Score 30; DB 7; Length 830;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
Db 73 GAAATTAATACGACTCACTATAGGAGACC 102

RESULT 62
LOCUS BE737520/c
DEFINITION 60130689F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640990 5',
mRNA sequence.
ACCESSION BE737520
VERSION BE737520.1 GI:10151512
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 803)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTp
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM281 row: g column: 09
High quality sequence start: 7
High quality sequence stop: 192.
Location/Qualifiers
1. .803
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/notes="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 909)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LCM346 row: a column: 23  
High quality sequence start: 3  
High quality sequence stop: 271.

FEATURES  
source

1..909  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:3640990"  
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/clone\_lib="NIH\_MGC\_39"  
/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 909;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
Db 120 GAAATTAATACGACTCACTATAGGAGACC 91

RESULT 63  
BE391677/c

LOCUS BE391677 932 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601284594F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3606310 5', mRNA sequence.

ACCESSION BE391677  
VERSION BE391677.1 GI:9337042  
KEYWORDS EST.

SOURCE  
ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 932)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LCM255 row: l column: 23  
High quality sequence start: 3  
High quality sequence stop: 166.

FEATURES  
source

1..932  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3606310"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 932;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
Db 118 GAAATTAATACGACTCACTATAGGAGACC 89

RESULT 64  
BE379428/c

LOCUS BE379428 944 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601237292F1 NIH\_MGC\_44 Homo sapiens CDNA clone IMAGE:3609287 5', mRNA sequence.

ACCESSION BE379428  
VERSION BE379428.1 GI:9324793  
KEYWORDS EST.

SOURCE  
ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 944)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LCM263 row: h column: 24  
High quality sequence start: 25  
High quality sequence stop: 644.

FEATURES  
source

1..944  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3609287"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"

/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
Query Match 55.6%; Score 30; DB 7; Length 944;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 119 GAAATTAATACGACTCACTATAGGAGACC 90

RESULT 65  
LOCUS BE515297/c 952 bp mRNA linear EST 07-AUG-2000  
DEFINITION 601235832F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3608286 5',  
mRNA sequence.

ACCESSION BE515297  
VERSION BE515297.1 GI:9722512  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 952)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LCM260 row: o column: 07  
High quality sequence stop: 447.  
Location/Qualifiers

FEATURES  
source

1..952  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3608286"  
/tissue\_type="endometrium, adenocarcinoma cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_44"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN  
Query Match 55.6%; Score 30; DB 7; Length 952;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 121 GAAATTAATACGACTCACTATAGGAGACC 92

RESULT 66  
LOCUS BE263035/c 978 bp mRNA linear EST 26-OCT-2000  
DEFINITION 601147095F1 NIH\_MGC\_19 Homo sapiens cDNA clone IMAGE:3162455 5',  
mRNA sequence.

ACCESSION BE263035  
VERSION BE263035.1 GI:9136565  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 978)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LCM121 row: n column: 24  
High quality sequence start: 94  
High quality sequence stop: 214.  
Location/Qualifiers

FEATURES  
source

1..978  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3162455"  
/tissue\_type="neuroblastoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_19"  
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 978;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
|||||  
Db 179 GAAATTAATACGACTCACTATAGGAGACC 150

RESULT 67  
BE391793/c

LOCUS BE391793 986 bp mRNA linear EST 21-JUL-2000  
DEFINITION 601282531F1 NIH\_MGC\_44 Homo sapiens cDNA clone IMAGE:3604422 5',  
mRNA sequence.

ACCESSION BE391793  
VERSION BE391793.1 GI:9337158  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 986)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM250 row: n column: 07  
 High quality sequence start: 53  
 High quality sequence stop: 187.

#### FEATURES

Location/Qualifiers

1..986

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:360442"

/tissue\_type="endometrium, adenocarcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_44"

/note="Organ: uterus; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 986;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

|||||

Db 153 GAAATTAATACGACTCACTATAGGAGACC 124

#### RESULT 68

BE749185/c

LOCUS

DEFINITION 601123490F1 NIH\_MGC\_5 Homo sapiens cDNA clone IMAGE:3348070 5',  
 mRNA sequence.

ACCESSION BE749185

VERSION BE749185.1 GI:10163177

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 986)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLCM140 row: d column: 23

High quality sequence start: 44

High quality sequence stop: 324.

#### FEATURES

source

1..986

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3348070"

/tissue\_type="carcinoma cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_5"

/note="Organ: cervix; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 986;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

|||||

Db 104 GAAATTAATACGACTCACTATAGGAGACC 75

#### RESULT 69

BE730535/c

LOCUS

DEFINITION 601562507F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3832128 5',  
 mRNA sequence.

ACCESSION BE730535

VERSION BE730535.1 GI:10144436

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 1064)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: ATCC/DCTP/DRP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)

Plate: LLCM508 row: n column: 01

High quality sequence start: 62

High quality sequence stop: 613.

#### FEATURES

source

1..1064

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3832128"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_20"

/note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 55.6%; Score 30; DB 7; Length 1064;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30

|||||

Db 108 GAAATTAATACGACTCACTATAGGAGACC 79



```

RESULT 70
BF689216/c
LOCUS
DEFINITION
602184894T1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4299407 3',
mRNA sequence.
ACCESSION
BF689216
VERSION
BF689216.1 GI:11974624
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1070)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L16W1156 row: k column: 24
High quality sequence start: 4
High quality sequence stop: 489.
Location/Qualifiers
1..1070
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4299407"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally_2:
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
ORIGIN
Query Match 55.6%; Score 30; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
|||||
Db 455 GAAATTAATACGACTCACTATAGGAGACC 426

RESULT 71
BQ102683/c
LOCUS
DEFINITION
BQ102683 Drosophila 8-12 hr embryonic cDNA library Drosophila
melanogaster cDNA 5', mRNA sequence.
ACCESSION
BQ102683
VERSION
BQ102683.1 GI:20144166
KEYWORDS
EST.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 451)
REFERENCE
1 (bases 1 to 451)
Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,
Mecherall,J.E. and Letsou,A.

TITLE
An automated screen for spatially restricted transcripts in
Drosophila embryogenesis
JOURNAL
Genome Res. (2002) In press
COMMENT
Contact: Letsou, A.
Department of Human Genetics
Eccles Institute of Human Genetics, University of Utah
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA
Tel: 801 581-4422
Fax: 801 581-7796
Email: alestou@genetics.utah.edu
Seq primer: SP6.
Location/Qualifiers
1..451
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/dev_stages="embryonic 8-12 hr post-fertilization"
/clone_lib="Drosophila 8-12 hr embryonic cDNA library"
/notes="Vector: plasmid pNB; see Brown, N.H. and Kafatos,
F.C. (1988) Functional cDNA libraries from Drosophila
embryos. J. Mol Biol. 203, 425-37."
ORIGIN
Query Match 54.1%; Score 29.2; DB 3; Length 451;
Best Local Similarity 88.6%; Pred. No. 3.2;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATT 35
|||||
Db 54 GAAATTAATACGACTCACTATAGGAGCCGCAAT 20

RESULT 72
BE946471
LOCUS
DEFINITION
BE946471 373 bp mRNA linear EST 03-OCT-2000
UI-M-BZ0-axu-e-01-0-UI.s1 NIH BMAP_MH12 Mus musculus cDNA clone
UI-M-BZ0-axu-e-01-0-UI 3', mRNA sequence.
ACCESSION
BE946471
VERSION
BE946471.1 GI:10524230
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 373)
REFERENCE
1 (bases 1 to 373)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: m5t@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
hippocampus tissue cDNA library preparation. M.B. Soares Lab Clone
distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
GENETICS. It should be noted that Bento Soares is generating a
small number of additional specialized non-redundant arrays of BMAP
cDNAs whose availability will be considered under appropriate and
limited collaborative arrangements
Seq primer: M13 Forward
POLYA=yes.
Location/Qualifiers
1..373
FEATURES
source

```

```

/notes/vectors/WT73D.pptx; Site 1: Not 1, Site 2: Eco RI;
The NIH MAP WH12 library is derived from most of
the hippocampus tissue. For a detailed description of the
library from which this clone was derived, please visit
our web site at brainset.eng.uiowa.edu.
TAG TISSUE=hippocampus
TAG LIB=NIH MAP_WH12
TAG SEQ=CGGNA"
TAG_SEQ=CGGNA"

```

**LOCUS** AG398203 /23 bp DNA linear GSS 21-DEC-2000  
**DEFINITION** *Mus musculus* molossinus DNA, clone:MSMg01-172D11.T7, genomic survey sequence.

**AUTHORS** Simin,K., Scuderi,A., Reamey,J., Dunn,D.M., Weiss,R.B.,  
Metherall,J.E. and Letsou,A.  
**TITLE** An automated screen for spatially restricted transcripts in  
Drosophila embryogenesis  
**JOURNAL** Genome Res. (2002) In press  
**COMMENT** Contact: Letsou, A.  
Department of Human Genetics  
Eccles Institute of Human Genetics, University of Utah  
15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA  
Tel: 801 581-4422  
Fax: 801 581-7796  
Email: aletsou@genetics.utah.edu  
Seq primer: SP6.  
**FEATURES**  
source  
1..452  
Location/Qualifiers  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/dev\_stage="embryonic 8-12 hr post-fertilization"  
/clone\_lib="Drosophila 8-12 hr embryonic cDNA library"  
/note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,  
F.C. (1988) Functional cDNA libraries from Drosophila  
embryos. J. Mol Biol. 203, 425-37."  
**ORIGIN**  
Query Match 53.0%; Score 28.6; DB 3; Length 452;  
Best Local Similarity 88.6%; Pred. No. 5.4;  
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
**QY** 1 GAAATTATACGACTCACTATAGGAGACCACTT 35  
|||||  
**Db** 59 GAAATTATACGACTCACTATAGGAGACCGGAAT 25  
|||||  
**RESULT 76**  
BE410822/c 214 bp mRNA linear EST 21-JUL-2000  
**LOCUS** 601301472F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:3636328 5',  
mRNA sequence.  
**DEFINITION** BE410822  
**ACCESSION** BE410822.1 GI:9347272  
**VERSION** EST.  
**KEYWORDS** Homo sapiens  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 214)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM333 row: o column: 17  
High quality sequence start: 63  
High quality sequence stop: 161.  
Location/Qualifiers  
**FEATURES**  
source  
1..214  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3636328"  
/tissue\_type="choriocarcinoma"  
/lab\_host="PH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_21"  
/note="Organ: placenta; Vector: pOTB7; Site: 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
for average insert size 1.8kb. Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
**ORIGIN**  
Query Match 52.6%; Score 28.4; DB 7; Length 214;  
Best Local Similarity 96.7%; Pred. No. 5.8;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**QY** 1 GAAATTATACGACTCACTATAGGAGACC 30  
|||||  
**Db** 131 GAAATTATACGACTCACTATAGGAGACC 102  
|||||  
**RESULT 77**  
CD625578 717 bp mRNA linear EST 12-JAN-2004  
**LOCUS** 55147850H1 FLP Homo sapiens cDNA, mRNA sequence.  
**DEFINITION** CD625578  
**ACCESSION** CD625578  
**VERSION** CD625578.1 GI:40273844  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 717)  
**AUTHORS** Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.  
**TITLE** Circular rapid amplification of cDNA ends for high-throughput  
extension cloning of partial genes  
**JOURNAL** Genomics 84 (1), 205-210 (2004)  
**PUBMED** 15203218  
**COMMENT** Contact: Fu GK  
Incyte Genomics, Inc.  
3160 Porter Dr., Palo Alto, CA 94304, USA  
Tel: 6508454102  
Email: gfu@incyte.com.  
**FEATURES**  
source  
1..717  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone\_lib="FLP"  
/note="Vector: pDrive Cloning Vector"  
**ORIGIN**  
Query Match 52.6%; Score 28.4; DB 5; Length 717;  
Best Local Similarity 76.1%; Pred. No. 6.9;  
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
**QY** 6 TAATACGACTCACTATAGGAGACCACTTGTGCAATATTCCTCCAC 51  
|||||  
**Db** 1 TAATACGACTCACTATAGGAGACCACTGTGAGGAGGTGCCCGAC 46  
|||||  
**RESULT 78**  
AG397294 730 bp DNA linear GSS 21-DEC-2004  
**LOCUS** AG397294  
**DEFINITION** Mus musculus molossinus DNA, clone:MSMg01-217P04.T7, genomic survey  
sequence.  
**ACCESSION** AG397294  
**VERSION** AG397294.1 GI:48032406  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus molossinus (Japanese wild mouse)  
**ORGANISM** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1  
**AUTHORS** Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,

Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.  
 Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis  
 Genome Res. 14 (12), 2439-2447 (2004)

JOURNAL PUBLISHED 15574823  
 REFERENCE 2 (bases 1 to 730)  
 AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  
 COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp  
 PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBACe3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI.

#### FEATURES

source  
 Location/Qualifiers  
 1..730  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-21P04.T7"  
 /sex="male"  
 /tissue type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

#### ORIGIN

Query Match 52.6%; Score 28.4; DB 14; Length 730;  
 Best Local Similarity 76.1%; Pred. No. 6.9;  
 Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 6 TAATACGACTCCTATAGGAGACACATTCTGCAATATCCCCAC 51  
 |||||  
 Db 18 TAATACGACTCCTATAGGAGAGGATCCCGGAATTTTACAC 63

RESULT 79  
 BE737118/c  
 LOCUS BE737118 784 bp mRNA linear EST 15-SEP-2000  
 DEFINITION 601304503F1 NIH\_MGC\_39 Homo sapiens cDNA clone IMAGE:3638784 5', mRNA sequence.  
 ACCESSION BE737118  
 VERSION BE737118.1 GI:10151110  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 784)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium (LLNL) at:

found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LICM440 row: f column: 01  
 High quality sequence start: 23  
 High quality sequence stop: 157.  
 Location/Qualifiers

#### FEATURES

source  
 1..784  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3638784"  
 /tissue\_type="adenocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_39"  
 /note="Organ: pancreas; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dr priming.  
 Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 52.6%; Score 28.4; DB 7; Length 784;  
 Best Local Similarity 96.7%; Pred. No. 7;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCTATAGGAGACC 30  
 |||||  
 Db 118 GAAATTAATACGACTCGCTATAGGAGACC 89

RESULT 80  
 BG491171/c  
 LOCUS BG491171 826 bp mRNA linear EST 27-MAR-2001  
 DEFINITION 602535205F1 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:4654152 5', mRNA sequence.  
 ACCESSION BG491171  
 VERSION BG491171.1 GI:13452683  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 826)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCFD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LICM1441 row: i column: 01  
 High quality sequence start: 46  
 High quality sequence stop: 145.  
 Location/Qualifiers

#### FEATURES

source  
 1..826  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4654152"  
 /tissue\_type="amelanotic melanoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_41"  
 /note="Organ: skin; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:  
GCCACGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 52.6%; Score 28.4; DB 2; Length 826;  
Best Local Similarity 96.7%; Pred. No. 7.1;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAATTATACGACTCACTATAGGAGACC 30  
|||||  
Db 111 GAAATTATACGACTCACTATAGGAGACC 82  
|||||

## RESULT 81

BE727309/c  
LOCUS BE727309 910 bp mRNA linear EST 15-SEP-2000  
DEFINITION 601560609F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:3830282 5',  
mRNA sequence.

ACCESSION BE727309

VERSION BE727309.1

KEYWORDS GI:10141402

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 910)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM504 row: a column: 03

High quality sequence start: 7

High quality sequence stop: 109.

## FEATURES

source

1..910  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3830282"  
/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_20"  
/note="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site: 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GCCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 52.6%; Score 28.4; DB 7; Length 910;  
Best Local Similarity 96.7%; Pred. No. 7.2;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAATTATACGACTCACTATAGGAGACC 30  
|||||

Db 75 GAAATTATACGACTCACTATAGAGACC 46  
|||||

## RESULT 82

BG490614/c

LOCUS BG490614

DEFINITION 602519576F1 NIH\_MGC\_18 Homo sapiens cDNA clone IMAGE:4638019 5',  
mRNA sequence.

ACCESSION BG490614

VERSION BG490614.1

KEYWORDS GI:13452124

SOURCE EST.

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1150)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTF/Gazdar

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1399 row: h column: 20

High quality sequence stop: 120.

## FEATURES

source

1..1150  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4638019"  
/tissue\_type="large cell carcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_18"  
/note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site: 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCACGAG(G). Library constructed by Ling Hong in the  
Laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

## ORIGIN

Query Match 52.6%; Score 28.4; DB 2; Length 1150;  
Best Local Similarity 96.7%; Pred. No. 7.4;  
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GAAATTATACGACTCACTATAGGAGACC 30  
|||||

Db 84 GAAATTATACGACTCACTATAGGAGACC 55  
|||||

## RESULT 83

DR138757/c

LOCUS DR138757

DEFINITION 49194855 Drosophila pseudoobscura embryonic cDNA library Drosophila  
pseudoobscura cDNA clone Al3 5', mRNA sequence.

ACCESSION DR138757

VERSION DR138757.1

KEYWORDS GI:67883847

SOURCE EST.

ORGANISM Drosophila pseudoobscura

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Richards S., Liu Y., Bettencourt B.R., Hradscky P., Letovsky S.,  
Nielsen R., Thornton K., Hubisz M.J., Chen R., Meisel R.P.,  
Couronne O., Hua S., Smith M.A., Zhang P., Liu J., Bussemaker H.J.,

van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E.,  
 Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,  
 Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,  
 Wheeler, D.A., Worley, K.C., Havlik, P., Durbin, K.J., Egan, A.,  
 Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,  
 Waldron, L., Verdusco, D., Clerc-Blankenburg, K.P., Dubchak, I.,  
 Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,  
 Gelbart, W., Weinstein, G.M., and Gibbs, R.A.  
 Comparative genome sequencing of *Drosophila pseudoobscura*:  
 Chromosomal, gene, and cis-element evolution  
 Genome Res. 15 (1), 1-18 (2005)  
 15632085  
 Contact: Stephen Richards  
 Human Genome Sequencing Center  
 Baylor College of Medicine  
 One Baylor Plaza, Houston, TX 77030, USA  
 Tel: 713-798-6667  
 Email: stephenr@bcm.tmc.edu  
 NCBI Trace Archive: 226708009  
 Insert Length: 1750 Std Error: 0.25.

## FEATURES

source  
 1..1201  
 /organism="Drosophila pseudoobscura"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7237"  
 /clone="Al3"  
 /dev\_stage="0-18h embryos"  
 /clone\_lib="Drosophila pseudoobscura embryonic cDNA  
 library"  
 /note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo  
 dt priming from poly A+ RNA, directionally cloned"

## ORIGIN

Query Match 52.6%; Score 28.4; DB 9; Length 1201;  
 Best Local Similarity 96.7%; Pred. No. 7.4;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30  
 |||||  
 Db 502 GAAATTTATACGACTCACTATAGGAGACC 473

RESULT 84  
 BQ102668/c  
 LOCUS BQ102668 403 bp mRNA linear EST 12-APR-2002  
 DEFINITION U08C0047 Drosophila 8-12 hr embryonic cDNA library Drosophila  
 melanogaster cDNA 5', mRNA sequence.

ACCESSION BQ102668  
 VERSION BQ102668.1 GI:20144151  
 KEYWORDS EST.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 403)  
 AUTHORS Simin, K., Scuderi, A., Reaney, J., Dunn, D.M., Weiss, R.B.,  
 Metherell, J.E. and Letsou, A.

TITLE An automated screen for spatially restricted transcripts in  
 Drosophila embryogenesis  
 JOURNAL Genome Res. (2002) In press  
 COMMENT Department of Human Genetics  
 Eccles Institute of Human Genetics, University of Utah  
 15 N 2030 EAST RM 2100, Salt Lake City, UT 84112-5330, USA  
 Tel: 801 581-4422  
 Fax: 801 581-7796  
 Email: aletsou@genetics.utah.edu  
 Seq primer: SP6

## FEATURES

source  
 1..403  
 /organism="Drosophila melanogaster"  
 /mol\_type="mRNA"

/db\_xref="taxon:7227"  
 /dev\_stage="embryonic 8-12 hr post-fertilization"  
 /clone\_lib="Drosophila 8-12 hr embryonic cDNA library"  
 /note="Vector: plasmid pNB; see Brown, N.H. and Kafatos,  
 F.C. (1988) Functional cDNA libraries from *Drosophila*  
 embryos. J. Mol Biol. 203, 425-37."

## ORIGIN

Query Match 52.2%; Score 28.2; DB 3; Length 403;  
 Best Local Similarity 90.9%; Pred. No. 7.6;  
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AATTAATACGACTCACTATAGGAGACCACTT 35  
 |||||  
 Db 51 AATTAATACGACTCACTATAGGAGACCGGAAT 19

## RESULT 85

CD629304  
 LOCUS CD629304 707 bp mRNA linear EST 12-JAN-2004  
 DEFINITION S514282SH1 FLP Homo sapiens cDNA, mRNA sequence.  
 ACCESSION CD629304  
 VERSION CD629304.1 GI:40277570  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 707)  
 AUTHORS Fu, G.K., Wang, J.T., Yang, J., Au-Young, J. and Stuve, L.L.  
 TITLE Circular rapid amplification of cDNA ends for high-throughput  
 extension cloning of partial genes  
 JOURNAL Genomics 84 (1), 205-210 (2004)  
 PUBMED 15203218  
 COMMENT Incyte Genomics, Inc.  
 Contact: Fu GK  
 3160 Porter Dr., Palo Alto, CA 94304, USA  
 Tel: 6508454102  
 Email: gfu@incyte.com.

## FEATURES

source  
 1..707  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone\_lib="FLP"  
 /note="Vector: pDrive Cloning Vector"

## ORIGIN

Query Match 52.2%; Score 28.2; DB 5; Length 707;  
 Best Local Similarity 73.5%; Pred. No. 8.3;  
 Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACTTGTGCAATATCCCACTGC 54  
 |||||  
 Db 1 TAATACGACTCACTATAGGAGACCACTGTGCTGAAAGTCGCTCAGC 49

## RESULT 86

AG399005  
 LOCUS AG399005 737 bp DNA linear GSS 21-DEC-2004  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-232110.T7, genomic survey  
 sequence.

ACCESSION AG399005  
 VERSION AG399005.1 GI:48037712  
 KEYWORDS GSS.  
 SOURCE Mus musculus molossinus  
 ORGANISM Mus musculus molossinus (Japanese wild mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,

Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and Shiroishi,T.  
 Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis  
 Genome Res. 14 (12), 2439-2447 (2004)  
 15574823  
 2 (bases 1 to 737)  
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.  
 Direct Submission  
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan  
 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
 (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 Tsukuba Institute, Bio Resource Center,  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp  
 PRIMERS  
 Sequencing : T7  
 LIBRARY  
 Vector : pBAC3.6  
 R.Site 1 : EcoRI  
 R.Site 2 : EcoRI

#### FEATURES

source  
 1..737  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-232110.T7"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

#### ORIGIN

Query Match 52.2%; Score 28.2; DB 14; Length 737;  
 Best Local Similarity 73.5%; Pred.No. 8.3;  
 Matches 36; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
 QY 6 TAATACGACTACTATAGGAGACCATTTGCAATATCCCACTGC 54  
 |||||  
 Db 18 TAATACGACTACTATAGGAGAGGACTCCGGGATTCATCACTAC 66  
 |||||

RESULT 87  
 BE749102/c  
 LOCUS 601123149F1 NIH\_MGC\_5 Homo sapiens cDNA clone IMAGE:3347988 5',  
 mRNA sequence.  
 BE749102  
 DEFINITION BE749102.1 GI:10163094  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1507)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium at:  
 http://image.llnl.gov

#### FEATURES

source

1..1507  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3347988"  
 /tissue\_type="carcinoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_5"  
 /note="Organ: cervix; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
 (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 52.2%; Score 28.2; DB 7; Length 1507;  
 Best Local Similarity 90.9%; Pred.No. 9.2;  
 Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GAATTAATACGACTCACTATAGGAGACCA 33  
 |||||  
 Db 68 GAATTAATACGACTCACTATAGGAGAACGGCA 36  
 |||||

#### RESULT 88

BE749102/c  
 LOCUS 602436407F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4554433 5',  
 mRNA sequence.  
 BE749102  
 DEFINITION BE749102.1 GI:13145090  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 385)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium at:  
 http://image.llnl.gov

#### FEATURES

source

1..385  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4554433"  
 /tissue\_type="leiomyosarcoma cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_46"  
 /note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size  
 GGCACGAG(G). Size-selected >500bp for average insert size

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
 Plate: LLCM140 row: a column: 13  
 High quality sequence start: 38  
 High quality sequence stop: 273.  
 Location/Qualifiers

1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 51.9%; Score 28; DB 2; Length 385;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 3 AATTAAATACGACTCTACTATAGGAGACC 30  
|||||  
Db 314 AATTAAATACGACTCTACTATAGGAGACC 287

RESULT 89

BG438290/c  
LOCUS  
DEFINITION BG438290 648 bp mRNA linear EST 14-MAR-2001  
TCB36.4\_C02.T7 Tribolium BAC library Tribolium castaneum genomic,  
genomic survey sequence.

ACCESSION

VERSION BG438290.1 GI:13344796

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE

1 (bases 1 to 648)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTF/Gazdar  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM1384 row: m column: 09  
High quality sequence start: 8  
High quality sequence stop: 128.

FEATURES

source

1..648

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4621616"

/tissue\_type="large cell carcinoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC 18"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 51.9%; Score 28; DB 2; Length 648;  
Best Local Similarity 100.0%; Pred. No. 9.7;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AATTAAATACGACTCTACTATAGGAGACC 30

|||||

Db 91 AATTAAATACGACTCTACTATAGGAGACC 64

RESULT 90

CW951343/c

LOCUS

DEFINITION TC36.4\_C02.T7 Tribolium BAC library Tribolium castaneum genomic,  
genomic survey sequence.

ACCESSION

VERSION CW951343.1 GI:56734380

KEYWORDS

SOURCE Tribolium castaneum (red flour beetle)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
Tenebrionidae; Tribolium.

REFERENCE

1 (bases 1 to 907)

AUTHORS

Savard, J. and Tautz, D.

TITLE

Tribolium castaneum BAC-ends sequencing project

JOURNAL

Unpublished (2003)

COMMENT

Contact: Savard, J.

Abteilung fur Evolutionsgenetik, AG Tautz

Institut fur Genetik, Universitat zu Koln

Weyertal 121, 50931 Koln, Germany

Tel: 49 221 470 6911

Fax: 49 221 470 5975

Email: [savard@uni-koeln.de](mailto:savard@uni-koeln.de)

Class: BAC ends

FEATURES

source

1..907

/organism="Tribolium castaneum"

/mol\_type="genomic DNA"

/strain="GA-2"

/db\_xref="taxon:7070"

/clone\_lib="Tribolium BAC library"

/note="vector: pBACE3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Library constructed by Exelixis Inc."

ORIGIN

Query Match 51.9%; Score 28; DB 13; Length 907;

Best Local Similarity 71.2%; Pred. No. 10;

Matches 37; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCCACTG 53

|||||

Db 66 AAATTAATACGACTCACTATAGGAGTCTATAGGCGATTATACGCTCGAATG 15

RESULT 91

AG375696

LOCUS

DEFINITION AG375696 704 bp DNA linear GSS 21-DEC-2004  
Mus musculus molossinus DNA, clone:MSMg01-182P08.TJ, genomic survey  
sequence.

ACCESSION

VERSION AG375696.1 GI:47986901

KEYWORDS

SOURCE GSS.

ORGANISM

Mus musculus molossinus (Japanese wild mouse)

Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Muridae; Mus.

REFERENCE

Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,

Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and

Shiroishi, T.

Contribution of Asian mouse subspecies Mus musculus molossinus to

genomic constitution of strain C57BL/6J, as defined by BAC-end

sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 704)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Title

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan



(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center, (RIKEN) 3-1-1  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

PRIMERS  
Sequencing : T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI

FEATURES  
source  
Location/Qualifiers  
1..704  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSMg01-182P08.TJ"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN  
Query Match 51.5%; Score 27.8; DB 14; Length 704;  
Best Local Similarity 74.5%; Pred. No. 12;  
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACACACATTGTGCAATATTCCTCCACT 52  
|||||  
DB 18 TAATACGACTCACTATAGGAGATCGCGGAATTCCTACCCACT 64  
|||||

RESULT 92  
AG366526 707 bp DNA linear GSS 21-DEC-2004  
LOCUS Mus musculus molossinus DNA, clone: MSMg01-169M02.T7, genomic survey  
DEFINITION sequence.  
ACCESSION AG366526.1 GI:47977731  
VERSION AG366526  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and  
Shiroishi, T.  
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)  
PUBMED 15574823  
REFERENCE 2 (bases 1 to 707)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

PRIMERS  
Sequencing : T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI

FEATURES  
source  
Location/Qualifiers  
1..707  
/organism="Mus musculus molossinus"  
/mol\_type="genomic DNA"  
/sub\_species="molossinus"  
/db\_xref="taxon:57486"  
/clone="MSMg01-169M02.T7"  
/sex="male"  
/tissue\_type="mixture of kidney and spleen"  
/clone\_lib="MSMg01 Mouse Male BAC Library"

ORIGIN  
Query Match 51.5%; Score 27.8; DB 14; Length 707;  
Best Local Similarity 74.5%; Pred. No. 12;  
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACACACATTGTGCAATATTCCTCCACT 52  
|||||  
DB 18 TAATACGACTCACTATAGGAGATCGCGGAATTCCTACCCACT 64  
|||||

RESULT 93  
AG409074 737 bp DNA linear GSS 21-DEC-2004  
LOCUS Mus musculus molossinus DNA, clone: MSMg01-268L24.T7, genomic survey  
DEFINITION sequence.  
ACCESSION AG409074  
VERSION AG409074.1 GI:48051760  
KEYWORDS GSS.  
SOURCE Mus musculus molossinus (Japanese wild mouse)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and  
Shiroishi, T.  
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to  
genomic constitution of strain C57BL/6J, as defined by BAC-end  
sequence-SNP analysis  
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)  
PUBMED 15574823  
REFERENCE 2 (bases 1 to 737)  
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
(E-mail: hattori@sc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC  
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
Tsukuba Institute, Bio Resource Center,  
The Institute of Physical and Chemical Research (RIKEN) 3-1-1  
Koyadai, Tsukuba, 305-0074 Japan  
phone: 81-298-36-9189, fax: 81-298-36-9199  
e-mail: abe@rtc.riken.jp

PRIMERS  
Sequencing : T7  
LIBRARY  
Vector : pBACe3.6  
R.Site 1 : EcoRI  
R.Site 2 : EcoRI

FEATURES  
source  
Location/Qualifiers  
1..737  
/organism="Mus musculus molossinus"

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/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-268L24.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

```

## ORIGIN

```

Query Match      51.5%; Score 27.8; DB 14; Length 737;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATTCCTCCACT 52
        |||||
Db      18 TAATACGACTCATTAGGAGAGGATCCGCGGAATCTTTCCCACT 64

```

```

RESULT 94
AG409684
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-269J20.T7, genomic survey
sequence.
ACCESSION AG409684
VERSION AG409684.1 GI:48052370
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
        Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
        Shiroishi,T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
        genomic constitution of strain C57BL/6J, as defined by BAC-end
        sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823

```

```

REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
        and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
        1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
        (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
        Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
        library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
        Tsukuba Institute, Bio Resource Center,
        The Institute of Physical and Chemical Research (RIKEN) 3-1-1
        Koyadai, Tsukuba, 305-0074 Japan
        phone: 81-298-36-9189, fax: 81-298-36-9199
        e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
            1..742
                /organism="Mus musculus molossinus"
                /mol_type="genomic DNA"
                /sub_species="molossinus"
                /db_xref="taxon:57486"
                /clone="MSMg01-269J20.T7"
                /sex="male"
                /tissue_type="mixture of kidney and spleen"
                /clone_lib="MSMg01 Mouse Male BAC Library"

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## ORIGIN

```

Query Match      51.5%; Score 27.8; DB 14; Length 742;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATTCCTCCACT 52
        |||||
Db      14 TAATACGACTCATTAGGAGAGATCCGCGGAATCTTCTCCTCACT 60

```

```

RESULT 95
AG357071
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-156E17.T7, genomic survey
sequence.
ACCESSION AG357071
VERSION AG357071.1 GI:47930381
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
        Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaki,K. and
        Shiroishi,T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
        genomic constitution of strain C57BL/6J, as defined by BAC-end
        sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823

```

```

REFERENCE
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
        and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
        1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
        (E-mail:hattori@psc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
        Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
        library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
        Tsukuba Institute, Bio Resource Center,
        The Institute of Physical and Chemical Research (RIKEN) 3-1-1
        Koyadai, Tsukuba, 305-0074 Japan
        phone: 81-298-36-9189, fax: 81-298-36-9199
        e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES Location/Qualifiers
            1..743
                /organism="Mus musculus molossinus"
                /mol_type="genomic DNA"
                /sub_species="molossinus"
                /db_xref="taxon:57486"
                /clone="MSMg01-156E17.T7"
                /sex="male"
                /tissue_type="mixture of kidney and spleen"
                /clone_lib="MSMg01 Mouse Male BAC Library"

```

## ORIGIN

```

Query Match      51.5%; Score 27.8; DB 14; Length 743;
Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

```

```

Qy      6 TAATACGACTCATTAGGAGACACATTGTGCAATATTCCTCCACT 52
        |||||
Db      17 TAATACGACTCATTAGGAGAGATCCGCGGAATCTTCTCCTCACT 63

```

```

RESULT 96
AG377287
LOCUS
DEFINITION
Mus musculus molossinus DNA, clone:MSMg01-185D18.T7, genomic survey
sequence.
ACCESSION
AG377287
VERSION
AG377287.1
KEYWORDS
GI:47988492
SOURCE
Mus musculus molossinus (Japanese wild mouse)
ORGANISM
Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
Shiroishi,T.
Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
Genome Res. 14 (12), 2439-2447 (2004)
15574823
2 (bases 1 to 767)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source
Location/Qualifiers
1..767
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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Best Local Similarity 74.5%; Pred. No. 12;
Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 6 TAATAGCACTACTATAGGAGACCATTTGTCGAATATTTCCCACT 52
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Db 31 TAATAGCACTACTATAGGAGGATCCGCGGAATTTCTTCCCACT 77
|||||
RESULT 97
CT010966
LOCUS
DEFINITION
KBRH118G04 genomic clone, KBRH (HindIII) BAC library Brassica rapa
subsp. pekinensis, genomic survey sequence.
ACCESSION
CT010966
VERSION
CT010966.1
KEYWORDS
GI:71479007
SOURCE
Brassica rapa subsp. pekinensis

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ORGANISM
Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE
1
Viehöver,P., Holtgraewe,D. and Weisshaar,B.
BAC end sequences of Brassica rapa
Unpublished
2 (bases 1 to 874)
Li,Y. and Weisshaar,B.
Direct Submission
Submitted (09-AUG-2005) Weisshaar B., Bielefeld University,
Institute for Genome Research, Universitätsstrasse 25, D-33594
Bielefeld, Germany
Contact: Bernd Weisshaar
Bielefeld University, Institute for Genome Research
Universitätsstrasse 25, D-33594 Bielefeld, Germany Email:
bernd.weisshaar@uni-bielefeld.de
BAC end sequences of Brassica rapa BAC clone KBRH118G04; generated
as contribution to the 'Multinational Brassica rapa Sequencing
Project' Seq primer: sp6B ATTTAGGTGACACTATAG
Class: BAC ends.
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Location/Qualifiers
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/cultivar="Chiifu"
/sub_species="pekinensis"
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GF-SCF-1002, Vector: pCUGIBac1"
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RESULT 98
CW946685
LOCUS
DEFINITION
TCB29.4 A01.T7 Tribolium BAC library Tribolium castaneum genomic,
genomic survey sequence.
ACCESSION
CW946685
VERSION
CW946685.1
KEYWORDS
GI:56729300
SOURCE
Tribolium castaneum (red flour beetle)
ORGANISM
Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
Tenebrionidae; Tribolium.
1 (bases 1 to 897)
Savard,J. and Tautz,D.
Tribolium castaneum BAC-ends sequencing project
Unpublished (2003)
Contact: Savard, J.
Abteilung für Evolutionsgenetik, AG Tautz
Institut für Genetik, Universität zu Köln
Weyertal 121, 50931 Köln, Germany
Tel: 49 221 470 6911
Fax: 49 221 470 5975
Email: savard@uni-koeln.de
Class: BAC ends.
FEATURES
source
Location/Qualifiers
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Matches 33; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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RESULT 99
BH501537
LOCUS BH501537 317 bp DNA linear GSS 13-DEC-2001
DEFINITION BOHSZ75TF BOHS Brassica oleracea genomic clone BOHSZ75, genomic
survey sequence.
ACCESSION BH501537
VERSION BH501537.1 GI:17709634
KEYWORDS GSS
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 317)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
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Location/Qualifiers
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ORIGIN
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Best Local Similarity 96.6%; Pred. NO. 15;
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Db 19 AATTAATACGACTCACTATAGGAGACGA 47

RESULT 100
BH523081
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DEFINITION BOGJM68TF BOGJ Brassica oleracea genomic clone BOGJM68, genomic
survey sequence.
ACCESSION BH523081

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VERSION BH523081.1 GI:17731166
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 317)
AUTHORS Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
TITLE Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
JOURNAL Genome Res. 15 (4), 487-495 (2005)
PUBMED 15805490
COMMENT Contact: Chris Town
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
FEATURES
source
Location/Qualifiers
1..317
/organism="Brassica oleracea"
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genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN
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Db 19 AATTAATACGACTCACTATAGGAGACGA 47

Search completed: May 19, 2006, 07:06:15
Job time : 3625.49 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 165.253 Seconds  
(without alignments)  
611.425 Million cell updates/sec

Title: US-10-665-708-11

Perfect score: 54

Sequence: 1 gaattataacgactcacta.....tgtgaattatccccactgc 54

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents\_NA.\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5/COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A/COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B/COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7/COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H/COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCFUS.COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP.COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE.COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	41	75.9	57	3	US-09-738-274-10	Sequence 10, Appl	
4	40	74.1	59	3	US-09-738-274-9	Sequence 9, Appl	
5	37.6	69.6	54	3	US-09-944-036-9	Sequence 9, Appl	
6	37.6	69.6	54	3	US-10-425-975-9	Sequence 9, Appl	
7	37	68.5	53	3	US-09-944-036-42	Sequence 42, Appl	
8	37	68.5	53	3	US-10-425-975-42	Sequence 42, Appl	
9	37	68.5	57	3	US-09-738-274-7	Sequence 7, Appl	
10	37	68.5	57	3	US-09-738-972-3	Sequence 3, Appl	
C	11	37	68.5	57	3	US-09-738-972-13	Sequence 13, Appl
	12	36	66.7	37	3	US-09-944-036-2	Sequence 2, Appl
	13	36	66.7	37	3	US-10-425-975-2	Sequence 2, Appl
	14	36	66.7	54	3	US-09-944-036-6	Sequence 6, Appl
	15	36	66.7	54	3	US-10-425-975-6	Sequence 6, Appl
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	17	35.8	66.3	53	3	US-09-944-036-36	Sequence 36, Appl
	18	35.8	66.3	53	3	US-10-425-975-34	Sequence 34, Appl
	19	35.8	66.3	53	3	US-10-425-975-36	Sequence 36, Appl
	20	35.4	65.6	54	3	US-09-493-491-49	Sequence 49, Appl
21	35.4	65.6	54	3	US-09-493-491A-49	Sequence 49, Appl	
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37	34	63.0	54	3	US-10-273-707-30	Sequence 30, Appl
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62	33	61.1	53	3	US-10-425-975-37	Sequence 37, Appl
63	33	61.1	55	2	US-08-162-836-14	Sequence 14, Appl
64	33	61.1	55	2	US-08-479-105A-1	Sequence 1, Appl
65	33	61.1	55	3	US-08-116-984A-13	Sequence 13, Appl
66	33	61.1	55	3	US-09-502-966-10	Sequence 10, Appl
67	33	61.1	55	3	US-09-944-036-44	Sequence 44, Appl
68	33	61.1	55	3	US-10-425-975-44	Sequence 44, Appl
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72	33	61.1	59	3	US-09-738-972-11	Sequence 11, Appl
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74	33	61.1	60	2	US-08-475-231-36	Sequence 36, Appl
75	33	61.1	62	2	US-08-345-861-1	Sequence 1, Appl
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77	33	61.1	63	3	US-09-953-321-5	Sequence 5, Appl
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79	33	61.1	67	3	US-09-518-813B-14	Sequence 14, Appl
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85	33	61.1	102	3	US-08-418-992-2	Sequence 2, Appl
86	33	61.1	109	2	US-08-538-875-5	Sequence 5, Appl
87	33	61.1	118	3	US-09-284-627-21	Sequence 21, Appl
88	33	61.1	144	3	US-09-655-378A-163	Sequence 163, Appl
89	33	61.1	146	2	US-08-902-623-44	Sequence 44, Appl
90	33	61.1	186	3	US-08-875-277A-12	Sequence 12, Appl
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92	33	61.1	187	2	US-08-877-109-7	Sequence 7, Appl
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98	33	61.1	2839	3	US-09-809-517A-36	Sequence 36, Appli	171	32.6	60.4	55	5	US-08-480-472A-21	Sequence 21, Appli
99	33	61.1	2865	3	US-09-795-872-9	Sequence 9, Appli	c 172	32	59.3	158	3	US-09-722-393A-6	Sequence 6, Appli
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110	33	61.1	4811	3	US-09-813-718-13	Sequence 13, Appli	183	31.8	58.9	3944	2	US-07-678-408A-1	Sequence 1, Appli
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114	33	61.1	4819	2	US-08-451-233-20	Sequence 20, Appli	187	31.6	58.5	760	3	US-09-043-506A-14	Sequence 14, Appli
115	33	61.1	4819	2	US-08-450-236-20	Sequence 20, Appli	188	31.6	58.5	5053	3	US-09-311-784A-35	Sequence 35, Appli
116	33	61.1	4819	2	US-08-235-403-20	Sequence 20, Appli	189	31.6	58.5	6200	3	US-09-439-523-1	Sequence 1, Appli
117	33	61.1	4877	3	US-09-813-718-11	Sequence 11, Appli	190	31.6	58.5	6200	3	US-09-711-202A-1	Sequence 1, Appli
118	33	61.1	4910	2	US-08-450-257-11	Sequence 11, Appli	191	31.6	58.5	6200	3	US-09-711-205A-1	Sequence 1, Appli
119	33	61.1	4910	2	US-08-450-246-11	Sequence 11, Appli	192	31.6	58.5	6200	3	US-09-993-241-1	Sequence 1, Appli
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122	33	61.1	4910	2	US-08-450-236-11	Sequence 11, Appli	195	31.4	58.1	619	3	US-09-043-506A-13	Sequence 13, Appli
123	33	61.1	4910	3	US-08-235-403-11	Sequence 11, Appli	196	31.4	58.1	629	2	US-08-300-265-2	Sequence 2, Appli
124	33	61.1	4977	2	US-08-450-257-14	Sequence 14, Appli	197	31.4	58.1	629	2	US-08-716-718-2	Sequence 2, Appli
125	33	61.1	4977	2	US-08-450-257-17	Sequence 17, Appli	198	31.4	58.1	629	3	US-09-438-836A-2	Sequence 2, Appli
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131	33	61.1	4977	2	US-08-451-233-17	Sequence 17, Appli	204	30.8	57.0	133	2	US-08-930-274-9	Sequence 9, Appli
132	33	61.1	4977	2	US-08-450-236-14	Sequence 14, Appli	c 205	30.8	57.0	135	2	US-08-930-274-10	Sequence 10, Appli
133	33	61.1	4977	2	US-08-450-236-17	Sequence 17, Appli	206	30.6	56.7	51	3	US-09-168-947-25	Sequence 25, Appli
134	33	61.1	4977	3	US-08-235-403-14	Sequence 14, Appli	207	30.6	56.7	1215	2	US-08-522-841-7	Sequence 7, Appli
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137	33	61.1	5018	3	US-09-813-718-9	Sequence 9, Appli	210	30.4	56.3	32	2	US-08-486-705-14	Sequence 14, Appli
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142	33	61.1	5098	2	US-08-450-236-10	Sequence 10, Appli	215	30.4	56.3	49	3	US-10-273-707-37	Sequence 37, Appli
143	33	61.1	5098	2	US-08-235-403-10	Sequence 10, Appli	216	30.4	56.3	50	3	US-09-944-036-8	Sequence 8, Appli
144	33	61.1	5174	3	US-09-813-718-1	Sequence 1, Appli	217	30.4	56.3	50	3	US-10-425-975-8	Sequence 8, Appli
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148	33	61.1	5574	2	US-08-451-233-22	Sequence 22, Appli	221	30.4	56.3	53	3	US-09-975-408-13	Sequence 13, Appli
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150	33	61.1	5574	3	US-08-235-403-22	Sequence 22, Appli	223	30.4	56.3	10494	4	US-10-138-727A-40	Sequence 40, Appli
151	33	61.1	5640	3	US-09-574-779B-133	Sequence 133, App	224	30.2	55.9	51	3	US-09-944-036-40	Sequence 40, Appli
152	33	61.1	6714	2	US-08-021-623C-5	Sequence 5, Appli	225	30.2	55.9	51	3	US-10-425-975-40	Sequence 40, Appli
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c 154	33	61.1	6873	3	US-09-131-028A-8	Sequence 8, Appli	227	30.2	55.9	52	3	US-09-493-491A-42	Sequence 42, Appli
c 155	33	61.1	8430	3	US-09-131-028A-6	Sequence 6, Appli	228	30.2	55.9	52	3	US-10-273-707-42	Sequence 42, Appli
156	33	61.1	8430	3	US-09-131-028A-10	Sequence 10, Appli	229	30.2	55.9	58	3	US-08-840-767-26	Sequence 26, Appli
157	33	61.1	13910	3	US-09-263-933-1	Sequence 1, Appli	c 230	30.2	55.9	3104	2	US-07-415-307A-1	Sequence 1, Appli
158	33	61.1	13910	3	US-09-263-933-8	Sequence 8, Appli	c 231	30.2	55.9	3104	2	US-08-371-320-1	Sequence 1, Appli
159	33	61.1	13910	3	US-09-263-933-15	Sequence 15, Appli	232	30.2	55.9	3613	3	US-10-622-064-19	Sequence 19, Appli
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162	33	61.1	13910	3	US-09-919-901-15	Sequence 15, Appli	235	30.2	55.9	5062	2	US-08-656-555-1	Sequence 1, Appli
163	33	61.1	13910	3	US-10-191-966-1	Sequence 1, Appli	236	30.2	55.9	5618	3	US-08-799-569-1	Sequence 1, Appli
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166	32.6	60.4	55	2	US-08-345-861-12	Sequence 12, Appli	c 239	30.2	55.9	7080	3	US-09-380-190A-21	Sequence 21, Appli
167	32.6	60.4	55	2	US-08-345-861-21	Sequence 21, Appli	240	30.2	55.9	11772	5	US-09-885-297B-17	Sequence 17, Appli
168	32.6	60.4	55	2	US-08-479-105A-12	Sequence 12, Appli	241	30	55.6	35	2	US-08-360-051A-24	Sequence 24, Appli
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243 30 55.6 48 3 US-09-049-325-1 Sequence 1, Appli  
244 30 55.6 70 3 US-09-648-569A-16 Sequence 16, Appli  
245 30 55.6 171 3 US-08-299-931-4 Sequence 4, Appli  
246 30 55.6 260 2 US-08-578-649-23 Sequence 23, Appli  
247 30 55.6 574 3 US-09-043-506A-6 Sequence 6, Appli  
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250 30 55.6 617 3 US-09-043-506A-9 Sequence 9, Appli  
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252 30 55.6 621 3 US-09-043-506A-16 Sequence 16, Appli  
253 30 55.6 626 3 US-09-043-506A-8 Sequence 8, Appli  
254 30 55.6 705 3 US-09-043-506A-4 Sequence 4, Appli  
255 30 55.6 806 3 US-10-138-184-31 Sequence 31, Appli  
256 30 55.6 996 3 US-09-151-999-25 Sequence 25, Appli  
257 30 55.6 996 3 US-09-418-221-23 Sequence 23, Appli  
258 30 55.6 996 3 US-09-569-386-25 Sequence 25, Appli  
259 30 55.6 996 3 US-09-724-964B-25 Sequence 25, Appli  
260 30 55.6 1467 3 US-09-800-170-27 Sequence 27, Appli  
261 30 55.6 2043 3 US-09-800-170-47 Sequence 47, Appli  
262 30 55.6 2336 2 US-08-389-564B-2 Sequence 2, Appli  
263 30 55.6 2336 3 US-08-466-047B-2 Sequence 2, Appli  
264 30 55.6 2462 3 US-09-496-445-5 Sequence 5, Appli  
265 30 55.6 2679 3 US-09-427-657-17 Sequence 17, Appli  
266 30 55.6 2939 2 US-08-119-512-2 Sequence 2, Appli  
267 30 55.6 2939 2 US-08-488-015B-2 Sequence 2, Appli  
268 30 55.6 2939 3 US-08-814-412-17 Sequence 17, Appli  
269 30 55.6 3228 3 US-09-636-215-701 Sequence 701, App  
270 30 55.6 3228 3 US-09-685-166A-701 Sequence 701, App  
271 30 55.6 3228 3 US-09-679-426-701 Sequence 701, App  
272 30 55.6 3228 3 US-09-759-143-701 Sequence 701, App  
273 30 55.6 3228 3 US-09-651-236-701 Sequence 701, App  
274 30 55.6 3228 3 US-09-657-279-701 Sequence 701, App  
275 30 55.6 3228 3 US-10-012-896-701 Sequence 701, App  
276 30 55.6 3228 5 US-10-144-678A-701 Sequence 701, App  
277 30 55.6 3594 3 US-09-710-279-3803 Sequence 3803, Ap  
278 30 55.6 3680 2 US-08-759-848-1 Sequence 1, Appli  
279 30 55.6 3680 7 PCT-US95-09383-1 Sequence 1, Appli  
280 30 55.6 3701 3 US-09-710-279-4342 Sequence 4342, Ap  
281 30 55.6 3853 3 US-08-801-092-5 Sequence 5, Appli  
282 30 55.6 3853 3 US-09-315-113-5 Sequence 5, Appli  
283 30 55.6 3853 3 US-09-315-116-5 Sequence 5, Appli  
284 30 55.6 4026 3 US-08-801-092-19 Sequence 19, Appli  
285 30 55.6 4026 3 US-09-315-113-19 Sequence 19, Appli  
286 30 55.6 4026 3 US-09-315-116-19 Sequence 19, Appli  
287 30 55.6 4069 3 US-09-170-496D-287 Sequence 287, App  
288 30 55.6 4069 3 US-09-170-496D-288 Sequence 288, App  
289 30 55.6 4069 3 US-09-364-425B-52 Sequence 52, Appli  
290 30 55.6 4069 3 US-09-364-425B-53 Sequence 53, Appli  
291 30 55.6 4249 3 US-08-801-092-33 Sequence 33, Appli  
292 30 55.6 4249 3 US-09-315-113-33 Sequence 33, Appli  
293 30 55.6 4249 3 US-09-315-116-33 Sequence 33, Appli  
294 30 55.6 4273 3 US-08-795-430-3 Sequence 3, Appli  
295 30 55.6 4273 3 US-09-355-430-3 Sequence 3, Appli  
296 30 55.6 4273 3 US-08-601-132-37 Sequence 37, Appli  
297 30 55.6 4273 3 US-08-671-573B-37 Sequence 37, Appli  
298 30 55.6 4273 3 US-09-631-092B-37 Sequence 37, Appli  
299 30 55.6 4273 3 US-09-534-376A-3 Sequence 3, Appli  
300 30 55.6 4395 3 US-10-023-649A-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-738-274-11  
; Sequence 11, Application US/09738274  
; Patent No. 6664081  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; NAME/KEY: oligonucleotide  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-738-274-11

Query Match 100.0%; Score 54; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11; Indels 0; Gaps 0;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATTTCCCACTGC 54  
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATTTCCCACTGC 54

RESULT 2  
US-09-738-274-8  
; Sequence 8, Application US/09738274  
; Patent No. 6664081  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 58  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; NAME/KEY: oligonucleotide  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-738-274-8

Query Match 77.8%; Score 42; DB 3; Length 58;  
Best Local Similarity 98.1%; Pred. No. 6.3e-07;  
Matches 53; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATTTCCCACTGC 54  
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTGCAATATTTCCCACTGC 53

RESULT 3  
US-09-738-274-10  
; Sequence 10, Application US/09738274  
; Patent No. 6664081  
; GENERAL INFORMATION:

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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-10
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Query Match 75.9%; Score 41; DB 3; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.5e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTTGTGCAATATTTCCCACTGC 54
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTTGTGCAATATTTCCCACTGC 57
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RESULT 4
US-09-738-274-9
; Sequence 9, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-9
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Query Match 74.1%; Score 40; DB 3; Length 59;
Best Local Similarity 93.1%; Pred. No. 3.7e-06;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTTGTGCAATATTTCCCACTGC 58
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RESULT 5
US-09-944-036-9
; Sequence 9, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-9
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Query Match 69.6%; Score 37.6; DB 3; Length 54;
Best Local Similarity 90.9%; Pred. No. 3.1e-05;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTTGTGCAATAT 44
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTTGATAATTT 44
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RESULT 6
US-10-425-975-9
; Sequence 9, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-9
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Query Match      69.6%; Score 37.6; DB 3; Length 54;
Best Local Similarity 90.9%; Pred. No. 3.1e-05;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 44
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAATT 44
    |||||

RESULT 7
US-09-944-036-42
; Sequence 42, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-42

Query Match      68.5%; Score 37; DB 3; Length 53;
Best Local Similarity 88.9%; Pred. No. 5.2e-05;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 45
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Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTCTTGATAATT 45
    |||||

RESULT 8
US-10-425-975-42
; Sequence 42, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-42

Query Match      68.5%; Score 37; DB 3; Length 53;
Best Local Similarity 88.9%; Pred. No. 5.2e-05;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATAT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAATT 45
    |||||

RESULT 9
US-09-738-274-7
; Sequence 7, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-7

Query Match      68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 5.3e-05;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 57
    |||||

RESULT 10
US-09-738-972-3
; Sequence 3, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
```

; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 57  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: promoter-primer  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-738-972-3

Query Match 68.5%; Score 37; DB 3; Length 57;  
Best Local Similarity 91.2%; Pred. No. 5.3e-05;  
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCAAGCCCATTTGTGCAATATTCCTCCACT 57  
|||||

## RESULT 11

US-09-738-972-13/c  
; Sequence 13, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 57  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: probe  
US-09-738-972-13

Query Match 68.5%; Score 37; DB 3; Length 57;  
Best Local Similarity 91.2%; Pred. No. 5.3e-05;  
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52  
|||||  
Db 57 GAAATTAATACGACTCACTATAGGAGACCAAGCCCATTTGTGCAATATTCCTCCACT 1  
|||||

## RESULT 12

US-09-944-036-2  
; Sequence 2, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 37  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter  
; OTHER INFORMATION: sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-09-944-036-2

Query Match 66.7%; Score 36; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||

## RESULT 13

US-10-425-975-2  
; Sequence 2, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 37  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter  
; OTHER INFORMATION: sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(29)  
US-10-425-975-2

Query Match 66.7%; Score 36; DB 3; Length 37;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||

## RESULT 14

US-09-944-036-6  
; Sequence 6, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie

APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; NAME/KEY: modified\_base  
; LOCATION: (46)  
; OTHER INFORMATION: Nebularine  
US-09-944-036-6

Query Match 66.7%; Score 36; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATG 36  
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATG 36

RESULT 15  
US-10-425-975-6  
; Sequence 6, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; NAME/KEY: modified\_base  
; LOCATION: (46)  
; OTHER INFORMATION: Nebularine  
US-10-425-975-6

Query Match 66.7%; Score 36; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATG 36  
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATG 36

RESULT 16  
US-09-944-036-34  
; Sequence 34, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; NAME/KEY: modified\_base  
; LOCATION: (45)  
; OTHER INFORMATION: Nebularine  
US-09-944-036-34

Query Match 66.3%; Score 35.8; DB 3; Length 53;  
Best Local Similarity 94.9%; Pred. No. 0.00015;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATGTC 39  
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATGTC 39

RESULT 17  
US-09-944-036-36  
; Sequence 36, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:

```
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: Promoter
; LOCATION: (1)..(33)
US-09-944-036-36

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39

RESULT 18
US-10-425-975-34
; Sequence 34, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: Promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (45)
; OTHER INFORMATION: Nebularine
US-10-425-975-34

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39

RESULT 19
US-10-425-975-36
; Sequence 36, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
```

```
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-36

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.00015;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGC 39

RESULT 20
US-09-493-491-49
; Sequence 49, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-49

Query Match          65.6%; Score 35.4; DB 3; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.00022;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTTCCCACTGC 54
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCAAAATTTCTTGTGCATCCAGCTTGC 54

RESULT 21
US-09-493-491A-49
; Sequence 49, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
```

; CURRENT APPLICATION NUMBER: US/09/493,491A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-09-493-491A-49

Query Match 65.6%; Score 35.4; DB 3; Length 54;  
Best Local Similarity 79.2%; Pred. No. 0.00022;  
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATCCCACTGC 54  
|||||  
DB 2 AAATTAATACGACTCACTATAGGAGACCACAAATCTTCTGCATCCAGCTTGC 54  
|||||

RESULT 22  
US-10-273-707-49  
; Sequence 49, Application US/10273707  
; Patent No. 6811985  
; GENERAL INFORMATION:  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-49

Query Match 65.6%; Score 35.4; DB 3; Length 54;  
Best Local Similarity 79.2%; Pred. No. 0.00022;  
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATCCCACTGC 54  
|||||  
DB 2 AAATTAATACGACTCACTATAGGAGACCACAAATCTTCTGCATCCAGCTTGC 54  
|||||

RESULT 23  
US-09-944-036-10  
; Sequence 10, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.

; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-10

Query Match 65.6%; Score 35.4; DB 3; Length 55;  
Best Local Similarity 97.3%; Pred. No. 0.00022;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37  
|||||  
DB 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37  
|||||

RESULT 24  
US-10-425-975-10  
; Sequence 10, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-10

Query Match 65.6%; Score 35.4; DB 3; Length 55;  
Best Local Similarity 97.3%; Pred. No. 0.00022;  
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACATTGT 37  
|||||

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGT 37

## RESULT 25

US-09-944-036-43  
; Sequence 43, Application US/09944036  
; Patent No. 6582920

## GENERAL INFORMATION:

; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-43

Query Match 64.8%; Score 35; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

## RESULT 26

US-09-738-274-12  
; Sequence 12, Application US/09738274  
; Patent No. 6664081

## GENERAL INFORMATION:

; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAI, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-738-274-12

Query Match 64.8%; Score 35; DB 3; Length 52;  
Best Local Similarity 80.4%; Pred. No. 0.00031;  
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCCAC 51

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGATGCTTGGCCCC 51

## RESULT 27

US-10-425-975-43  
; Sequence 43, Application US/10425975  
; Patent No. 6946254

## GENERAL INFORMATION:

; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-43

Query Match 64.8%; Score 35; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

Db 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35

## RESULT 28

US-09-944-036-35  
; Sequence 35, Application US/09944036  
; Patent No. 6582920

## GENERAL INFORMATION:

; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 53

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-35
```

```
Query Match          64.4%; Score 34.8; DB 3; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00037;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTC 46
      |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTC 46
      |||||
```

```
RESULT 29
US-10-425-975-35
; Sequence 35, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-35
```

```
Query Match          64.4%; Score 34.8; DB 3; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.00037;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTC 46
      |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTGTGCAATATTC 46
      |||||
```

```
RESULT 30
US-09-944-036-33
; Sequence 33, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
```

```
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-33
```

```
Query Match          63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00053;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTG 36
      |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTG 36
      |||||
```

```
RESULT 31
US-10-425-975-33
; Sequence 33, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-33
```

```
Query Match          63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.00053;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTG 36
      |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTG 36
      |||||

RESULT 32
US-10-140-545-48
; Sequence 48, Application US/10140545
; Patent No. 6943242
; GENERAL INFORMATION:
```

```

; APPLICANT: Daniel, Stevan G
; APPLICANT: Turner, Leah
; APPLICANT: Samartzidou, Hrisi
; APPLICANT: Houts, Thomas M
; TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION
; TITLE OF INVENTION: ANALYSIS SYSTEMS
; FILE REFERENCE: PB0120
; CURRENT APPLICATION NUMBER: US/10/140,545
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 60/289,202
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/312,420
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; TYPE: DNA
; LENGTH: 62
; ORGANISM: Saccharomyces cerevisiae
US-10-140-545-48

Query Match      63.7%; Score 34.4; DB 3; Length 62;
Best Local Similarity 97.2%; Pred. No. 0.00054;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTTG 36
   |||||
Db 15 GAAATTAATACGACTCACTATAGGAGACCAATTTG 50

RESULT 33
US-09-944-036-38
; Sequence 38, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-38

Query Match      63.0%; Score 34; DB 3; Length 53;
Best Local Similarity 88.1%; Pred. No. 0.00075;
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATTTGCAAT 42
   |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATTTGCAAT 42

RESULT 34
US-10-425-975-38
; Sequence 38, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-38

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51
   |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51

RESULT 35
US-09-493-491-27
; Sequence 27, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-27

Query Match      63.0%; Score 34; DB 3; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.00076;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51
   |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCAATTTGCAATATTTCCAC 51

```





```
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-45

Query Match          63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34

RESULT 40
US-09-738-972-2
; Sequence 2, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-2

Query Match          63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34

RESULT 41
US-09-738-972-12/c
; Sequence 12, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-45
```

```
US-09-738-972-12

Query Match          63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 42
US-09-493-491-33
; Sequence 33, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
US-09-493-491-33

Query Match          62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCACCTTCTG 38

RESULT 43
US-09-493-491A-36
; Sequence 36, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-09-493-491A-36
```

```
Query Match          62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACACCTTCTG 38
    |||||

RESULT 44
US-10-273-707-36
; Sequence 36, Application US/10273707
; Patent No. 6811985
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match          62.6%; Score 33.8; DB 3; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.0009;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAATTAATACGACTCACTATAGGAGACACATTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACACCTTCTG 38
    |||||

RESULT 45
US-10-001-407-19
; Sequence 19, Application US/10001407
; Patent No. 6870045
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
```

```
; OTHER INFORMATION: primer sequence
US-10-001-407-19

Query Match          61.5%; Score 33.2; DB 3; Length 58;
Best Local Similarity 92.1%; Pred. No. 0.0016;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACATTGTG 38
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACCTG 38
    |||||

RESULT 46
US-09-944-036-4
; Sequence 4, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-4

Query Match          61.1%; Score 33; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACACCA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACACCA 33
    |||||

RESULT 47
US-09-738-274-36
; Sequence 36, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 33
; TYPE: DNA
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; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-09-738-274-36

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

## RESULT 48

US-09-738-972-10  
; Sequence 10, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE OF INVENTION: AVIUM COMPLEX SPECIES  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-09-738-972-10

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

## RESULT 49

US-10-001-407-29  
; Sequence 29, Application US/10001407  
; Patent No. 6870045  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Yeasing  
; APPLICANT: Burrell, Terrie  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; FILE REFERENCE: GP117-03.UT  
; CURRENT APPLICATION NUMBER: US/10/001,407  
; CURRENT FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/242,620  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/280,058  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: HIV-2  
US-10-001-407-29

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

## RESULT 50

US-10-425-975-4  
; Sequence 4, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter  
US-10-425-975-4

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.0017;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

## RESULT 51

US-09-425-585-15  
; Sequence 15, Application US/09425585  
; Patent No. 6348315  
; GENERAL INFORMATION:  
; APPLICANT: PLUCKTHUN, ANDREAS  
; APPLICANT: HANES, JOZEF  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING  
; FILE REFERENCE: PLUCK/1  
; CURRENT APPLICATION NUMBER: US/09/425,585  
; CURRENT FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: PCT/EP98/02420  
; PRIOR FILING DATE: 1998-04-23  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 41  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide T7B  
US-09-425-585-15

```
Query Match          61.1%; Score 33; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 52
US-09-953-321-15
; Sequence 15, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 41
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide T7B
US-09-953-321-15

Query Match          61.1%; Score 33; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 5 GAAATTAATACGACTCACTATAGGAGACCACA 37

RESULT 53
US-08-678-735A-9
; Sequence 9, Application US/08678735A
; Patent No. 6150179
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,735A
; FILING DATE: 1996-JUL-11
; CLASSIFICATION: 436
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-678-735A-9

Query Match          61.1%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 54
US-08-418-992-9
; Sequence 9, Application US/08418992
; Patent No. 6341256
; GENERAL INFORMATION:
; APPLICANT: Deem, Michael W.
; APPLICANT: Rothberg, Jonathan M.
; APPLICANT: Went, Gregory T.
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/418,992
; FILING DATE: On Even Date Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirostock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-418-992-9

Query Match          61.1%; Score 33; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 0.0018;
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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
Db 6 GAAATTATACGACTCACTATAGGAGACCACA 38

## RESULT 55

US-09-518-813B-15

; Sequence 15, Application US/09518813B

; Patent No. 6927025

; GENERAL INFORMATION:

; APPLICANT: CARR, Francis Joseph

; APPLICANT: CARTER, Graham

; APPLICANT: HAMILTON, Anita Anne

; APPLICANT: ADAIR, Fiona Suzanne

; APPLICANT: WILLIAMS, Stephen

; TITLE OF INVENTION: METHODS FOR PROTEIN SCREENING

; FILE REFERENCE: 112408-122

; CURRENT APPLICATION NUMBER: US/09/518,813B

; CURRENT FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: PCT/GB98/02649

; PRIOR FILING DATE: 1998-09-03

; PRIOR APPLICATION NUMBER: US 60/070,063

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,062

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,037

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: US 60/070,050

; PRIOR FILING DATE: 1997-12-30

; PRIOR APPLICATION NUMBER: GB 9718552.4

; PRIOR FILING DATE: 1997-09-03

; PRIOR APPLICATION NUMBER: GB 9719834.5

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: GB 9720184.2

; PRIOR FILING DATE: 1997-09-14

; PRIOR APPLICATION NUMBER: GB 9720522.3

; PRIOR FILING DATE: 1997-09-29

; PRIOR APPLICATION NUMBER: GB 9720523.1

; PRIOR FILING DATE: 1997-09-29

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 50

; TYPE: DNA

; ORGANISM: synthetic oligonucleotide

US-09-518-813B-15

Query Match 61.1%; Score 33; DB 3; Length 50;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
Db 15 GAAATTATACGACTCACTATAGGAGACCACA 47

## RESULT 56

US-08-902-623-33

; Sequence 33, Application US/08902623

; Patent No. 5922545

; GENERAL INFORMATION:

; APPLICANT: MATTHEAKIS, LARRY C.

; APPLICANT: DOWER, WILLIAM J.

; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY

; TITLE OF INVENTION: LIBRARIES

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP

; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR

; CITY: SAN FRANCISCO

; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,623  
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/586,176

; FILING DATE: 17-JAN-1996

; APPLICATION NUMBER: US 08/300,262

; FILING DATE: 02-SEP-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/144,775

; FILING DATE: US 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/12206

; FILING DATE: US 25-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: DUNN, TRACY J.

; REGISTRATION NUMBER: 34,587

; REFERENCE/DOCKET NUMBER: 16528X-003230US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 51 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-902-623-33

Query Match 61.1%; Score 33; DB 2; Length 51;

Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTATACGACTCACTATAGGAGACCACA 33  
Db 6 GAAATTATACGACTCACTATAGGAGACCACA 38

## RESULT 57

US-09-944-036-41

; Sequence 41, Application US/09944036

; Patent No. 6582920

; GENERAL INFORMATION:

; APPLICANT: YANG, Yeasing Y.

; APPLICANT: BRENTANO, Steven T.

; APPLICANT: BABOLA, Odile

; APPLICANT: TRAN, Nathalie

; APPLICANT: VERNET, Guy

; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF

; FILE REFERENCE: GP114-02.UT

; CURRENT APPLICATION NUMBER: US/09/944,036

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/229,790

; PRIOR FILING DATE: 2000-09-01

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 41

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase

; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-41

Query Match 61.1%; Score 33; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 58  
US-10-425-975-41  
; Sequence 41, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-41

Query Match 61.1%; Score 33; DB 3; Length 51;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 59  
US-09-944-036-39  
; Sequence 39, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790

; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-39

Query Match 61.1%; Score 33; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 60  
US-10-425-975-39  
; Sequence 39, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-39

Query Match 61.1%; Score 33; DB 3; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 61  
US-09-944-036-37  
; Sequence 37, Application US/09944036  
; Patent No. 6582920  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.

```
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-37

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB      1  GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 62
US-10-425-975-37
; Sequence 37, Application US/10425975
; Patent No. 6946254
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-37

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB      1  GAAATTAATACGACTCACTATAGGAGACCACA 33

; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-37

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
```

```
Db      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 63
US-08-162-836-14
; Sequence 14, Application US/08162836
; Patent No. 5554516
; GENERAL INFORMATION:
; APPLICANT: Daniel L. Kacian
; APPLICANT: Diane L. McAllister
; APPLICANT: Sherrol H. McDonough
; APPLICANT: Nani Bhushan Dattagupta
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
; TITLE OF INVENTION: METHOD, COMPOSITION AND KIT
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/162,836
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/879,686
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-162-836-14

Query Match          61.1%; Score 33; DB 2; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
DB      1  GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
RESULT 64
US-08-479-105A-1
; Sequence 1, Application US/08479105A
; Patent No. 5908744
; GENERAL INFORMATION:
; APPLICANT: Diane L. McAllister
; APPLICANT: Philip Hammond
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: AMPLIFICATION
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
```



STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: MS DOS (5.0)  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/479,105A  
FILING DATE: June 6, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/345,861  
FILING DATE: No. 5908744ember 28, 1994  
APPLICATION NUMBER: 07/925,405  
FILING DATE: August 4, 1992  
APPLICATION NUMBER: 07/855,732  
FILING DATE: March 19, 1992  
APPLICATION NUMBER: 07/550,837  
FILING DATE: July 10, 1990  
APPLICATION NUMBER: 07/379,501  
FILING DATE: July 11, 1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Heber, Sheldon O.  
REGISTRATION NUMBER: 38,179  
REFERENCE/DOCKET NUMBER: 213/067  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-479-105A-1

Query Match 61.1%; Score 33; DB 2; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 65  
US-08-116-984A-13  
; Sequence 13, Application US/08116984A  
; Patent No. 6136529  
; GENERAL INFORMATION:  
; APPLICANT: Philip W. Hammond  
; TITLE OF INVENTION: NUCLEIC ACID PROBES TO  
; TITLE OF INVENTION: MYCOBACTERIUM AVIUM  
; TITLE OF INVENTION: COMPLEX  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/116,984A  
FILING DATE: September 3, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 203/188  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 55  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-116-984A-13

Query Match 61.1%; Score 33; DB 3; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 66  
US-09-502-966-10  
; Sequence 10, Application US/09502966  
; Patent No. 6245519  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: McDONOUGH, Sherrol H.  
; APPLICANT: NELSON, No. 6245519man C.  
; TITLE OF INVENTION: PROTECTION PROBES  
; FILE REFERENCE: GP102-02 UT  
; CURRENT APPLICATION NUMBER: US/09/502,966  
; CURRENT FILING DATE: 2000-02-11  
; EARLIER APPLICATION NUMBER: 60/120,019 US  
; EARLIER FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: a synthetic  
; OTHER INFORMATION: amplification primer  
US-09-502-966-10

Query Match 61.1%; Score 33; DB 3; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 67  
US-09-944-036-44  
; Sequence 44, Application US/09944036  
; Patent No. 6582920

GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-44

Query Match 61.1%; Score 33; DB 3; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 68  
US-10-425-975-44  
; Sequence 44, Application US/10425975  
; Patent No. 6946254  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 55  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase  
; OTHER INFORMATION: target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-44

Query Match 61.1%; Score 33; DB 3; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 69  
US-08-480-472A-1  
; Sequence 1, Application US/08480472A  
; Patent No. 7009041  
; GENERAL INFORMATION:  
; APPLICANT: Sherrol H. McDonough  
; APPLICANT: Daniel L. Kacian  
; APPLICANT: Nanibhushan Battagupta  
; APPLICANT: Diane L. McAllister  
; APPLICANT: Philip Hammond  
; APPLICANT: Thomas B. Ryder  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE  
; TITLE OF INVENTION: AMPLIFICATION  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/480,472A  
; FILING DATE: June 6, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/345,861  
; FILING DATE: No. 7009041ember 28, 1994  
; APPLICATION NUMBER: 07/925,405  
; FILING DATE: August 4, 1992  
; APPLICATION NUMBER: 07/855,732  
; FILING DATE: March 19, 1992  
; APPLICATION NUMBER: 07/550,837  
; FILING DATE: July 10, 1990  
; APPLICATION NUMBER: 07/379,501  
; FILING DATE: July 11, 1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Heber, Sheldon O.  
; REGISTRATION NUMBER: 38,179  
; REFERENCE/DOCKET NUMBER: 213/066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 55 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-480-472A-1

Query Match 61.1%; Score 33; DB 5; Length 55;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

```
RESULT 70
US-10-001-407-18
; Sequence 18, Application US/10001407
; Patent No. 6870045
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03 UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
; OTHER INFORMATION: SEQ ID NO:13
US-10-001-407-18

Query Match      61.1%; Score 33; DB 3; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 71
US-09-738-972-1
; Sequence 1, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: promoter-primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-1

Query Match      61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 72
US-09-738-972-11/c
; Sequence 11, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-11

Query Match      61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 59 GAAATTAATACGACTCACTATAGGAGACCACA 27

RESULT 73
US-07-971-819A-36
; Sequence 36, Application US/07971819A
; Patent No. 5420029
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Lawyer, Frances C.
; APPLICANT: Stoffel, Susanne
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
; TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/971,819A
; FILING DATE: 19930203
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 bases
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-07-971-819A-36

Query Match          61.1%; Score 33; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 74
US-08-475-231-36
; Sequence 36, Application US/08475231
; Patent No. 5624833
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Lawyer, Frances C.
; APPLICANT: Stoffel, Susanne
; TITLE OF INVENTION: Purified Thermostable Nucleic Acid
; TITLE OF INVENTION: Polymerase Enzyme from Thermotoga Maritima
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,231
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,819
; FILING DATE: 03-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stacey R. Sias, Ph.D.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 814-2977
; TELEX:
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-475-231-36

Query Match          61.1%; Score 33; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 75
US-08-345-861-1

; Sequence 1, Application US/08345861
; Patent No. 5766849
; GENERAL INFORMATION:
; APPLICANT: Sherrol H. McDonough
; APPLICANT: Daniel L. Kacian
; APPLICANT: Nanibhushan Dattagupta
; APPLICANT: Diane L. McAllister
; APPLICANT: Philip Hammond
; APPLICANT: Thomas B. Ryder
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,861
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,405
; FILING DATE: August 4, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 197/136
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 552-8400
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-345-861-1

Query Match          61.1%; Score 33; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 76
US-09-425-585-5
; Sequence 5, Application US/09425585
; Patent No. 6348315
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: HANES, JOZEF
; TITLE OF INVENTION: METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; FILE REFERENCE: PLUCK/1
; CURRENT APPLICATION NUMBER: US/09/425,585
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: PCT/EP98/02420
; PRIOR FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 63
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide ON3
US-09-425-585-5

Query Match      61.1%; Score 33; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 77
US-09-953-321-5
; Sequence 5, Application US/09953321
; Patent No. 6589741
; GENERAL INFORMATION:
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: (POLY) PEPTIDES THAT INTERACT WITH TARGET MOLECULES
; CURRENT APPLICATION NUMBER: US/09/953,321
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 09/425,585
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide ON3
US-09-953-321-5

Query Match      61.1%; Score 33; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 78
US-10-124-663A-2
; Sequence 2, Application US/10124663A
; Patent No. 7011958
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Method for Improving the Stability of Linear DNA in Cell-free in
; TITLE OF INVENTION: transcription/translation systems
; FILE REFERENCE: RDID 010490US
; CURRENT APPLICATION NUMBER: US/10/124,663A
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sense primer
US-10-124-663A-2

Query Match      61.1%; Score 33; DB 5; Length 66;
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 26 GAAATTAATACGACTCACTATAGGAGACCACA 58

RESULT 79
US-09-518-813B-14
; Sequence 14, Application US/09518813B
; Patent No. 6927025
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: CARTER, Graham
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: WILLIAMS, Stephen
; TITLE OF INVENTION: METHODS FOR PROTEIN SCREENING
; FILE REFERENCE: 112408-122
; CURRENT APPLICATION NUMBER: US/09/518,813B
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: PCT/GB98/02649
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: US 60/070,063
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,062
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,037
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: US 60/070,050
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: GB 9718552.4
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: GB 9719834.5
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: GB 9720184.2
; PRIOR FILING DATE: 1997-09-14
; PRIOR APPLICATION NUMBER: GB 9720522.3
; PRIOR FILING DATE: 1997-09-29
; PRIOR APPLICATION NUMBER: GB 9720523.1
; PRIOR FILING DATE: 1997-09-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 67
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-518-813B-14

Query Match      61.1%; Score 33; DB 3; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 15 GAAATTAATACGACTCACTATAGGAGACCACA 47

RESULT 80
US-09-486-356-16
; Sequence 16, Application US/09486356
; Patent No. 6383770
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6383770en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCT-U
; CURRENT APPLICATION NUMBER: US/09/486,356
```

```
; CURRENT FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: PCT/US98/18124
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-09-486-356-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 41
   |||||
Db 2 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 42
   |||||

RESULT 81
US-09-577-528B-16
; Sequence 16, Application US/09577528B
; Patent No. 6689573
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6689573en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCTPR
; CURRENT APPLICATION NUMBER: US/09/577,528B
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-09-577-528B-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 41
   |||||
Db 2 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 42
   |||||

RESULT 82
US-10-208-557-16
; Sequence 16, Application US/10208557
; Patent No. 6905837
; GENERAL INFORMATION:
; APPLICANT: Roberts, Richard J.
; APPLICANT: Byrd, Devon R.
; APPLICANT: Morgan, Richard D.
; APPLICANT: Patti, Jay
; APPLICANT: No. 6905837en, Christopher J.
; TITLE OF INVENTION: Method For Screening Restriction Endonucleases
; FILE REFERENCE: NEB-130PCT-U
; CURRENT APPLICATION NUMBER: US/10/208,557
; CURRENT FILING DATE: 2002-07-30
; PRIOR APPLICATION NUMBER: US/09/486,356
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: PCT/US98/18124
; PRIOR FILING DATE: 1998-09-01
```

```
; PRIOR APPLICATION NUMBER: 60/135,541
; PRIOR FILING DATE: 1999-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 75
; TYPE: DNA
; ORGANISM: Pseudomonas alcaligenes
US-10-208-557-16

Query Match 61.1%; Score 33; DB 3; Length 75;
Best Local Similarity 87.8%; Pred. No. 0.002;
Matches 36; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 41
   |||||
Db 2 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAA 42
   |||||

RESULT 83
US-08-902-623-24
; Sequence 24, Application US/08902623
; Patent No. 5922545
; GENERAL INFORMATION:
; APPLICANT: MATTHEAKIS, LARRY C.
; APPLICANT: DOWER, WILLIAM J.
; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/902,623
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/586,176
; FILING DATE: 17-JAN-1996
; APPLICATION NUMBER: US 08/300,262
; FILING DATE: 02-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/144,775
; FILING DATE: US 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/12206
; FILING DATE: US 25-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, TRACY J.
; REGISTRATION NUMBER: 34,587
; REFERENCE/DOCKET NUMBER: 16528X-003230US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 90 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-902-623-24

Query Match 61.1%; Score 33; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.002;
```

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 84  
US-08-678-735A-2  
; Sequence 2, Application US/08678735A  
; Patent No. 6150179  
; GENERAL INFORMATION:  
; APPLICANT: Deem, Michael W.  
; APPLICANT: Rothberg, Jonathan M.  
; APPLICANT: Went, Gregory T.  
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE  
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE  
; TITLE OF INVENTION: DETERMINATION  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 1996-JUL-11  
; APPLICATION NUMBER: US/08/678,735A  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7934-035  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-678-735A-2

Query Match 61.1%; Score 33; DB 3; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 85  
US-08-418-992-2  
; Sequence 2, Application US/08418992  
; Patent No. 6341256  
; GENERAL INFORMATION:  
; APPLICANT: Deem, Michael W.  
; APPLICANT: Rothberg, Jonathan M.  
; APPLICANT: Went, Gregory T.  
; TITLE OF INVENTION: CONSENSUS CONFIGURATIONAL BIAS MONTE  
; TITLE OF INVENTION: CARLO METHOD AND SYSTEM FOR PHARMACOPHORE STRUCTURE  
; TITLE OF INVENTION: DETERMINATION  
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/418,992  
; FILING DATE: On Even Date Herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7934-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-08-418-992-2

Query Match 61.1%; Score 33; DB 3; Length 102;  
Best Local Similarity 100.0%; Pred. No. 0.0021;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 6 GAAATTAATACGACTCACTATAGGAGACCACA 38

RESULT 86  
US-08-538-875-5/c  
; Sequence 5, Application US/08538875  
; Patent No. 5773582  
; GENERAL INFORMATION:  
; APPLICANT: Shin, Hang-Cheol  
; APPLICANT: Shin, Nam-Kyu  
; APPLICANT: Lee, Inkyung  
; APPLICANT: Kang, Sungzong  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR MUTAINS  
; NUMBER OF SEQUENCES: 73  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Shin, Hang-Cheol  
; STREET: Jukong Gocheung Apt. 1014-806, Haan-dong  
; CITY: Kwangmyung-shi  
; STATE: Kyungki-do  
; COUNTRY: Republic of Korea  
; ZIP: 423-060  
; ADDRESSEE: Shin, Nam-Kyu  
; STREET: #181-404 Sadang-4-dong, Dongjak-ku  
; CITY: Seoul  
; STATE:  
; COUNTRY: Republic of Korea  
; ZIP: 156-094  
; ADDRESSEE: Lee, Inkyung  
; STREET: 11/2, #302-39 Juan-4-dong, Nam-ku  
; CITY: Incheon  
; STATE:  
; COUNTRY: Republic of Korea  
; ZIP: 402-204  
; ADDRESSEE: Kang, Sungzong

```
; STREET: #84-4 Daeshin-dong, Seodaemun-ku
; CITY: Seoul
; STATE:
; COUNTRY: Republic of Korea
; ZIP: 120-160
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 3.5inch 2.0Mb storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/538,875
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,336
; FILING DATE:
; APPLICATION NUMBER: KR 93-1751
; FILING DATE: 9-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: T7 promoter region DNA
; US-08-538-875-5
;
; Query Match 61.1%; Score 33; DB 2; Length 109;
; Best Local Similarity 100.0%; Pred. No. 0.0021;
; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
; DB 91 GAAATTAATACGACTCACTATAGGAGACCACA 59
;
; RESULT 87
; US-09-284-627-21
; Sequence 21, Application US/09284627
; Patent No. 6361943
; GENERAL INFORMATION:
; APPLICANT: Mitsubishi Chemical Corporation
; TITLE OF INVENTION: Molecule assigning genotype to
; phenotype and use thereof
;
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mitsubishi Chemical Corporation
; STREET: 5-2, Marunouchi 2-chome
; CITY: Chiyoda-ku
; STATE: Tokyo
; COUNTRY: JAPAN
; ZIP: 103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,627
; FILING DATE: 02-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 1996274855
; FILING DATE: 17.10.96
; INFORMATION FOR SEQ ID NO: 21:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 118
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: synthetic DNA
; FEATURE:
; OTHER INFORMATION: includes a promoter region of T7
; RNA polymerase, a kozak sequence, and a DNA sequence
; corresponding to amino acid numbers 1-25 of a human tau protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
; US-09-284-627-21
;
; Query Match 61.1%; Score 33; DB 3; Length 118;
; Best Local Similarity 100.0%; Pred. No. 0.0021;
; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
; DB 9 GAAATTAATACGACTCACTATAGGAGACCACA 41
;
; RESULT 88
; US-09-655-378A-163
; Sequence 163, Application US/09655378A
; Patent No. 6673616
; GENERAL INFORMATION:
; APPLICANT: BROW, MARY ANN D.
; LYAMICHEV, VICTOR I.
; OLIVE, DAVID M.
; TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
; PATHOGENS
;
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/655,378A
; FILING DATE: 05-Sep-2000
; CLASSIFICATION: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: FORS-01756
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 163:
; US-09-655-378A-163
;
; Query Match 61.1%; Score 33; DB 3; Length 144;
; Best Local Similarity 100.0%; Pred. No. 0.0022;
; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
; DB 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
```



Db 16 GAAATTAATACGACTCACTATAGGGAGACCACA 48

## RESULT 89

US-08-902-623-44  
; Sequence 44, Application US/08902623  
; Patent No. 5922545  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEAKIS, LARRY C.  
; APPLICANT: DOWER, WILLIAM J.  
; TITLE OF INVENTION: IN VITRO PEPTIDE AND ANTIBODY DISPLAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW LLP  
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: U.S.A.  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/902,623  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/586,176  
; FILING DATE: 17-JAN-1996  
; APPLICATION NUMBER: US 08/300,262  
; FILING DATE: 02-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/144,775  
; FILING DATE: US 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/12206  
; FILING DATE: US 25-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DUNN, TRACY J.  
; REGISTRATION NUMBER: 34,587  
; REFERENCE/DOCKET NUMBER: 16528X-003230US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 146 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-902-623-44

Query Match 61.1%; Score 33; DB 2; Length 146;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

Db 6 GAAATTAATACGACTCACTATAGGGAGACCACA 38

## RESULT 90

US-08-875-277A-12  
; Sequence 12, Application US/08875277A  
; Patent No. 6171808  
; GENERAL INFORMATION:  
; APPLICANT: SOUIRELL, DAVID J.  
; APPLICANT: LOWE, CHRISTOPHER R.  
; APPLICANT: WHITE, PETER J.  
; APPLICANT: MURRAY, JAMES A.H.

; TITLE OF INVENTION: MUTANT LUCIFERASES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/875,277A  
; FILING DATE: 01-OCT-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9501172.2  
; FILING DATE: 20-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9508301.0  
; FILING DATE: 24-APR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CRAWFORD, ARTHUR R.  
; REGISTRATION NUMBER: 25,327  
; REFERENCE/DOCKET NUMBER: 124-588  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 186 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "PLASMID"  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 124..186  
US-08-875-277A-12

Query Match 61.1%; Score 33; DB 3; Length 186;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

Db 39 GAAATTAATACGACTCACTATAGGGAGACCACA 71

## RESULT 91

US-08-096-182A-7  
; Sequence 7, Application US/08096182A  
; Patent No. 5439808  
; GENERAL INFORMATION:  
; APPLICANT: Blake, Milan S.

; APPLICANT: Tai, Joseph Y.  
; APPLICANT: Qi, Huilin L.  
; APPLICANT: Liang, Shu-Mei  
; APPLICANT: Hronowski, Lucjan J.J.  
; APPLICANT: Pullen, Jeffrey K.

; TITLE OF INVENTION: Method for the High Level Expression,  
; Purification and Refolding of the Outer Membrane Group B  
; TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Ave., Suite 600  
; CITY: Washington  
; STATE: D.C.

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; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/096.182A
; FILING DATE: 23-JUL-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..187
; US-08-096-182A-7

Query Match 61.1%; Score 33; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACA 33
Db 16 GAAATTAAATAGCACTCACTATAGGAGACCACA 48

RESULT 92
US-08-877-109-7
; Sequence 7, Application US/08877109
; Patent No. 5747287
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Huilin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
; TITLE OF INVENTION: Porin Proteins from Neisseria meningitidis
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877.109
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/431,264
; FILING DATE: 28-APR-1995
; APPLICATION NUMBER: 08/096.182
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; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..187
; US-08-877-109-7

Query Match 61.1%; Score 33; DB 2; Length 187;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATAGCACTCACTATAGGAGACCACA 33
Db 16 GAAATTAAATAGCACTCACTATAGGAGACCACA 48

RESULT 93
US-08-798-760-7
; Sequence 7, Application US/08798760
; Patent No. 6013267
; GENERAL INFORMATION:
; APPLICANT: Blake, Milan S.
; APPLICANT: Tai, Joseph Y.
; APPLICANT: Qi, Huilin L.
; APPLICANT: Liang, Shu-Mei
; APPLICANT: Hronowski, Lucjan J.J.
; APPLICANT: Pullen, Jeffrey K.
; TITLE OF INVENTION: Method for the High Level Expression,
; TITLE OF INVENTION: Purification and Refolding of the Outer Membrane Group B
; TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798.760
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1438.0060002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; FEATURE:
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NAME/KEY: CDS  
LOCATION: 101..187  
US-08-798-760-7

Query Match 61.1%; Score 33; DB 3; Length 187;  
Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
DB 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 94

PCT-US94-08327-7  
Sequence 7, Application PC/TUS9408327  
GENERAL INFORMATION:  
APPLICANT: The Rockefeller University  
APPLICANT: 1230 York Avenue  
APPLICANT: New York, New York 10021  
APPLICANT: United States of America  
APPLICANT: 12103 Indian Creek Court  
APPLICANT: Beltsville, Maryland 20705  
APPLICANT: United States of America  
APPLICANT: Tai, Joseph Y.  
APPLICANT: Qi, Huilin L.  
APPLICANT: Liang, Shu-Mei  
APPLICANT: Hronowski, Lucjan J.J.  
APPLICANT: Pullen, Jeffrey K.  
TITLE OF INVENTION: Method for the High Level  
TITLE OF INVENTION: Expression,  
TITLE OF INVENTION: Purification and Refolding of the Outer Membrane  
TITLE OF INVENTION: Group B  
TITLE OF INVENTION: Porin Proteins from Neisseria Meningitidis  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Ave., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/08327  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,182  
FILING DATE: 23 July 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1438.006PC00  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 187 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 101..187  
PCT-US94-08327-7

Query Match 61.1%; Score 33; DB 7; Length 187;

Best Local Similarity 100.0%; Pred. No. 0.0023;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
DB 16 GAAATTAATACGACTCACTATAGGAGACCACA 48

RESULT 95

US-08-178-477B-33  
Sequence 33, Application US/08178477B  
Patent No. 5756343  
GENERAL INFORMATION:  
APPLICANT: WU, CARL; CLOS, JOACHIM;  
APPLICANT: WESTWOOD, J. TIMOTHY.; RABINDRAN, SRIDHAR  
TITLE OF INVENTION: CELL STRESS  
TITLE OF INVENTION: TRANSCRIPTIONAL FACTORS  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORGAN & FINNEGAN  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/178,477B  
FILING DATE: 07-JAN-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/617,910  
FILING DATE: 26-NOV-1990  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: CAROL M. GRUPPI  
REGISTRATION NUMBER: 37,341  
REFERENCE/DOCKET NUMBER: 2026-4103US1  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: (DNA) genomic  
US-08-178-477B-33

Query Match 61.1%; Score 33; DB 2; Length 278;  
Best Local Similarity 100.0%; Pred. No. 0.0025;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
DB 18 GAAATTAATACGACTCACTATAGGAGACCACA 50

RESULT 96

US-08-014-944-1  
Sequence 1, Application US/08014944  
Patent No. 5376549  
GENERAL INFORMATION:  
APPLICANT: Guilfoyle, Richard A.  
APPLICANT: Smith, Lloyd M.  
TITLE OF INVENTION: CLONING VECTOR  
NUMBER OF SEQUENCES: 6

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: QUARLES & BRADY
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: United States
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/014,944
; FILING DATE: 19930205
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 96-296-9243-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 277-5591
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: RNA (genomic)
;
US-08-014-944-1

Query Match 61.1%; Score 33; DB 2; Length 451;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 24 GAAATTAATACGACTCACTATAGGAGACCACA 56

RESULT 97
US-09-450-972-6
; Sequence 6, Application US/09450972
; Patent No. 6440728
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PHAGE VECTORS AND METHODS OF USE
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/450,972
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/072,222
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/049,072
; FILING DATE: 09-JUN-1997
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 967 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
;
US-09-450-972-6

Query Match 61.1%; Score 33; DB 3; Length 967;
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```
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; Best Local Similarity 100.0%; Pred. No. 0.0032;
; Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 673 GAAATTAATACGACTCACTATAGGAGACCACA 705

RESULT 98
US-09-809-517A-36
; Sequence 36, Application US/09809517A
; Patent No. 6753136
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b.
; FILE REFERENCE: MORPHO/11
; CURRENT APPLICATION NUMBER: US/09/809,517A
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 2839
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vector
;
US-09-809-517A-36

Query Match 61.1%; Score 33; DB 3; Length 2839;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
Db 14 GAAATTAATACGACTCACTATAGGAGACCACA 46

RESULT 99
US-09-795-872-9
; Sequence 9, Application US/09795872
; Patent No. 6653068
; GENERAL INFORMATION:
; APPLICANT: Frisch, Christian
; APPLICANT: Kretzschmar, Titus
; APPLICANT: Hoss, Adolf
; APPLICANT: Von Ruden, Thomas
; TITLE OF INVENTION: Generation of specific binding partners binding to (poly)peptides
; FILE REFERENCE: Morpho/10
; CURRENT APPLICATION NUMBER: US/09/795,872
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/EP00/06137
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: EP 99 11 2815.8
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2865
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2865)
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: expression vector
;
US-09-795-872-9
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Query Match      61.1%; Score 33; DB 3; Length 2865;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATACGACTCACTATAGGGAGACCACA 33
Db 14 GAAATTAAATACGACTCACTATAGGGAGACCACA 46

RESULT 100
US-09-795-872-8
; Sequence 8, Application US/09795872
; Patent No. 6653068
; GENERAL INFORMATION:
; APPLICANT: Frisch, Christian
; APPLICANT: Kretschmar, Titus
; APPLICANT: Hoss, Adolf
; APPLICANT: Von Ruden, Thomas
; TITLE OF INVENTION: Generation of specific binding partners binding to (poly)peptides
; FILE REFERENCE: Morpho/10
; CURRENT APPLICATION NUMBER: US/09/795,872
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/EP00/06137
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: EP 99 11 2815.8
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 2869
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(2869)
; OTHER INFORMATION: synthetic construct
; OTHER INFORMATION: expression vector
US-09-795-872-8

Query Match      61.1%; Score 33; DB 3; Length 2869;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAAATACGACTCACTATAGGGAGACCACA 33
Db 14 GAAATTAAATACGACTCACTATAGGGAGACCACA 46

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Search completed: May 19, 2006, 01:01:36  
Job time : 167.253 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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306.314 Million cell updates/sec

Title: US-10-665-708-11  
Perfect score: 54  
Sequence: 1 gaattaatacagctacta.....tgtgcaatattcccaatgc 54

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues  
Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : Published Applications\_NA\_Main:\*

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3:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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9:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
16:	/EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	54	100.0	54 3 US-09-738-274-11 Sequence 11, Appl
2	54	100.0	54 10 US-10-665-708-11 Sequence 11, Appl
3	42	77.8	58 3 US-09-738-274-8 Sequence 8, Appl
4	42	77.8	58 10 US-10-665-708-8 Sequence 8, Appl
5	41	75.9	57 3 US-09-738-274-10 Sequence 10, Appl
6	41	75.9	57 10 US-10-665-708-10 Sequence 10, Appl
7	40	74.1	59 3 US-09-738-274-9 Sequence 9, Appl
8	40	74.1	59 10 US-10-665-708-9 Sequence 9, Appl
9	37.6	69.6	54 3 US-09-944-036-9 Sequence 9, Appl
10	37.6	69.6	54 7 US-10-425-975-9 Sequence 9, Appl
11	37.6	69.6	54 13 US-11-145-272-9 Sequence 9, Appl
12	37	68.5	53 3 US-09-944-036-42 Sequence 42, Appl
13	37	68.5	53 7 US-10-425-975-42 Sequence 42, Appl
14	37	68.5	53 13 US-11-145-272-42 Sequence 42, Appl
15	37	68.5	57 3 US-09-738-972-3 Sequence 3, Appl
16	37	68.5	57 3 US-09-738-972-13 Sequence 13, Appl
17	37	68.5	57 3 US-09-738-274-7 Sequence 7, Appl

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ALIGNMENTS

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US-09-738-274-11  
; Sequence 11, Application US/09738274  
; Publication No. US20030165824A1

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; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GPI07-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; PRIOR FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
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; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
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US-09-738-274-11

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; Publication No. US20030165824A1
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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
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; TYPE: DNA
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; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
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; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
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Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy      1  GAAATTAATACGACTCACTATAGGAGACCACCA---CATTGTGCAATATATCCCACTGC 54
|||||
Db      1  GAAATTAATACGACTCACTATAGGAGACCACACCAATTGTGCAATATATCCCACTGC 57

RESULT 6
US-10-665-708-10
; Sequence 10, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
```

```
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-10

Query Match      75.9%; Score 41; DB 10; Length 57;
Best Local Similarity 94.7%; Pred. No. 1.9e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 57

RESULT 7
US-09-738-274-9
; Sequence 9, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-9

Query Match      74.1%; Score 40; DB 3; Length 59;
Best Local Similarity 93.1%; Pred. No. 4.6e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58

RESULT 8
US-10-665-708-9
; Sequence 9, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
```

```
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-9

Query Match      74.1%; Score 40; DB 10; Length 59;
Best Local Similarity 93.1%; Pred. No. 4.6e-05;
Matches 54; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 54
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 58

RESULT 9
US-09-944-036-9
; Sequence 9, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-9

Query Match      69.6%; Score 37.6; DB 3; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 44
    |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCA---CATTGTGCAATATTTCCCACTGC 44

RESULT 10
US-10-425-975-9
; Sequence 9, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
```

```
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-9
```

```
Query Match          69.6%; Score 37.6; DB 7; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATGTGCAATAT 44
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATGTGCAATAT 44
|||||
```

```
RESULT 11
US-11-145-272-9
; Sequence 9, Application US/11/45272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-9
```

```
Query Match          69.6%; Score 37.6; DB 13; Length 54;
Best Local Similarity 90.9%; Pred. No. 0.00037;
Matches 40; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATGTGCAATAT 44
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATGTGCAATAT 44
|||||
```

```
RESULT 12
US-09-944-036-42
; Sequence 42, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-42
```

```
Query Match          68.5%; Score 37; DB 3; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAATGTGCAATAT 45
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCAATCTTTGATAAAT 45
|||||
```

```
RESULT 13
US-10-425-975-42
; Sequence 42, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-42

Query Match          68.5%; Score 37; DB 7; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAAATT 45

RESULT 14
US-11-145-272-42
; Sequence 42, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; PRIORITY FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-42

Query Match          68.5%; Score 37; DB 13; Length 53;
Best Local Similarity 88.9%; Pred. No. 0.00063;
Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATT 45
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGATAAATT 45

RESULT 15
US-09-738-972-3
; Sequence 3, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
```

```
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-3

Query Match          68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 57

RESULT 16
US-09-738-972-13/c
; Sequence 13, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-13

Query Match          68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 GAAATTAATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTTCCCACT 52
    |||||
Db 57 GAAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATTTCCCACT 1

RESULT 17
US-09-738-274-7
; Sequence 7, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
```

```
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-7

Query Match      68.5%; Score 37; DB 3; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 57
    |||||||

RESULT 18
US-10-862-026-3
; Sequence 3, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-862-026-3

Query Match      68.5%; Score 37; DB 9; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 57
    |||||||

RESULT 19
US-10-862-026-13/c
; Sequence 13, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
```

```
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: probe
; LOCATION: (1)..(33)
US-10-862-026-13

Query Match      68.5%; Score 37; DB 9; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
    |||||||
Db 57 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 1
    |||||||

RESULT 20
US-10-665-708-7
; Sequence 7, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAI, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-665-708-7

Query Match      68.5%; Score 37; DB 10; Length 57;
Best Local Similarity 91.2%; Pred. No. 0.00064;
Matches 52; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

Qy 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 52
    |||||||
Db 1 GAAATTATACGACTCACTATAGGAGACCA-----CATTGTGCAATATTCCTCCACT 57
    |||||||

RESULT 21
US-09-944-036-2
; Sequence 2, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
```

```
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-09-944-036-2
```

```
Query Match 66.7%; Score 36; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
```

```
RESULT 22
US-10-425-975-2
; Sequence 2, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter
; NAME/KEY: promoter
; LOCATION: (1)..(29)
US-10-425-975-2
```

```
Query Match 66.7%; Score 36; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
```

```
RESULT 23
US-11-145-272-2
; Sequence 2, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 37
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter
US-11-145-272-2
```

```
Query Match 66.7%; Score 36; DB 13; Length 37;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
|||||
DB 1 GAAATTAATACGACTCACTATAGGAGACCATTTG 36
```

```
RESULT 24
US-09-944-036-6
; Sequence 6, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Nebularine
US-09-944-036-6
```

```
Query Match          66.7%; Score 36; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 25
US-10-425-975-6
; Sequence 6, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (46)
; OTHER INFORMATION: Nebularine
US-10-425-975-6

Query Match          66.7%; Score 36; DB 7; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 26
US-11-145-272-6
; Sequence 6, Application US/11145272
; Publication No. US2005027227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
```

```
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; NAME/KEY: misc_feature
; LOCATION: (46)..(46)
; OTHER INFORMATION: Nebularine
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-6

Query Match          66.7%; Score 36; DB 13; Length 54;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 27
US-09-944-036-34
; Sequence 34, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; NAME/KEY: modified_base
; LOCATION: (45)
; OTHER INFORMATION: Nebularine
US-09-944-036-34

Query Match          66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTGTC 39
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTATGC 39
```



```

RESULT 28
US-09-944-036-36
; Sequence 36, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-36

Query Match      66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39

RESULT 29
US-10-425-975-34
; Sequence 34, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-34

Query Match      66.3%; Score 35.8; DB 3; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39

RESULT 30
US-10-425-975-36
; Sequence 36, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-36

Query Match      66.3%; Score 35.8; DB 7; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39

RESULT 31
US-11-145-272-34
; Sequence 34, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
US-11-145-272-34

```

```

; OTHER INFORMATION: Nebularine
US-10-425-975-34

Query Match      66.3%; Score 35.8; DB 7; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39

RESULT 30
US-10-425-975-36
; Sequence 36, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-36

Query Match      66.3%; Score 35.8; DB 7; Length 53;
Best Local Similarity 94.9%; Pred. No. 0.0018;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39
Db 1 GAAATTAATACGACTCACTATAGGAGACCATGTCG 39

RESULT 31
US-11-145-272-34
; Sequence 34, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
US-11-145-272-34

```

; PRIOR APPLICATION NUMBER: 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for Gag target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; OTHER INFORMATION:  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (45)..(45)  
; OTHER INFORMATION: Nebularine  
US-11-145-272-34

Query Match 66.3%; Score 35.8; DB 13; Length 53;  
Best Local Similarity 94.9%; Pred. No. 0.0018;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39

RESULT 32  
US-11-145-272-36  
; Sequence 36, Application US/11145272  
; Publication No. US2005022727A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations  
; FILE REFERENCE: GP114-04.DV2  
; CURRENT APPLICATION NUMBER: US/11/145,272  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 10/425,975  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for Gag target sequence  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; OTHER INFORMATION:  
US-11-145-272-36

Query Match 66.3%; Score 35.8; DB 13; Length 53;  
Best Local Similarity 94.9%; Pred. No. 0.0018;  
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGC 39

RESULT 33  
US-10-500-646-241  
; Sequence 241, Application US/10500646  
; Publication No. US20050069890A1  
; GENERAL INFORMATION:  
; APPLICANT: MABILAT, Claude  
; APPLICANT: DESVARENNE, Sabine  
; APPLICANT: BABOLA, Odile  
; APPLICANT: LACROIX, Bruno  
; APPLICANT: BELLO PIGEM, Natalia  
; TITLE OF INVENTION: Method for the detection and/or identification of the original animal species in animal matter contained in a sample  
; FILE REFERENCE: 120162  
; CURRENT APPLICATION NUMBER: US/10/500,646  
; CURRENT FILING DATE: 2004-07-02  
; PRIOR APPLICATION NUMBER: FR 0200265  
; PRIOR FILING DATE: 2002-01-10  
; NUMBER OF SEQ ID NOS: 276  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 241  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: primer sequence CBHT7 20  
US-10-500-646-241

Query Match 65.6%; Score 35.4; DB 10; Length 53;  
Best Local Similarity 86.7%; Pred. No. 0.0026;  
Matches 39; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATT 45  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAGATGATATT 45

RESULT 34  
US-10-273-707-49  
; Sequence 49, Application US/10273707  
; Publication No. US20030104448A1  
; GENERAL INFORMATION:  
; APPLICANT: HARVEY, Richard, C.  
; APPLICANT: CLARK, JR., Thomas, J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS  
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE  
; FILE REFERENCE: GP097-03.DV1  
; CURRENT APPLICATION NUMBER: US/10/273,707  
; CURRENT FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: 09/493,491  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/117,640 US  
; PRIOR FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 54  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: construct  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1)..(28)  
US-10-273-707-49

Query Match 65.6%; Score 35.4; DB 6; Length 54;  
Best Local Similarity 79.2%; Pred. No. 0.0026;  
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCCCACTGC 54  
Db 2 AAATTAATACGACTCACTATAGGAGACCACAAATTTCTTGCATCCCACTTGC 54

```

RESULT 35
US-10-978-145-49
; Sequence 49, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/978,145
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1998-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-978-145-49

Query Match          65.6%; Score 35.4; DB 10; Length 54;
Best Local Similarity 79.2%; Pred. No. 0.0026;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY  2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATCCCACTGC 54
    |||||||
DB   2 AAATTAATACGACTCACTATAGGAGACCACTTGTGCAATATCCCACTGC 54
    |||||||

RESULT 36
US-09-944-036-10
; Sequence 10, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-10

Query Match          65.6%; Score 35.4; DB 3; Length 55;
Best Local Similarity 79.2%; Pred. No. 0.0026;
Matches 42; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

```

```

Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
    |||||||
DB   1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
    |||||||

RESULT 37
US-10-425-975-10
; Sequence 10, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-10

Query Match          65.6%; Score 35.4; DB 7; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
    |||||||
DB   1 GAAATTAATACGACTCACTATAGGAGACCACTTGT 37
    |||||||

RESULT 38
US-11-145-272-10
; Sequence 10, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70

```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-10

Query Match          65.6%; Score 35.4; DB 13; Length 55;
Best Local Similarity 97.3%; Pred. No. 0.0026;
Matches 36; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATTGT 37
    |||||
Db 1 GAAATTAATAGCACTCACTATAGGAGACCACACTGT 37

RESULT 39
US-09-944-036-43
; Sequence 43, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-43

Query Match          64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35
    |||||
Db 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35

RESULT 40
US-09-738-274-12
; Sequence 12, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
```

```
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-274-12

Query Match          64.8%; Score 35; DB 3; Length 52;
Best Local Similarity 80.4%; Pred. No. 0.0036;
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATTGTGCAATATTCGCCAC 51
    |||||
Db 1 GAAATTAATAGCACTCACTATAGGAGACCACATGCATCAGGCTTGGCCCC 51

RESULT 41
US-10-425-975-43
; Sequence 43, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-43

Query Match          64.8%; Score 35; DB 7; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35
    |||||
Db 1 GAAATTAATAGCACTCACTATAGGAGACCACATT 35

RESULT 42
US-10-665-708-12
```

; Sequence 12, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02 UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; PRIOR FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-665-708-12

Query Match 64.8%; Score 35; DB 10; Length 52;  
Best Local Similarity 80.4%; Pred. No. 0.0036;  
Matches 41; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
  
QY 1 GAAATTATACGACTCACTATAGGAGACCATTTGCAATATTCCTCCAC 51  
|||||  
DB 1 GAAATTATACGACTCACTATAGGAGACCATGTCATGCTGGGCC 51  
|||||

RESULT 43  
US-11-145-272-43  
; Sequence 43, Application US/11145272  
; Publication No. US2005022727A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations  
; FILE REFERENCE: GP114-04.DV2  
; CURRENT APPLICATION NUMBER: US/11/145,272  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US/10/425,975  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 52  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
; OTHER INFORMATION:

US-11-145-272-43  
  
Query Match 64.8%; Score 35; DB 13; Length 52;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GAAATTATACGACTCACTATAGGAGACCATTT 35  
|||||  
DB 1 GAAATTATACGACTCACTATAGGAGACCATTT 35  
|||||  
  
RESULT 44  
US-09-944-036-35  
; Sequence 35, Application US/09944036  
; Patent No. US20020055095A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-35

Query Match 64.4%; Score 34.8; DB 3; Length 53;  
Best Local Similarity 84.8%; Pred. No. 0.0043;  
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 GAAATTATACGACTCACTATAGGAGACCATTTGCAATATTC 46  
|||||  
DB 1 GAAATTATACGACTCACTATAGGAGACCATGCTCCTTC 46  
|||||  
  
RESULT 45  
US-10-425-975-35  
; Sequence 35, Application US/10425975  
; Publication No. US20030228574A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 53

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-35

Query Match          64.4%; Score 34.8; DB 7; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.0043;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTC 46
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTC 46
    |||||

RESULT 46
US-11-145-272-35
; Sequence 35, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-35

Query Match          64.4%; Score 34.8; DB 13; Length 53;
Best Local Similarity 84.8%; Pred. No. 0.0043;
Matches 39; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTC 46
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTGCAATATTC 46
    |||||

RESULT 47
US-09-944-036-33
; Sequence 33, Application US/09944036
; Patent No. US2002005095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
```

```
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-33

Query Match          63.7%; Score 34.4; DB 3; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.0062;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTG 36
    |||||

RESULT 48
US-10-425-975-33
; Sequence 33, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-33

Query Match          63.7%; Score 34.4; DB 7; Length 54;
Best Local Similarity 97.2%; Pred. No. 0.0062;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTGTG 36
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTGTG 36
    |||||

RESULT 49
US-11-145-272-33
```

Sequence 33, Application US/11145272  
Publication No. US2005022727A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations  
FILE REFERENCE: GP114-04.DV2  
CURRENT APPLICATION NUMBER: US/11/145,272  
CURRENT FILING DATE: 2005-06-03  
PRIOR APPLICATION NUMBER: US 10/425,975  
PRIOR FILING DATE: 2003-04-28  
PRIOR APPLICATION NUMBER: 09/944,036  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 33  
LENGTH: 54  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer for Gag target sequence  
FEATURE:  
NAME/KEY: promoter  
LOCATION: (1)..(33)  
OTHER INFORMATION:  
US-11-145-272-33

Query Match 63.7%; Score 34.4; DB 13; Length 54;  
Best Local Similarity 97.2%; Pred. No. 0.0062;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

RESULT 50  
US-10-140-545-48  
Sequence 48, Application US/10140545  
Publication No. US2003017526A1  
GENERAL INFORMATION:  
APPLICANT: Daniel, Steven G  
APPLICANT: Turner, Leah  
APPLICANT: Samartzidou, Hrisi  
APPLICANT: Houts, Thomas M  
TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION  
FILE REFERENCE: PB0120  
CURRENT APPLICATION NUMBER: US/10/140,545  
CURRENT FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: US 60/289,202  
PRIOR FILING DATE: 2001-05-07  
PRIOR APPLICATION NUMBER: US 60/312,420  
PRIOR FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 62  
TYPE: DNA  
ORGANISM: Saccharomyces cerevisiae  
US-10-140-545-48

Query Match 63.7%; Score 34.4; DB 7; Length 62;  
Best Local Similarity 97.2%; Pred. No. 0.0064;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36

Db 15 GAAATTAATACGACTCACTATAGGAGACCACTTG 50  
|||||  
RESULT 51  
US-11-013-179-48  
Sequence 48, Application US/11013179  
Publication No. US20050095640A1  
GENERAL INFORMATION:  
APPLICANT: SAMARTZIDOU, Hrisi  
APPLICANT: TURNER, Leah  
APPLICANT: HOUTS, Thomas  
TITLE OF INVENTION: DESIGN OF ARTIFICIAL GENES FOR USE AS CONTROLS IN GENE EXPRESSION  
FILE REFERENCE: PB0120  
CURRENT APPLICATION NUMBER: US/11/013,179  
CURRENT FILING DATE: 2004-12-15  
PRIOR APPLICATION NUMBER: US 10/140,545  
PRIOR FILING DATE: 2002-05-07  
PRIOR APPLICATION NUMBER: US 60/289,202  
PRIOR FILING DATE: 2001-05-07  
PRIOR APPLICATION NUMBER: US 60/312,420  
PRIOR FILING DATE: 2001-08-15  
NUMBER OF SEQ ID NOS: 60  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 48  
LENGTH: 62  
TYPE: DNA  
ORGANISM: Saccharomyces cerevisiae  
US-11-013-179-48

Query Match 63.7%; Score 34.4; DB 13; Length 62;  
Best Local Similarity 97.2%; Pred. No. 0.0064;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTTG 36  
|||||  
Db 15 GAAATTAATACGACTCACTATAGGAGACCACTTG 50

RESULT 52  
US-09-944-036-38  
Sequence 38, Application US/09944036  
Patent No. US2002005095A1  
GENERAL INFORMATION:  
APPLICANT: YANG, Yeasing Y.  
APPLICANT: BRENTANO, Steven T.  
APPLICANT: BABOLA, Odile  
APPLICANT: TRAN, Nathalie  
APPLICANT: VERNET, Guy  
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
FILE REFERENCE: GP114-02.UT  
CURRENT APPLICATION NUMBER: US/09/944,036  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: US 60/229,790  
PRIOR FILING DATE: 2000-09-01  
NUMBER OF SEQ ID NOS: 70  
SOFTWARE: PatentIn ver. 2.1  
SEQ ID NO 38  
LENGTH: 53  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Oligonucleotide primer for Protease target  
OTHER INFORMATION: sequence  
NAME/KEY: promoter  
LOCATION: (1)..(33)  
US-09-944-036-38

Query Match 63.0%; Score 34; DB 3; Length 53;

Best Local Similarity 88.1%; Pred. No. 0.0088;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**Qy**

1 GAAATTAAACGACTCACTATAGGGAGACCACATTGTGCAAT 42  
|||||

**Db**

1 GAAATTAAACGACTCACTATAGGGAGACCACCATCCATT 42  
|||||

## RESULT 53

```

US-10-425-975-38
; Sequence 38, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-38

```

Query Match 63.0%; Score 34; DB 7; Length 53;  
Best Local Similarity 88.1%; Pred. No. 0.0088;  
Matches 37; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGGAGACCACATTGTGCAAT 42

Db 1 GAAATTAATACGACTCACTATAGGGAGACCACATTCCATT 42

RESULT 54

```

RES001_34
US-11-145-272-38
: Sequence 38, Application US/11145272
: Publication No. US20050227227A1
: GENERAL INFORMATION:
: APPLICANT: YANG, Yeasing Y.
: APPLICANT: BRENTANO, Steven T.
: APPLICANT: BABOLA, Odile
: APPLICANT: TRAN, Nathalie
: APPLICANT: VERNET, Guy
: TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
: TITLE OF INVENTION: with drug-resistance mutations
: FILE REFERENCE: GP114-04.DV2
: CURRENT APPLICATION NUMBER: US/11/145,272
: CURRENT FILING DATE: 2005-06-03
: PRIOR APPLICATION NUMBER: US 10/425,975
: PRIOR FILING DATE: 2003-04-28
: PRIOR APPLICATION NUMBER: 09/944,036
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 60/229,790
: PRIOR FILING DATE: 2000-09-01
: NUMBER OF SEQ ID NOS: 70

```

```
; SOFTWARE: PatentIn version 3.1
```

```

; SEQ ID NO 38
;
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Protease target sequence
;
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
;
US-11-145-272-38

```

Query Match 63.0%; Score 34; DB 13; Length 53;  
Best Local Similarity 88.1%; Pred. No. 0.0088;  
Matches 37: Conservative 0; Mismatches 5; Indels

QY 1 GAAATTAAACGACTCACTATAGGGAGCCACATTGTGCAAT 42  
|||||

pb 1 GAAATTAAACGACTCACTATAGGGAGCCACATTCCATT 42  
|||||

RESULT 55

```

US-10-273-707-30
; Sequence 30, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1993-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
; US-10-273-707-30

```

Query Match 63.0%; Score 34; DB 6; Length 54;  
Best Local Similarity 80.0%; Pred. No. 0.0088:

	Qy	2	AAATTAATACGACTCATATAGGGAGACCACATTGTGCAATATATCCCCAC	51			
Matches	40	Conservative	0	Mismatches	10	Indels	0
	Db	2	AAATTAATACGACTCATATAGGGAGACCACAGAGGGTGAATTTGGGCACAC	51			

## RESULT 56

```

US-10-978-145-30
; Sequence 30, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; TITLE OF INVENTION: FOR CANCER IN A BIOLOGICAL SAMPLE
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/978,145
; CURRENT FILING DATE: 2004-10-28

```



```
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: construct
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-978-145-30
```

```
Query Match 63.0%; Score 34; DB 10; Length 54;
Best Local Similarity 80.0%; Pred. No. 0.0088;
Matches 40; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
```

```
Qy 2 AAATTAATACGACTCACTATAGGAGACACATTTGTGAATATCCGCAC 51
|||||
Db 2 AAATTAATACGACTCACTATAGGAGACACATTTGTGAATATCCGCAC 51
|||||
```

```
RESULT 57
US-09-944-036-45
; Sequence 45, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-45
```

```
Query Match 63.0%; Score 34; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCCACAT 34
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCCACAT 34
|||||
```

```
RESULT 58
US-10-425-975-45
; Sequence 45, Application US/10425975
; Publication No. US20030228574A1
```

```
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-45
```

```
Query Match 63.0%; Score 34; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCCACAT 34
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCCACAT 34
|||||
```

```
RESULT 59
US-11-145-272-45
; Sequence 45, Application US/11145272
; Publication No. US20050227227A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-45
```

```
Query Match      63.0%; Score 34; DB 13; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 60
US-09-738-972-2
; Sequence 2, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-2

Query Match      63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 61
US-09-738-972-12/c
; Sequence 12, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-12

Query Match      63.0%; Score 34; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCACAT 28

RESULT 62
US-10-862-026-2
; Sequence 2, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-862-026-2

Query Match      63.0%; Score 34; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACAT 34
    |||||

RESULT 63
US-10-862-026-12/c
; Sequence 12, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: Gp119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 61
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-862-026-12

Query Match      63.0%; Score 34; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GAAATTAATACGACTCACTATAGGAGACCAT 34
    |||||
Db 61 GAAATTAATACGACTCACTATAGGAGACCAT 28

RESULT 64
US-10-273-707-36
; Sequence 36, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-273-707-36

Query Match 62.6%; Score 33.8; DB 6; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.01;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 65
US-10-778-145-36
; Sequence 36, Application US/10978145
; Publication No. US20050118630A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US/10/273,707
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(28)
US-10-778-145-36

Query Match 62.6%; Score 33.8; DB 6; Length 52;
Best Local Similarity 94.6%; Pred. No. 0.01;
Matches 35; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38
    |||||
Db 2 AAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 66
US-10-001-407-19
; Sequence 19, Application US/10001407
; Publication No. US2002017127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP117-03 UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
; OTHER INFORMATION: primer sequence
US-10-001-407-19

Query Match 61.5%; Score 33.2; DB 6; Length 58;
Best Local Similarity 92.1%; Pred. No. 0.018;
Matches 35; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTG 38
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCATTTGTG 38

RESULT 67
US-09-765-555-66
; Sequence 66, Application US/09765555
; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 09/620,897
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 5731
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2C7-SiD
US-09-765-555-66
```

Query Match 61.5%; Score 33.2; DB 3; Length 5731;  
Best Local Similarity 75.9%; Pred. No. 0.046; 13; Indels 0; Gaps 0;  
Matches 41; Conservative 0; Mismatches 13; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAATATTCCCACTGC 54  
|||||  
Db 858 GAAATTAATACGACTCACTATAGGAGACCAAGCTGCTAGCATGGCCGCTGC 911  
|||||

RESULT 68  
US-09-738-972-10  
; Sequence 10, Application US/09738972  
; Patent No. US20020012918A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-09-738-972-10

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||

RESULT 69  
US-09-944-036-4  
; Sequence 4, Application US/09944036  
; Patent No. US2002005095A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/09/944,036  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-09-944-036-4

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||

RESULT 70  
US-09-738-274-36  
; Sequence 36, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-09-738-274-36

Query Match 61.1%; Score 33; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||  
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
|||||

RESULT 71  
US-10-001-407-29  
; Sequence 29, Application US/10001407  
; Publication No. US20020177127A1  
; GENERAL INFORMATION:  
; APPLICANT: Yang, Yeasing  
; APPLICANT: Burrell, Terrie  
; TITLE OF INVENTION: Compositions and Methods for Detecting  
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)  
; FILE REFERENCE: GP117-03.UT  
; CURRENT APPLICATION NUMBER: US/10/001,407  
; CURRENT FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: 60/242,620  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/280,058  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: HIV-2  
US-10-001-407-29

Query Match 61.1%; Score 33; DB 6; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGGAGACCACA 33  
|||||  
Db 1 GAAATTATACGACTCACTATAGGGAGACCACA 33

RESULT 72  
US-10-425-975-4  
; Sequence 4, Application US/10425975  
; Publication No. US20030228574A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF  
; FILE REFERENCE: GP114-02.UT  
; CURRENT APPLICATION NUMBER: US/10/425,975  
; CURRENT FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US/09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: US 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: T7 promoter  
; NAME/KEY: promoter  
; LOCATION: (1)..(33)  
US-10-425-975-4

Query Match 61.1%; Score 33; DB 7; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGGAGACCACA 33  
|||||  
Db 1 GAAATTATACGACTCACTATAGGGAGACCACA 33

RESULT 73  
US-10-862-026-10  
; Sequence 10, Application US/10862026  
; Publication No. US20040224348A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/10/862,026  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-10-862-026-10

Query Match 61.1%; Score 33; DB 9; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTATACGACTCACTATAGGGAGACCACA 33  
|||||  
Db 1 GAAATTATACGACTCACTATAGGGAGACCACA 33

RESULT 74  
US-10-665-708-36  
; Sequence 36, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAN, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 36  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: promoter  
US-10-665-708-36

Query Match 61.1%; Score 33; DB 10; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.019;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTATACGACTCACTATAGGGAGACCACA 33  
|||||  
Db 1 GAAATTATACGACTCACTATAGGGAGACCACA 33

RESULT 75  
US-11-145-272-4  
; Sequence 4, Application US/11145272  
; Publication No. US2005022727A1  
; GENERAL INFORMATION:  
; APPLICANT: YANG, Yeasing Y.  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: BABOLA, Odile  
; APPLICANT: TRAN, Nathalie  
; APPLICANT: VERNET, Guy  
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations  
; FILE REFERENCE: GP114-04.DV2  
; CURRENT APPLICATION NUMBER: US/11/145,272  
; CURRENT FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: US 10/425,975  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: 09/944,036  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 60/229,790  
; PRIOR FILING DATE: 2000-09-01  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 33  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:



```
US-11-142-790-3
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Inferring Function from Shotgun Sequencing Data
; FILE REFERENCE: NEB-248-US
; CURRENT APPLICATION NUMBER: US/11/142,790
; PRIOR FILING DATE: 2005-06-01
; PRIOR APPLICATION NUMBER: 60/576,196
; PRIOR FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 42
; TYPE: DNA
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: T7 universal primer
US-11-142-790-3

Query Match          61.1%; Score 33; DB 16; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.02; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 81
US-09-944-036-41
; Sequence 41, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-41

Query Match          61.1%; Score 33; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 82
US-10-425-975-41
; Sequence 41, Application US/10425975
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Reverse Transcriptase target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
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; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-944-036-37

```

```

Query Match          61.1%; Score 33; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
    |||||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

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RESULT 88
US-10-425-975-37
; Sequence 37, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-10-425-975-37

```

```

Query Match          61.1%; Score 33; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
    |||||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

```

```

RESULT 89
US-11-145-272-37
; Sequence 37, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer for Protease target sequence
; NAME/KEY: promoter
; LOCATION: (1)..(33)
; OTHER INFORMATION:
US-11-145-272-37

Query Match          61.1%; Score 33; DB 13; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33
    |||||||
DB 1 GAAATTAATACGACTCACTATAGGGAGACCACA 33

RESULT 90
US-09-944-036-44
; Sequence 44, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence

```

```
; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-09-944-036-44

Query Match      61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 91
US-10-425-975-44
; Sequence 44, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 44
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Reverse Transcriptase
; OTHER INFORMATION: target sequence
; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-10-425-975-44

Query Match      61.1%; Score 33; DB 7; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 92
US-11-145-272-44
; Sequence 44, Application US/11145272
; Publication No. US2005022727A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: Amplification of HIV-1 sequences for detection of sequences associated with drug-resistance mutations
; FILE REFERENCE: GP114-04.DV2
; CURRENT APPLICATION NUMBER: US/11/145,272
; CURRENT FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: US 10/425,975
; PRIOR FILING DATE: 2003-04-28

; NAME/KEY: promoter
; LOCATION: (1)...(33)
US-09-944-036-44

Query Match      61.1%; Score 33; DB 3; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 93
US-10-001-407-18
; Sequence 18, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
; OTHER INFORMATION: SEQ ID NO:13
US-10-001-407-18

Query Match      61.1%; Score 33; DB 6; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
    |||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 94
US-10-500-646-234
; Sequence 234, Application US/10500646
; Publication No. US20050069890A1
; GENERAL INFORMATION:
; APPLICANT: MABILAT, Claude
; APPLICANT: DESVARENNE, Sabine
; APPLICANT: BABOLA, Odile
; APPLICANT: LACROIX, Bruno
```

```
; APPLICANT: BELLO PIGEM, Natalia
; TITLE OF INVENTION: Method for the detection and/or identification of the original an
; FILE REFERENCE: 120162
; CURRENT APPLICATION NUMBER: US/10/500,646
; PRIOR FILING DATE: 2004-07-02
; PRIOR APPLICATION NUMBER: FR 0200265
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 58
; TYPE: DNA
; ORGANISM: primer sequence CBHT7
US-10-500-646-234

Query Match          61.1%; Score 33; DB 10; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 95
US-09-738-972-1
; Sequence 1, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; NAME/KEY: promoter
; LOCATION: (1)..(33)
US-09-738-972-1

Query Match          61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 96
US-09-738-972-11/c
; Sequence 11, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; PRIOR FILING DATE: 2000-12-15
```

```
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-11

Query Match          61.1%; Score 33; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
|||||
Db 59 GAAATTAATACGACTCACTATAGGAGACCACA 27

RESULT 97
US-10-862-026-1
; Sequence 1, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: promoter-primer
; NAME/KEY: promoter
; LOCATION: (1)..(33)
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; Sequence 11, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GPI19-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
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; Sequence 5, Application US/09953321
; Patent No. US20020115083A1
; GENERAL INFORMATION:
; APPLICANT: HANES, JOZEF
; APPLICANT: JERMUTUS, LUTZ
; TITLE OF INVENTION: NOVEL METHODS FOR IDENTIFYING NUCLEIC ACID MOLECULES ENCODING
; FILE REFERENCE: PLUCK/1 CON2
; CURRENT APPLICATION NUMBER: US/09/953,321
; PRIOR APPLICATION NUMBER: 2001-09-14
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Oligonucleotide ON3
US-09-953-321-5

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; Sequence 2, Application US/10124663
; Publication No. US20030073201A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Method for Improving the Stability of Linear DNA in Cell-free in
; FILE REFERENCE: RDID 010490S
; CURRENT APPLICATION NUMBER: US/10/124,663
; CURRENT FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.1
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GenCore version 5.1.8  
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Searched: 224314 seqs, 3527956 residues

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Listing first 300 summaries

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SUMMARIES

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6	33	61.1	8810	US-11-258-704-40	Sequence 40, Appli
7	33	61.1	8819	US-11-258-704-41	Sequence 41, Appli
8	30.8	57.0	2338	US-11-246-999-148	Sequence 148, App
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111	21.4	39.6	5833	7	US-11-254-173-46	Sequence 46, Appl	184	21.4	39.6	12649	7	US-11-024-545-38	Sequence 38, App
112	21.4	39.6	5833	7	US-11-264-784-131	Sequence 131, App	185	21.4	39.6	12649	7	US-11-185-301-27	Sequence 27, Appl
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c 294 19.2 35.2 1674 7 US-11-263-057-22  
c 295 19.2 35.2 1674 7 US-11-263-057-22  
c 296 19.2 35.2 1674 7 US-11-263-057-22  
c 297 19.2 35.2 1674 7 US-11-263-057-22  
c 298 19.2 35.2 1674 7 US-11-263-057-22  
c 299 19.2 35.2 1674 7 US-11-263-057-22  
c 300 19.2 35.2 1674 7 US-11-263-057-22

ALIGNMENTS

RESULT 1  
US-10-953-688A-5  
; Sequence 5, Application US/10953688A  
; Publication No. US20060099602A1  
; GENERAL INFORMATION:  
; APPLICANT: Precision System Science Co., Ltd  
; APPLICANT: National Institute of Advanced Industrial Science and Technology  
; TITLE OF INVENTION: Nucleic acid library and protein library  
; FILE REFERENCE: PCT03-1004-US  
; CURRENT APPLICATION NUMBER: US/10/953,688A  
; CURRENT FILING DATE: 2004-09-29  
; PRIOR APPLICATION NUMBER: JP 2002-095285

Sequence 81701, A  
Sequence 2957, Ap  
Sequence 51, Appl  
Sequence 85, Appl  
Sequence 151, Appl  
Sequence 46, Appl  
Sequence 81996, A  
Sequence 2840, Ap  
Sequence 82281, A  
Sequence 444, App  
Sequence 5194, Ap  
Sequence 22, Appl  
Sequence 7, Appl  
Sequence 1361, Ap  
Sequence 82221, A  
Sequence 78985, A  
Sequence 78111, A  
Sequence 279, App  
Sequence 77878, A  
Sequence 3, Appl  
Sequence 77984, A  
Sequence 78208, A  
Sequence 4802, Ap  
Sequence 81292, A  
Sequence 3169, Ap  
Sequence 2, Appl  
Sequence 82708, A  
Sequence 79862, A  
Sequence 77398, A  
Sequence 4885, Ap  
Sequence 2497, Ap  
Sequence 34, Appl  
Sequence 29, Appl  
Sequence 37, Appl  
Sequence 1764, Ap  
Sequence 80397, A  
Sequence 3540, Ap  
Sequence 77915, A  
Sequence 33, Appl  
Sequence 82728, A  
Sequence 1218, Ap  
Sequence 4214, Ap  
Sequence 5983, Ap  
Sequence 54, Appl  
Sequence 173824, A  
Sequence 77193, A  
Sequence 166655, A  
Sequence 75863, A  
Sequence 101, App  
Sequence 191177, A  
Sequence 327, App  
Sequence 109, App  
Sequence 1807, App  
Sequence 528, App  
Sequence 2499, Ap  
Sequence 3362, Ap

Query Match 61.1%; Score 33; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 2  
US-10-953-688A-6  
; Sequence 6, Application US/10953688A  
; Publication No. US20060099602A1  
; GENERAL INFORMATION:  
; APPLICANT: Precision System Science Co., Ltd  
; APPLICANT: National Institute of Advanced Industrial Science and Technology  
; TITLE OF INVENTION: Nucleic acid library and protein library  
; FILE REFERENCE: PCT03-1004-US  
; CURRENT APPLICATION NUMBER: US/10/953,688A  
; CURRENT FILING DATE: 2004-09-29  
; PRIOR APPLICATION NUMBER: JP 2002-095285  
; PRIOR FILING DATE: 2002-03-29  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 6  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: upstream primer for 1st PCR

US-10-953-688A-6  
Query Match 61.1%; Score 33; DB 6; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.5e-05;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33  
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 3  
US-10-472-003-6  
; Sequence 6, Application US/10472003  
; Publication No. US20060099577A1  
; GENERAL INFORMATION:  
; APPLICANT: RiNA Netzwerk TNA-Technologien GmbH  
; APPLICANT: Erdmann, Volker  
; APPLICANT: Stiege, Wolfgang  
; TITLE OF INVENTION: Method for Preparative Production of Long Nucleic Acids by PCR  
; FILE REFERENCE: RNA/US/0308 / 00140/019001  
; CURRENT APPLICATION NUMBER: US/10/472,003  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: DE 101 13 265  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: DE 101 51 071  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: DE 101 45 014  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 75

```
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
; NAME/KEY: primer bind
; LOCATION: (1)..(75)
US-10-472-003-6

Query Match          61.1%; Score 33; DB 6; Length 75;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 1 GAAATTAATACGACTCACTATAGGAGACCACA 33

RESULT 4
US-10-953-688A-2
; Sequence 2, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; PRIOR FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(534)
; OTHER INFORMATION: Description of Artificial Sequence: His-labeled avidin gene
US-10-953-688A-2

Query Match          61.1%; Score 33; DB 6; Length 651;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 5
US-10-953-688A-3
; Sequence 3, Application US/10953688A
; Publication No. US20060099602A1
; GENERAL INFORMATION:
; APPLICANT: Precision System Science Co., Ltd
; TITLE OF INVENTION: Nucleic acid library and protein library
; FILE REFERENCE: PCT03-1004-US
; CURRENT APPLICATION NUMBER: US/10/953,688A
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: JP 2002-095285
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(537)
; OTHER INFORMATION: Description of Artificial Sequence: HA-labeled avidin gene
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```
US-10-953-688A-3

Query Match          61.1%; Score 33; DB 6; Length 654;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 13 GAAATTAATACGACTCACTATAGGAGACCACA 45

RESULT 6
US-11-258-704-40
; Sequence 40, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Stoop, Johan
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENES
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
; LENGTH: 8810
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH50
US-11-258-704-40

Query Match          61.1%; Score 33; DB 7; Length 8810;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
   |||||||
Db 5216 GAAATTAATACGACTCACTATAGGAGACCACA 5248

RESULT 7
US-11-258-704-41
; Sequence 41, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Zhan-Bin
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENES
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 8819
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH58
US-11-258-704-41

Query Match          61.1%; Score 33; DB 7; Length 8819;
Best Local Similarity 100.0%; Pred. No. 7.1e-05;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGGAGACCACA 33
```



```
Db      6810 GAAATTAATACGACTCACTATAGGAGACCACA 6842
|||||
RESULT 8
US-11-246-999-148
; Sequence 148, Application US/11246999
; Publication No. US20060099622A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 12 Human Secreted Proteins
; FILE REFERENCE: PF489P2
; CURRENT APPLICATION NUMBER: US/11/246,999
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/09/984,130
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 60/243,792
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 09/836,353
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/198,407
; PRIOR FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: PCT/US99/25031
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: 60/105,971
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 148
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (6)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (18)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (23)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (25)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
```

```
; NAME/KEY: SITE
; LOCATION: (26)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (27)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (28)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (29)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (33)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (37)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (38)
; OTHER INFORMATION: n equals a,t,g, or c
US-11-246-999-148

Query Match      57.0%; Score 30.8; DB 7; Length 2338;
Best Local Similarity 83.3%; Pred. No. 0.00038;
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1 GAAATTAATACGACTCACTATAGGAGACCACATTGTGCAAT 42
        |||||
Db      107 GAAATTAATACGACTCACTATAGGAGACCACCGCTTGATAT 148

RESULT 9
US-11-258-392-2
; Sequence 2, Application US/11258392
; Publication No. US20060099193A1
; GENERAL INFORMATION:
; APPLICANT: SUGAYA, IKUKO
; APPLICANT: SUGAYA, KIMINOBU
; TITLE OF INVENTION: METHODS AND MATERIALS FOR SUPPRESSING PAIN
; FILE REFERENCE: 10669-009
; CURRENT APPLICATION NUMBER: US/11/258,392
; PRIOR FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 60/621,903
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 3780
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Cloning vector sequence
US-11-258-392-2

Query Match          55.9%; Score 30.2; DB 7; Length 3780;
Best Local Similarity 91.4%; Pred. No. 0.00078;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACCACTT 35
    |||||
Db 2778 GAAATTAATACGACTCACTATAGGAGACCGGAAT 2812

RESULT 10
US-11-283-332A-24
; Sequence 24, Application US/11283332A
; Publication No. US20060099686A1
; GENERAL INFORMATION:
; APPLICANT: Scil Proteins GmbH
; APPLICANT: Fiedler, Markus
; APPLICANT: Fiedler, Ulrike
; APPLICANT: Rudolph, Rainer
; TITLE OF INVENTION: Generation of artificial binding proteins based on ubiquitin protein
; FILE REFERENCE: P17437
; CURRENT APPLICATION NUMBER: US/11/283,332A
; CURRENT FILING DATE: 2005-11-18
; PRIOR APPLICATION NUMBER: DE 103 24 447.6
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 42
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized flanking oligonucleotide
US-11-283-332A-24

Query Match          55.6%; Score 30; DB 7; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 5 GAAATTAATACGACTCACTATAGGAGACC 34

RESULT 11
US-11-267-871-716
; Sequence 716, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 716
; LENGTH: 3821
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pNAUT hGH vector
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```
US-11-267-871-716

Query Match          55.6%; Score 30; DB 7; Length 3821;
Best Local Similarity 100.0%; Pred. No. 0.00094;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 480 GAAATTAATACGACTCACTATAGGAGACC 509

RESULT 12
US-11-258-392-3
; Sequence 3, Application US/11258392
; Publication No. US20060099193A1
; GENERAL INFORMATION:
; APPLICANT: SUGAYA, IKUKO
; APPLICANT: SUGAYA, KIMINOBU
; TITLE OF INVENTION: METHODS AND MATERIALS FOR SUPPRESSING PAIN
; FILE REFERENCE: 10669-009
; CURRENT APPLICATION NUMBER: US/11/258,392
; CURRENT FILING DATE: 2005-10-24
; PRIOR APPLICATION NUMBER: 60/621,903
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 3
; LENGTH: 5933
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: cloning vector sequence
US-11-258-392-3

Query Match          55.6%; Score 30; DB 7; Length 5933;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGAGACC 30
    |||||
Db 858 GAAATTAATACGACTCACTATAGGAGACC 887

RESULT 13
US-11-233-094-37
; Sequence 37, Application US/11233094
; Publication No. US20060094041A1
; GENERAL INFORMATION:
; APPLICANT: MARUYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081USO
; CURRENT APPLICATION NUMBER: US/11/233,094
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-233-094-37

Query Match          49.6%; Score 26.8; DB 7; Length 53;
Best Local Similarity 93.3%; Pred. No. 0.0053;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 6 TAATACGACTCTATAGGAGACACATT 35  
|||||  
Db 6 TAATACGACTCTATAGGAGACGCAATT 35

RESULT 14  
US-11-313-849-37  
; Sequence 37, Application US/11313849  
; Publication No. US2006009637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081U50  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2003-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-313-849-37

Query Match 49.6%; Score 26.8; DB 7; Length 53;  
Best Local Similarity 93.3%; Pred. No. 0.0053; Mismatches 2; Indels 0; Gaps 0;

QY 6 TAATACGACTCTATAGGAGACACATT 35  
|||||  
Db 6 TAATACGACTCTATAGGAGACGCAATT 35

RESULT 15  
US-11-260-844-35  
; Sequence 35, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-35

Query Match 48.1%; Score 26; DB 7; Length 97;  
Best Local Similarity 70.0%; Pred. No. 0.014; Mismatches 15; Indels 0; Gaps 0;

QY 5 TTAATACGACTCTATAGGAGACACATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 8 TTAATACGACTCTATAGGAGGACGATCGGACAATCTCCTTACCCGC 57

RESULT 16  
US-11-260-844-36  
; Sequence 36, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 36  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-36

Query Match 48.1%; Score 26; DB 7; Length 97;  
Best Local Similarity 70.0%; Pred. No. 0.014; Mismatches 15; Indels 0; Gaps 0;

QY 5 TTAATACGACTCTATAGGAGACACATTGTGCAATATTTCCCACTGC 54  
|||||  
Db 8 TTAATACGACTCTATAGGAGGACGATCGGACAATCTCCTTACCCGC 57

RESULT 17  
US-11-260-844-39  
; Sequence 39, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 95  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-39

Query Match 46.7%; Score 25.2; DB 7; Length 95;  
Best Local Similarity 78.9%; Pred. No. 0.029; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAGACCACTTGTGCAAT 42  
| | | | | | | | | | | | | | | | | | | | | |  
Db 6 TTAATACGACTCACTATAGGAGACGATGCGGCAAT 43  
| | | | | | | | | | | | | | | | | | | | | |  
RESULT 18  
US-11-260-844-38  
; Sequence 38, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 38  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-38

Query Match 46.7%; Score 25.2; DB 7; Length 97;  
Best Local Similarity 78.9%; Pred. No. 0.029;  
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAGACCACTTGTGCAAT 42  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 TTAATACGACTCACTATAGGAGACGATGCGGCAAT 45  
| | | | | | | | | | | | | | | | | | | | | |

RESULT 19  
US-11-260-844-41  
; Sequence 41, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 54, 58, 79, 81, 83, 86, 90, 94  
; OTHER INFORMATION: n = any of a, c, g, or t

US-11-260-844-41

Query Match 46.7%; Score 25.2; DB 7; Length 97;  
Best Local Similarity 78.9%; Pred. No. 0.029;  
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAGACCACTTGTGCAAT 42  
| | | | | | | | | | | | | | | | | | | | | |  
Db 8 TTAATACGACTCACTATAGGAGACGATGCGGCAAT 45  
| | | | | | | | | | | | | | | | | | | | | |

RESULT 20  
US-10-472-003-7  
; Sequence 7, Application US/10472003  
; Publication No. US20060099577A1  
; GENERAL INFORMATION:  
; APPLICANT: Rina Netzwerk TNA-Technologien GmbH  
; APPLICANT: Merk, Helmut  
; APPLICANT: Erdmann, Volker  
; APPLICANT: Stiege, Wolfgang  
; TITLE OF INVENTION: Method for Preparative Production of Long Nucleic Acids by PCR  
; FILE REFERENCE: RNA/US/0308 / 00140/019001  
; CURRENT APPLICATION NUMBER: US/10/472,003  
; CURRENT FILING DATE: 2003-09-15  
; PRIOR APPLICATION NUMBER: DE 101 13 265  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: DE 101 51 071  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: DE 101 45 014  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 47  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Primer  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: (1)..(47)  
US-10-472-003-7

Query Match 46.3%; Score 25; DB 6; Length 47;  
Best Local Similarity 100.0%; Pred. No. 0.028;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGGG 25  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GAAATTAATACGACTCACTATAGGG 25  
| | | | | | | | | | | | | | | | | | | | | |

RESULT 21  
US-11-219-635-11  
; Sequence 11, Application US/11219635  
; Publication No. US20060100218A1  
; GENERAL INFORMATION:  
; APPLICANT: IBRAHIM, PRABHA  
; APPLICANT: BREMER, RYAN  
; APPLICANT: GILLETTE, SAM  
; APPLICANT: CHO, HANNA  
; APPLICANT: NESPI, MARIKA  
; APPLICANT: MAMO, SHUMEYE  
; APPLICANT: ZHANG, CHAO  
; APPLICANT: ARTIS, DEAN R.  
; APPLICANT: LEE, BYUNGHUN  
; APPLICANT: ZUCKERMAN, REBECCA  
; TITLE OF INVENTION: PDE4B INHIBITORS  
; FILE REFERENCE: 039363-1111  
; CURRENT APPLICATION NUMBER: US/11/219,635  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: 60/607,407  
; PRIOR FILING DATE: 2004-09-03

; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 11  
; LENGTH: 391  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (108)..(170)  
US-11-219-635-11

Query Match 46.3%; Score 25; DB 7; Length 391;  
Best Local Similarity 100.0%; Pred. No. 0.053; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 16 GAAATTAATACGACTCACTATAGG 40

RESULT 22  
US-11-245-473-14  
; Sequence 14, Application US/11245473  
; Publication No. US20060094085A1  
; GENERAL INFORMATION:  
; APPLICANT: Berry, Alan  
; APPLICANT: Burlingame, Richard P.  
; APPLICANT: Millis, James R.  
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE  
; FILE REFERENCE: 3161-18-C1  
; CURRENT APPLICATION NUMBER: US/11/245,473  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US/10/024,460  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; TYPE: DNA  
; LENGTH: 2184  
; ORGANISM: Escherichia coli  
US-11-245-473-14

Query Match 46.3%; Score 25; DB 7; Length 2184;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 23  
US-11-245-473-17  
; Sequence 17, Application US/11245473  
; Publication No. US20060094085A1  
; GENERAL INFORMATION:  
; APPLICANT: Berry, Alan  
; APPLICANT: Burlingame, Richard P.  
; APPLICANT: Millis, James R.  
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE  
; FILE REFERENCE: 3161-18-C1  
; CURRENT APPLICATION NUMBER: US/11/245,473  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US/10/024,460  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; TYPE: DNA  
; LENGTH: 2184  
; ORGANISM: Escherichia coli  
US-11-245-473-17

Query Match 46.3%; Score 25; DB 7; Length 2184;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 24  
US-11-245-473-20  
; Sequence 20, Application US/11245473  
; Publication No. US20060094085A1  
; GENERAL INFORMATION:  
; APPLICANT: Berry, Alan  
; APPLICANT: Burlingame, Richard P.  
; APPLICANT: Millis, James R.  
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE  
; FILE REFERENCE: 3161-18-C1  
; CURRENT APPLICATION NUMBER: US/11/245,473  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US/10/024,460  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; TYPE: DNA  
; LENGTH: 2184  
; ORGANISM: Escherichia coli  
US-11-245-473-20

Query Match 46.3%; Score 25; DB 7; Length 2184;  
Best Local Similarity 100.0%; Pred. No. 0.09; Mismatches 0; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 25  
US-11-245-473-23  
; Sequence 23, Application US/11245473  
; Publication No. US20060094085A1  
; GENERAL INFORMATION:  
; APPLICANT: Berry, Alan  
; APPLICANT: Burlingame, Richard P.  
; APPLICANT: Millis, James R.  
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE  
; FILE REFERENCE: 3161-18-C1  
; CURRENT APPLICATION NUMBER: US/11/245,473  
; PRIOR FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US/10/024,460  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14

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; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-23

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 26
US-11-245-473-26
; Sequence 26, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-26

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 27
US-11-245-473-29
; Sequence 29, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
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; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Escherichia coli
US-11-245-473-29

Query Match          46.3%; Score 25; DB 7; Length 2184;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||||
Db 32 GAAATTAATACGACTCACTATAGG 56

RESULT 28
US-11-267-871-718/c
; Sequence 718, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 718
; LENGTH: 5236
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pET - 24 vector
US-11-267-871-718

Query Match          46.3%; Score 25; DB 7; Length 5236;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAATTAATACGACTCACTATAGG 25
    |||||||
Db 258 GAAATTAATACGACTCACTATAGG 234

RESULT 29
US-11-301-554-785
; Sequence 785, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
```

; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 785  
; LENGTH: 5502  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-301-554-785

Query Match 46.3%; Score 25; DB 7; Length 5502;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 4979 GAAATTAATACGACTCACTATAGG 5003

RESULT 30  
US-11-301-554-784  
; Sequence 784, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongcong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Carter, Darick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.478C21  
; CURRENT APPLICATION NUMBER: US/11/301,554  
; PRIOR FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13

; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 784  
; LENGTH: 6353  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-301-554-784

Query Match 46.3%; Score 25; DB 7; Length 6353;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 4979 GAAATTAATACGACTCACTATAGG 5003

RESULT 31  
US-11-196-366-3/C  
; Sequence 3, Application US/11196366  
; Publication No. US20060099710A1  
; GENERAL INFORMATION:  
; APPLICANT: DONNELLY, MARK I.  
; APPLICANT: JOACHIMIAK, ANDRZEJ  
; TITLE OF INVENTION: A VECTOR FOR IMPROVED IN VIVO PRODUCTION OF PROTEINS  
; FILE REFERENCE: 21416-99616  
; CURRENT APPLICATION NUMBER: US/11/196,366  
; CURRENT FILING DATE: 2005-08-03  
; PRIOR APPLICATION NUMBER: 60/626,800  
; PRIOR FILING DATE: 2004-11-10  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn ver. 3.3  
; SEQ ID NO 3  
; LENGTH: 6441  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: pMCSG19 nucleotide sequence  
US-11-196-366-3

Query Match 46.3%; Score 25; DB 7; Length 6441;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAATTAATACGACTCACTATAGG 25  
Db 1536 GAAATTAATACGACTCACTATAGG 1512

RESULT 32  
US-11-245-473-13  
; Sequence 13, Application US/11245473  
; Publication No. US20060094085A1  
; GENERAL INFORMATION:  
; APPLICANT: Berry, Alan  
; APPLICANT: Burlingame, Richard P.  
; APPLICANT: Millis, James R.  
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE  
; FILE REFERENCE: 3161-18-C1  
; CURRENT APPLICATION NUMBER: US/11/245,473  
; CURRENT FILING DATE: 2005-10-05  
; PRIOR APPLICATION NUMBER: US/10/024,460  
; PRIOR FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 7408  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: RBS  
; LOCATION: (1240)..(1245)  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: (1185)..(1181)  
; FEATURE:  
; NAME/KEY: conflict  
; LOCATION: (2509)..(2510)  
US-11-245-473-13

Query Match 46.3%; Score 25; DB 7; Length 7408;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTAATACGACTCACTATAGG 25  
Db 1161 GAATTAATACGACTCACTATAGG 1185

RESULT 33  
US-11-233-094-39  
; Sequence 39, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; PRIOR FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-39

Query Match 45.6%; Score 24.6; DB 7; Length 53;  
Best Local Similarity 87.1%; Pred. No. 0.042;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACATG 36  
Db 6 TAATACGACTCACTATAGGAGATCATG 36

RESULT 34  
US-11-313-849-39  
; Sequence 39, Application US/11313849  
; Publication No. US20060099637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI

; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-313-849-39

Query Match 45.6%; Score 24.6; DB 7; Length 53;  
Best Local Similarity 87.1%; Pred. No. 0.042;  
Matches 27; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACATG 36  
Db 6 TAATACGACTCACTATAGGAGATCATG 36

RESULT 35  
US-11-233-094-40  
; Sequence 40, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-40

Query Match 44.8%; Score 24.2; DB 7; Length 53;  
Best Local Similarity 89.7%; Pred. No. 0.062;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGAGACCACAT 34  
Db 6 TAATACGACTCACTATAGGAGAGTATAT 34

RESULT 36  
US-11-233-094-41  
; Sequence 41, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094



; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; TYPE: DNA  
; LENGTH: 53  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-41

Query Match 44.8%; Score 24.2; DB 7; Length 53;  
Best Local Similarity 89.7%; Pred. No. 0.062;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 TAATACGACTCACTATAGGAGACCACAT 34  
|||||  
Db 6 TAATACGACTCACTATAGGAGATATAT 34  
|||||

RESULT 37  
US-11-313-849-40  
; Sequence 40, Application US/11313849  
; Publication No. US20060099637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081USO  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-313-849-40

Query Match 44.8%; Score 24.2; DB 7; Length 53;  
Best Local Similarity 89.7%; Pred. No. 0.062;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 TAATACGACTCACTATAGGAGACCACAT 34  
|||||  
Db 6 TAATACGACTCACTATAGGAGATATAT 34  
|||||

RESULT 38  
US-11-313-849-41  
; Sequence 41, Application US/11313849  
; Publication No. US20060099637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081USO  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-313-849-41

Query Match 44.8%; Score 24.2; DB 7; Length 53;  
Best Local Similarity 89.7%; Pred. No. 0.062;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 TAATACGACTCACTATAGGAGACCACAT 34  
|||||  
Db 6 TAATACGACTCACTATAGGAGATATAT 34  
|||||

RESULT 39  
US-11-233-094-44  
; Sequence 44, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081USO  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 44  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-44

Query Match 44.4%; Score 24; DB 7; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.075;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 TAATACGACTCACTATAGGAGAC 29  
|||||  
Db 6 TAATACGACTCACTATAGGAGAC 29  
|||||

RESULT 40  
US-11-313-849-44  
; Sequence 44, Application US/11313849  
; Publication No. US20060099637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081USO  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44



; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-42

Query Match 43.3%; Score 23.4; DB 7; Length 53;  
Best Local Similarity 96.0%; Pred. No. 0.13; Mismatches 0; Indels 1; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACC 30  
|||||  
DB 6 TAATACGACTCACTATAGGAGACC 30

RESULT 45  
US-11-313-849-42  
; Sequence 42, Application US/11313849  
; Publication No. US20060099637A1  
; GENERAL INFORMATION:  
; APPLICANT: MARUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081U50  
; CURRENT APPLICATION NUMBER: US/11/313,849  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-313-849-42

Query Match 43.3%; Score 23.4; DB 7; Length 53;  
Best Local Similarity 96.0%; Pred. No. 0.13; Mismatches 0; Indels 1; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACC 30  
|||||  
DB 6 TAATACGACTCACTATAGGAGACC 30

RESULT 46  
US-10-541-993-4/c  
; Sequence 4, Application US/10541993  
; Publication No. US20060099670A1  
; GENERAL INFORMATION:  
; APPLICANT: Matuschek, Markus  
; APPLICANT: Heinekamp, Thorsten  
; APPLICANT: Schmidt, Andre  
; APPLICANT: Brakhage, Axel  
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus  
; TITLE OF INVENTION: Blakesles, corresponding organisms, and the use of the same  
; FILE REFERENCE: 13311-00010-US  
; CURRENT APPLICATION NUMBER: US/10/541,993

; CURRENT FILING DATE: 2005-07-08  
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100  
; PRIOR FILING DATE: 2004-01-09  
; PRIOR APPLICATION NUMBER: DE 103 00 649.4  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: DE 103 41 272.7  
; PRIOR FILING DATE: 2003-09-08  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 11611  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Vector  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (227)..(227)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (318)..(318)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (526)..(526)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8946)..(8946)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10028)..(10028)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-541-993-4

Query Match 43.3%; Score 23.4; DB 6; Length 11611;  
Best Local Similarity 67.3%; Pred. No. 0.68; Mismatches 33; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGACCACATTTGTGCAATATATCCCACTGC 54  
|||||  
DB 8291 TAATACGACTCACTATAGGATCCTTTAGTAGGGTTAATTGCGGCCGC 8243

RESULT 47  
US-11-193-682-4  
; Sequence 4, Application US/11193682  
; Publication No. US20060094110A1  
; GENERAL INFORMATION:  
; APPLICANT: MCGARRITY, Gerard J.  
; APPLICANT: GARCIA-BLANCO, Mariano  
; TITLE OF INVENTION: USE OF SPLICEOSOME MEDIATED RNA TRANS-SPLICING FOR IMMUNOTHERAPY  
; FILE REFERENCE: 027705.00102  
; CURRENT APPLICATION NUMBER: US/11/193,682  
; CURRENT FILING DATE: 2005-07-29  
; PRIOR APPLICATION NUMBER: US 60/592,607  
; PRIOR FILING DATE: 2004-07-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: unable to identify  
US-11-193-682-4

Query Match 42.6%; Score 23; DB 7; Length 23;  
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28  
|||||  
Db 1 TAATACGACTCACTATAGGGAGA 23

RESULT 48  
US-11-260-844-17  
; Sequence 17, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG.3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Primer  
US-11-260-844-17

Query Match 42.6%; Score 23; DB 7; Length 40;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 49  
US-11-233-094-36  
; Sequence 36, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARYUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 36  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-36

Query Match 42.6%; Score 23; DB 7; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28

Db 6 TAATACGACTCACTATAGGGAGA 28  
|||||

RESULT 50  
US-11-233-094-38  
; Sequence 38, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARYUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-38

Query Match 42.6%; Score 23; DB 7; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28  
|||||  
Db 6 TAATACGACTCACTATAGGGAGA 28

RESULT 51  
US-11-233-094-43  
; Sequence 43, Application US/11233094  
; Publication No. US20060094041A1  
; GENERAL INFORMATION:  
; APPLICANT: MARYUYAMA, TAKAHIRO  
; APPLICANT: ISHIGURO, TAKAHIRO  
; APPLICANT: TAYA, TOSHIKI  
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN  
; FILE REFERENCE: 220081US0  
; CURRENT APPLICATION NUMBER: US/11/233,094  
; CURRENT FILING DATE: 2005-09-23  
; PRIOR APPLICATION NUMBER: US/10/085,056  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-58143  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 53  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic DNA  
US-11-233-094-43

Query Match 42.6%; Score 23; DB 7; Length 53;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGA 28  
|||||  
Db 6 TAATACGACTCACTATAGGGAGA 28

```
RESULT 52
US-11-313-849-36
; Sequence 36, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-36

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
Db 6 TAATACGACTCACTATAGGAGA 28

RESULT 53
US-11-313-849-38
; Sequence 38, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-38

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
Db 6 TAATACGACTCACTATAGGAGA 28
```

```
; Sequence 43, Application US/11313849
; Publication No. US20060099637A1
; GENERAL INFORMATION:
; APPLICANT: MARIYAMA, TAKAHIRO
; APPLICANT: ISHIGURO, TAKAHIRO
; APPLICANT: TAYA, TOSHIKI
; TITLE OF INVENTION: OLIGONUCLEOTIDE AND METHOD FOR DETECTING VEROTOXIN
; FILE REFERENCE: 220081US0
; CURRENT APPLICATION NUMBER: US/11/313,849
; PRIOR FILING DATE: 2005-12-22
; PRIOR APPLICATION NUMBER: US/10/085,056
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: JP 2001-58143
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-11-313-849-43

Query Match          42.6%; Score 23; DB 7; Length 53;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGAGA 28
   |||||
Db 6 TAATACGACTCACTATAGGAGA 28

RESULT 55
US-11-260-844-57
; Sequence 57, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Apramer
US-11-260-844-57

Query Match          42.6%; Score 23; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27
   |||||
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 56
US-11-260-844-24
; Sequence 24, Application US/11260844
```

; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 24  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-24

Query Match 42.6%; Score 23; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 57  
US-11-260-844-34  
; Sequence 34, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-34

Query Match 42.6%; Score 23; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 7 TTAATACGACTCACTATAGGGAG 29

RESULT 58  
US-11-260-844-37

; Sequence 37, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 37  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-37

Query Match 42.6%; Score 23; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 59  
US-11-260-844-52  
; Sequence 52, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 52  
; LENGTH: 96  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-52

Query Match 42.6%; Score 23; DB 7; Length 96;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 60

US-11-260-844-25  
; Sequence 25, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-25

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 61  
US-11-260-844-27  
; Sequence 27, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-27

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 62  
US-11-260-844-28  
; Sequence 28, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-28

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 63  
US-11-260-844-29  
; Sequence 29, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-29

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30





Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27  
Db 8 TTAATACGACTCACTATAGGAG 30

## RESULT 68

US-11-260-844-46  
; Sequence 46, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; PRIOR FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 46  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-46

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27  
Db 8 TTAATACGACTCACTATAGGAG 30

## RESULT 69

US-11-260-844-49  
; Sequence 49, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; PRIOR FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
; NAME/KEY: misc\_feature  
; LOCATION: 45, 49, 52, 54, 55, 67, 72..75, 81, 83, 85, 97

; OTHER INFORMATION: n = any of a, c, g, or t  
US-11-260-844-49

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27  
Db 8 TTAATACGACTCACTATAGGAG 30

## RESULT 70

US-11-260-844-50  
; Sequence 50, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; PRIOR FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 50  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-50

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TTAATACGACTCACTATAGGAG 27  
Db 8 TTAATACGACTCACTATAGGAG 30

## RESULT 71

US-11-260-844-51  
; Sequence 51, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; PRIOR FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 51  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-51

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 72
US-11-260-844-53
; Sequence 53, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 45, 48, 50, 57, 59, 60, 74, 80, 84, 94, 96
; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-53

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 73
US-11-260-844-55
; Sequence 55, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-55

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 74
US-11-260-844-56
; Sequence 56, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 97
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-56

Query Match      42.6%; Score 23; DB 7; Length 97;
Best Local Similarity 100.0%; Pred.No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGAG 27
Db 8 TTAATACGACTCACTATAGGAG 30

RESULT 75
US-11-260-844-58
; Sequence 58, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
```

; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 58  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-58

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

## RESULT 76

US-11-260-844-60  
; Sequence 60, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 60  
; LENGTH: 97  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-60

Query Match 42.6%; Score 23; DB 7; Length 97;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

## RESULT 77

US-11-260-844-26  
; Sequence 26, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3

; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-26

Query Match 42.6%; Score 23; DB 7; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

## RESULT 78

US-11-260-844-33  
; Sequence 33, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27  
; PRIOR APPLICATION NUMBER: US/10/442,289  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/276,147  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: GB 9806530.3  
; PRIOR FILING DATE: 1998-03-26  
; NUMBER OF SEQ ID NOS: 61  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 33  
; LENGTH: 98  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer  
US-11-260-844-33

Query Match 42.6%; Score 23; DB 7; Length 98;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27  
|||||  
Db 8 TTAATACGACTCACTATAGGGAG 30

## RESULT 79

US-11-260-844-61  
; Sequence 61, Application US/11260844  
; Publication No. US20060093602A1  
; GENERAL INFORMATION:  
; APPLICANT: Life, Paul F  
; APPLICANT: Rees, Edward S  
; APPLICANT: Rhodes, Andrew D  
; TITLE OF INVENTION: Oncostatin M Antagonists  
; FILE REFERENCE: 1430-282 / PG 3728US  
; CURRENT APPLICATION NUMBER: US/11/260,844  
; CURRENT FILING DATE: 2005-10-27

```
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
; NAME/KEY: misc_feature
; LOCATION: 42, 46, 54..56, 59, 62, 72, 79, 80
; OTHER INFORMATION: n = any of a, c, g, or t
US-11-260-844-61

Query Match          42.6%; Score 23; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 80
US-11-260-844-19
; Sequence 19, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-11-260-844-19

Query Match          42.6%; Score 23; DB 7; Length 105;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TTAATACGACTCACTATAGGGAG 27
|||||
Db 8 TTAATACGACTCACTATAGGGAG 30

RESULT 81
US-11-217-529-78404
; Sequence 78404, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78404
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78404

Query Match          42.6%; Score 23; DB 7; Length 1701;
Best Local Similarity 68.1%; Pred. No. 0.55;
Matches 32; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 4 ATTAATACGACTCACTATAGGGAGACCAACCATTTGTGCAATATTTCCCA 50
|||||
Db 948 AATAATAGGATTGAAGACGGTACATCATCATGATGCAATATTTTCCA 994

RESULT 82
US-10-511-937-3082
; Sequence 3082, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3082
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-3082

Query Match          41.5%; Score 22.4; DB 6; Length 63;
Best Local Similarity 95.8%; Pred. No. 0.36;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TAATACGACTCACTATAGGGAGAC 29
|||||
Db 14 TAATACGACTCACTATAGGGAGC 37

RESULT 83
US-10-511-937-3105
; Sequence 3105, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
```

APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
APPLICANT: Wohlgemuth, Jay  
APPLICANT: Fry, Kirk  
APPLICANT: Woodward, Robert  
APPLICANT: Ly, Ngoc  
APPLICANT: Prentice, James  
APPLICANT: Morris, MacDonald  
APPLICANT: Rosenberg, Steven  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
FILE REFERENCE: 50661200104  
CURRENT APPLICATION NUMBER: US/10/511,937  
CURRENT FILING DATE: 2004-10-19  
PRIOR APPLICATION NUMBER: PCT/US2003/012946  
PRIOR FILING DATE: 2003-04-24  
PRIOR APPLICATION NUMBER: US 10/131,831  
PRIOR FILING DATE: 2002-04-24  
PRIOR APPLICATION NUMBER: US 10/325,899  
PRIOR FILING DATE: 2002-12-20  
NUMBER OF SEQ ID NOS: 3117  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3105  
LENGTH: 63  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-511-937-3105

Query Match 41.5%; Score 22.4; DB 6; Length 63;  
Best Local Similarity 95.8%; Pred. No. 0.36; Mismatches 0; Indels 1; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 0;  
Qy 6 TAATACGACTCACTATAGGGAGAC 29  
Db 14 TAATACGACTCACTATAGGGAGGC 37

RESULT 84  
US-10-524-399-1  
Sequence 1, Application US/10524399  
Publication No. US2006009591A1  
GENERAL INFORMATION:  
APPLICANT: KRAUSE, Andreas  
APPLICANT: NIESE, Detlef  
APPLICANT: RAULF, Friedrich  
APPLICANT: SCHERER, Andreas  
TITLE OF INVENTION: Diagnosis of chronic rejection  
FILE REFERENCE: 4-32608A  
CURRENT APPLICATION NUMBER: US/10/524,399  
CURRENT FILING DATE: 2005-02-11  
PRIOR APPLICATION NUMBER: US 60/405,225  
PRIOR FILING DATE: 2002-08-22  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1  
LENGTH: 63  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Primer sequence  
US-10-524-399-1

Query Match 41.5%; Score 22.4; DB 6; Length 63;  
Best Local Similarity 95.8%; Pred. No. 0.36; Mismatches 0; Indels 1; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 1; Gaps 0;  
Qy 6 TAATACGACTCACTATAGGGAGAC 29  
Db 14 TAATACGACTCACTATAGGGAGGC 37

RESULT 85  
US-11-217-529-2644  
Sequence 2644, Application US/11217529

Publication No. US20060099612A1  
GENERAL INFORMATION:  
APPLICANT: SUNTORY LIMITED  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: S-38-285  
CURRENT APPLICATION NUMBER: US/11/217,529  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: US 10/932,182  
PRIOR FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 2644  
LENGTH: 3915  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
NAME/KEY: modified base  
LOCATION: (73)..(122)  
FEATURE:  
OTHER INFORMATION: a, c, g, t, unknown, or other  
NAME/KEY: modified base  
LOCATION: (1668)..(1721)  
OTHER INFORMATION: a, c, g, t, unknown, or other  
US-11-217-529-2644

Query Match 41.5%; Score 22.4; DB 7; Length 3915;  
Best Local Similarity 66.7%; Pred. No. 1.3; Mismatches 32; Conservative 0; Mismatches 16; Indels 0; Gaps 0;  
Qy 1 GAAATTATACGACTCACTATAGGAGACCATTCGCAATATCCC 48  
Db 3466 GAAAGCAATACGAGTCATTAATAGTAAGAACAAAGATTCAGTTTACC 3513

RESULT 86  
US-10-900-453-1  
Sequence 1, Application US/10900453  
Publication No. US20060099601A1  
GENERAL INFORMATION:  
APPLICANT: RABBANI, ELAZAR  
APPLICANT: STAVRIANOPOULOS, JANNIS G.  
APPLICANT: DONEGAN, JAMES J.  
APPLICANT: COLEMAN, JACK  
TITLE OF INVENTION: DETECTION AND QUANTIFICATION PROCESS FOR NUCLEIC  
TITLE OF INVENTION: ACIDS IN LIBRARY  
FILE REFERENCE: EN2-60 (D2)  
CURRENT APPLICATION NUMBER: US/10/900,453  
CURRENT FILING DATE: 2004-07-27  
PRIOR APPLICATION NUMBER: 09/896,897  
PRIOR FILING DATE: 2001-06-30  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 1  
LENGTH: 44  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Bacteriophage  
OTHER INFORMATION: T7 Promoter with a C9 3' Tail  
US-10-900-453-1

Query Match 41.1%; Score 22.2; DB 6; Length 44;  
Best Local Similarity 88.9%; Pred. No. 0.39; Mismatches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 6 TAATACGACTCACTATAGGAGACAC 32  
Db 14 TAATACGACTCACTATAGGATCCCC 40



```

RESULT 93
US-11-260-844-48
; Sequence 48, Application US/11260844
; Publication No. US20060093602A1
; GENERAL INFORMATION:
; APPLICANT: Life, Paul F
; APPLICANT: Rees, Edward S
; APPLICANT: Rhodes, Andrew D
; TITLE OF INVENTION: Oncostatin M Antagonists
; FILE REFERENCE: 1430-282 / PG 3728US
; CURRENT APPLICATION NUMBER: US/11/260,844
; CURRENT FILING DATE: 2005-10-27
; PRIOR APPLICATION NUMBER: US/10/442,289
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/276,147
; PRIOR FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: GB 9806530.3
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 98
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Aptamer
US-11-260-844-48

Query Match 39.6%; Score 21.4; DB 7; Length 98;
Best Local Similarity 66.0%; Pred. No. 1.1;
Matches 31; Conservative 0; Mismatches 16; Indels 0

Qy 5 TTAATAGACTCACTATAGGAGACCAATTGTGCAATATTTCCCAAC 51
|||||
Db 8 TTAATAGACTCACTATAGGAGGACGATGCGTTTAACTCCCAAC 54
|||||

RESULT 94
US-10-980-856-34
; Sequence 34, Application US/10980856
; Publication No. US20060094026A1
; GENERAL INFORMATION:
; APPLICANT: LU, YI
; APPLICANT: LIU, JUEWEN
; TITLE OF INVENTION: NUCLEIC ACID ENZYME LIGHT-UP SENSOR UTILIZING
; FILE REFERENCE: ILL05-052-US
; CURRENT APPLICATION NUMBER: US/10/980,856
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34
; LENGTH: 105
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide sequence
US-10-980-856-34

Query Match 39.6%; Score 21.4; DB 6; Length 105;
Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 1; Indels 0

Qy 6 TAATACGACTCACTATAGGAGA 28
|||||
Db 12 TAATACGACTCACTATAGGAAGA 34
|||||

RESULT 95
US-10-980-856-35
; Sequence 35, Application US/10980856
; Publication No. US20060094026A1
; GENERAL INFORMATION:

```

```
; APPLICANT: LU, YI
; APPLICANT: LIU JUWEN
; TITLE OF INVENTION: NUCLEIC ACID ENZYME LIGHT-UP SENSOR UTILIZING INVASIVE DNA
; FILE REFERENCE: IL05-052-US
; CURRENT APPLICATION NUMBER: US/10/980,856
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 107
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic polynucleotide sequence
US-10-980-856-35

Query Match          39.6%; Score 21.4; DB 6; Length 107;
Best Local Similarity 95.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 TAATACGACTCACTATAGGAGGA 28
Db      12 TAATACGACTCACTATAGGAAGA 34

RESULT 96
US-11-217-529-5480
; Sequence 5480, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5480
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5480

Query Match          39.6%; Score 21.4; DB 7; Length 222;
Best Local Similarity 80.6%; Pred. No. 1.4;
Matches 25; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      6 TAATACGACTCACTATAGGAGACCACATTTG 36
Db      11 TAATACGACTCACTACAGGGATCAACACTG 41

RESULT 97
US-11-265-954-5/c
; Sequence 5, Application US/11265954
; Publication No. US20060094052A1
; GENERAL INFORMATION:
; APPLICANT: Kelman, zvi
; APPLICANT: Shin, Jae-Ho
; TITLE OF INVENTION: PCR-BASED SUBSTRATE PREPARATION FOR HELICASE ASSAYS
; FILE REFERENCE: 4115-210
; CURRENT APPLICATION NUMBER: US/11/265,954
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: US 60/624,571
; PRIOR FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 5
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 226
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-265-954-5

Query Match          39.6%; Score 21.4; DB 7; Length 226;
Best Local Similarity 95.7%; Pred. No. 1.4;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 TAATACGACTCACTATAGGAGGA 28
Db      201 TAATACGACTCACTATAGGGCGA 179

RESULT 98
US-11-245-514-10
; Sequence 10, Application US/11245514
; Publication No. US20060099621A1
; GENERAL INFORMATION:
; APPLICANT: Schuetz, Ekkehard
; APPLICANT: Iakoubov, Leonid
; APPLICANT: Urnovitz, Howard
; APPLICANT: Chronix Biomedical
; TITLE OF INVENTION: Detection of Nucleic Acids to Assess Risk for
; FILE OF INVENTION: Creutzfeldt-Jakob Disease
; FILE REFERENCE: 018651-000810US
; CURRENT APPLICATION NUMBER: US/11/245,514
; CURRENT FILING DATE: 2005-10-07
; PRIOR APPLICATION NUMBER: US 60/616,726
; PRIOR FILING DATE: 2004-10-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence 2
; OTHER INFORMATION: present in presumptive Creutzfeldt-Jakob Disease
; OTHER INFORMATION: (CJD) derived from PCR products using primers
; OTHER INFORMATION: 75P/83R
US-11-245-514-10

Query Match          39.6%; Score 21.4; DB 7; Length 320;
Best Local Similarity 95.7%; Pred. No. 1.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      6 TAATACGACTCACTATAGGAGGA 28
Db      24 TAATACGACTCACTATAGGGCGA 46

RESULT 99
US-09-949-925-25/c
; Sequence 25, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
```



;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,165  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,164  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,167  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,162  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,161  
;; PRIOR FILING DATE: 1998-01-30  
;; PRIOR APPLICATION NUMBER: US 60/073,170  
;; PRIOR FILING DATE: 1998-01-30  
;; NUMBER OF SEQ ID NOS: 298  
;; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 25  
; LENGTH: 1076  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (910)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (912)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (958)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: SITE  
; LOCATION: (1038)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-949-925-25

Query Match 39.6%; Score 21.4; DB 1; Length 1076;

Best Local Similarity 95.7%; Pred. No. 2.2; Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TAATACGACTCACTATAGGGAGA 28  
|||  
DB 800 TAATACGACTCACTATAGGGCGA 778

## RESULT 100

US-11-315-766-11/c  
; Sequence 11, Application US/11315766  
; Publication No. US20060101544A1  
; GENERAL INFORMATION:  
; APPLICANT: Butler, Karlene H.  
; APPLICANT: Cahoon, Edgar B.  
; APPLICANT: Cahoon, Rebecca E.  
; APPLICANT: Famodu, Omolayo O.  
; APPLICANT: Hall, Sarah E.  
; TITLE OF INVENTION: Phospholipid:diacylglycerol Acetyltransferases  
; FILE REFERENCE: BB1486 US NA  
; CURRENT APPLICATION NUMBER: US/11/315,766  
; CURRENT FILING DATE: 2005-12-22  
; PRIOR APPLICATION NUMBER: US/10/321,802  
; PRIOR FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 11  
; LENGTH: 1475  
; TYPE: DNA  
; ORGANISM: Vernonia mespilifolia  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1471)  
; OTHER INFORMATION: n = a, c, g or t  
US-11-315-766-11

Query Match 39.6%; Score 21.4; DB 7; Length 1475;

Best Local Similarity 95.7%; Pred. No. 2.4;

Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 6 TAATACGACTCACTATAGGGAGA 28  
|||  
DB 1456 TAATACGACTCACTATAGGGCGA 1434

Search completed: May 19, 2006, 05:38:15  
Job time : 35.506 secs

**This Page Blank (uspto)**

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:23:06 ; Search time 873.946 Seconds  
(without alignments)  
1829.273 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacggaaggccttctg 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 300 summaries

Database :

GenEmbl.\*

1: gb\_env.\*

2: gb\_pat.\*

3: gb\_ph.\*

4: gb\_pl.\*

5: gb\_pr.\*

6: gb\_ro.\*

7: gb\_sts.\*

8: gb\_sy.\*

9: gb\_un.\*

10: gb\_vi.\*

11: gb\_ov.\*

12: gb\_hcg.\*

13: gb\_in.\*

14: gb\_on.\*

15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	25	100.0	25	2	AR438653 Sequence
2	25	100.0	25	2	AX166855 Sequence
3	25	100.0	541	15	AF547926
4	25	100.0	1456	15	MCAD16S
5	25	100.0	1459	15	MCO16S
6	24	96.0	24	2	AR438654
7	24	96.0	24	2	AX166856
8	24	96.0	1460	15	MSGRGDSB
9	24	96.0	1479	15	MSGRR16S
10	23.4	93.6	268	15	M95469 Mycobacteri
11	23.4	93.6	293	1	AJ404591 Unculture
12	23.4	93.6	316	15	Y09325 M.fortuitum
13	23.4	93.6	388	1	AY395145 Unculture
14	23.4	93.6	393	1	BSSMKN23
15	23.4	93.6	394	1	AY395154 Bacterium s
16	23.4	93.6	395	1	AY43901 Unculture
17	23.4	93.6	395	1	AY395151 Unculture
18	23.4	93.6	396	1	X78655 Bacterium s

19	23.4	93.6	400	1	DQ221681
20	23.4	93.6	403	15	AY234665 Bacterium
21	23.4	93.6	407	15	AY792017 Mycobacte
22	23.4	93.6	410	1	BSSMKN12
23	23.4	93.6	411	15	DQ063154
24	23.4	93.6	411	15	DQ063199 Actinobac
25	23.4	93.6	411	15	AY792013 Mycobacte
26	23.4	93.6	416	1	AM085786 Unculture
27	23.4	93.6	418	1	AM085788 Unculture
28	23.4	93.6	418	15	AY673261 Mycobacte
29	23.4	93.6	421	1	AM085770 Unculture
30	23.4	93.6	422	15	AJ786807 Mycobacte
31	23.4	93.6	423	15	AY673205 Mycobacte
32	23.4	93.6	423	15	AY673206 Mycobacte
33	23.4	93.6	423	15	AY673207 Mycobacte
34	23.4	93.6	424	15	DQ063156 Actinobac
35	23.4	93.6	424	15	AY673287 Streptosp
36	23.4	93.6	425	1	AY394635 Unculture
37	23.4	93.6	426	15	AY673136 Mycobacte
38	23.4	93.6	428	15	AB106918 Gram-posi
39	23.4	93.6	428	15	DQ063058 Actinobac
40	23.4	93.6	430	15	AJ786822 Mycobacte
41	23.4	93.6	430	15	AY673202 Mycobacte
42	23.4	93.6	431	15	AB106919 Gram-posi
43	23.4	93.6	432	1	AF078232 Grassland
44	23.4	93.6	433	15	AY673198 Mycobacte
45	23.4	93.6	433	15	AY673266 Mycobacte
46	23.4	93.6	435	15	DQ063195 Actinobac
47	23.4	93.6	435	15	AY234692 Bacterium
48	23.4	93.6	435	15	AY673233 Mycobacte
49	23.4	93.6	436	15	DQ063046 Actinobac
50	23.4	93.6	436	15	AY673199 Mycobacte
51	23.4	93.6	436	15	AY673304 Mycobacte
52	23.4	93.6	437	1	AF078419 Grassland
53	23.4	93.6	441	15	AB232370 Mycobacte
54	23.4	93.6	442	15	AY306201 Mycobacte
55	23.4	93.6	444	15	AY306205 Mycobacte
56	23.4	93.6	445	15	AB106917 Gram-posi
57	23.4	93.6	445	15	DQ067466 Mycobacte
58	23.4	93.6	450	15	MS91016SR
59	23.4	93.6	450	15	MSP16SR
60	23.4	93.6	450	15	AY358002 Actinobac
61	23.4	93.6	454	15	AJ746062 Mycobacte
62	23.4	93.6	456	15	AY358001 Actinobac
63	23.4	93.6	459	1	AJ609008 Unculture
64	23.4	93.6	459	15	AY754884 Mycobacte
65	23.4	93.6	459	15	AY754885 Mycobacte
66	23.4	93.6	464	15	AB118817 Denitrify
67	23.4	93.6	464	15	DQ142669 Mycobacte
68	23.4	93.6	464	15	DQ142672 Mycobacte
69	23.4	93.6	466	15	DQ067465 Mycobacte
70	23.4	93.6	466	15	AY524839 Mycobacte
71	23.4	93.6	468	15	DQ154332 Soil bact
72	23.4	93.6	473	1	AY043719 Unculture
73	23.4	93.6	474	1	DQ136108 Unculture
74	23.4	93.6	474	15	AY792024 Mycobacte
75	23.4	93.6	476	15	AY559492 Mycobacte
76	23.4	93.6	478	1	AY251205 Unculture
77	23.4	93.6	481	15	MSP413603
78	23.4	93.6	495	15	AY943206 Mycobacte
79	23.4	93.6	496	1	DQ154344 Unculture
80	23.4	93.6	498	15	AY215287 Mycobacte
81	23.4	93.6	498	15	AY215324 Mycobacte
82	23.4	93.6	498	15	AY215336 Mycobacte
83	23.4	93.6	499	1	DQ154566 Unculture
84	23.4	93.6	499	15	DQ154328 Soil bact
85	23.4	93.6	500	15	AY215236 Mycobacte
86	23.4	93.6	500	1	UEU233561 unculture
87	23.4	93.6	500	15	AF498660 Mycobacte
88	23.4	93.6	500	15	AF498661 Mycobacte
89	23.4	93.6	500	15	AY162027 Mycobacte
90	23.4	93.6	500	15	AY162030 Mycobacte
91	23.4	93.6	500	15	AY215218 Mycobacte

92	23.4	93.6	500	15	AV215228	Mycobacte	165	23.4	93.6	540	15	AF547958	Mycobacte
93	23.4	93.6	500	15	AV215234	Mycobacte	166	23.4	93.6	540	15	AF547961	Mycobacte
94	23.4	93.6	500	15	AV215235	Mycobacte	167	23.4	93.6	540	15	AF547963	Mycobacte
95	23.4	93.6	500	15	AV215237	Mycobacte	168	23.4	93.6	540	15	AF547964	Mycobacte
96	23.4	93.6	500	15	AV215245	Mycobacte	169	23.4	93.6	540	15	AF547972	Mycobacte
97	23.4	93.6	500	15	AV215247	Mycobacte	170	23.4	93.6	540	15	AF547981	Mycobacte
98	23.4	93.6	500	15	AV215251	Mycobacte	171	23.4	93.6	540	15	AV438068	Mycobacte
99	23.4	93.6	500	15	AV215252	Mycobacte	172	23.4	93.6	540	15	AV438071	Mycobacte
100	23.4	93.6	500	15	AV215266	Mycobacte	173	23.4	93.6	540	15	AY438077	Mycobacte
101	23.4	93.6	500	15	AV215280	Mycobacte	174	23.4	93.6	541	15	AF547943	Mycobacte
102	23.4	93.6	500	15	AV215285	Mycobacte	175	23.4	93.6	541	15	AY438067	Mycobacte
103	23.4	93.6	500	15	AV215286	Mycobacte	176	23.4	93.6	542	15	AF547897	Mycobacte
104	23.4	93.6	500	15	AV215288	Mycobacte	177	23.4	93.6	542	15	AF547917	Mycobacte
105	23.4	93.6	500	15	AV215289	Mycobacte	178	23.4	93.6	542	15	AF547918	Mycobacte
106	23.4	93.6	500	15	AV215290	Mycobacte	179	23.4	93.6	542	15	AF547980	Mycobacte
107	23.4	93.6	500	15	AV215291	Mycobacte	180	23.4	93.6	542	15	AY438079	Mycobacte
108	23.4	93.6	500	15	AV215292	Mycobacte	181	23.4	93.6	551	1	AY725804	Unculture
109	23.4	93.6	500	15	AV215293	Mycobacte	182	23.4	93.6	552	15	AY438073	Mycobacte
110	23.4	93.6	500	15	AV215304	Mycobacte	183	23.4	93.6	552	15	AY438074	Mycobacte
111	23.4	93.6	500	15	AV215316	Mycobacte	184	23.4	93.6	576	15	AY367021	Mycobacte
112	23.4	93.6	500	15	AV215320	Mycobacte	185	23.4	93.6	588	15	AJ627393	Mycobacte
113	23.4	93.6	500	15	AV215323	Mycobacte	186	23.4	93.6	611	1	DQ149896	Unculture
114	23.4	93.6	500	15	AV215331	Mycobacte	187	23.4	93.6	616	1	AY242618	Unculture
115	23.4	93.6	500	15	AV215346	Mycobacte	188	23.4	93.6	619	1	AY242619	Unculture
116	23.4	93.6	500	15	AV215348	Mycobacte	189	23.4	93.6	629	1	DQ149899	Unculture
117	23.4	93.6	500	15	AV215371	Mycobacte	190	23.4	93.6	629	1	DQ149915	Unculture
118	23.4	93.6	501	15	AF498655	Mycobacte	191	23.4	93.6	629	1	DQ149916	Unculture
119	23.4	93.6	501	15	AV112744	Mycobacte	192	23.4	93.6	631	1	AY307880	Unculture
120	23.4	93.6	501	15	AV215219	Mycobacte	193	23.4	93.6	636	1	DQ149894	Unculture
121	23.4	93.6	501	15	AV215226	Mycobacte	194	23.4	93.6	660	1	AY242620	Unculture
122	23.4	93.6	501	15	AV215229	Mycobacte	195	23.4	93.6	676	15	AY368530	Mycobacte
123	23.4	93.6	501	15	AV215238	Mycobacte	196	23.4	93.6	685	1	AY881659	Unculture
124	23.4	93.6	501	15	AV215370	Mycobacte	197	23.4	93.6	737	1	AY154573	Unculture
125	23.4	93.6	503	15	AV215227	Mycobacte	198	23.4	93.6	740	1	AF145831	Metal-con
126	23.4	93.6	503	15	AV215249	Mycobacte	199	23.4	93.6	749	15	AJ784807	Mycobacte
127	23.4	93.6	503	15	AV148214	Mycobacte	200	23.4	93.6	761	15	AJ746076	Mycobacte
128	23.4	93.6	508	15	AV148214	Mycobacte	201	23.4	93.6	761	15	AJ746076	Mycobacte
129	23.4	93.6	509	15	AV215212	Mycobacte	202	23.4	93.6	773	15	AJ746072	Mycobacte
130	23.4	93.6	511	15	AV039467	Earthworm	203	23.4	93.6	804	15	AJ746074	Mycobacte
131	23.4	93.6	512	15	AV215272	Mycobacte	204	23.4	93.6	810	15	AJ746058	Mycobacte
132	23.4	93.6	512	15	AV943205	Mycobacte	205	23.4	93.6	810	15	AJ746059	Mycobacte
133	23.4	93.6	513	15	DQ081189	Mycobacte	206	23.4	93.6	813	15	AJ746070	Mycobacte
134	23.4	93.6	513	15	AV215273	Mycobacte	207	23.4	93.6	815	15	AJ746064	Mycobacte
135	23.4	93.6	514	15	AV215276	Mycobacte	208	23.4	93.6	815	1	AY154519	Unculture
136	23.4	93.6	519	15	MSU19366	Unculture	209	23.4	93.6	815	15	AJ746069	Mycobacte
137	23.4	93.6	519	15	AJ746067	Mycobacte	210	23.4	93.6	824	15	AJ746060	Mycobacte
138	23.4	93.6	530	1	AY725810	Unculture	211	23.4	93.6	828	15	AJ746061	Mycobacte
139	23.4	93.6	530	15	AY039507	Soil bact	212	23.4	93.6	828	15	AJ746073	Mycobacte
140	23.4	93.6	532	15	DQ124114	Mycobacte	213	23.4	93.6	836	15	AF131354	Catellato
141	23.4	93.6	534	15	MFO416908	Mycobacte	214	23.4	93.6	878	15	AY429701	Mycobacte
142	23.4	93.6	535	1	AY148216	Unculture	215	23.4	93.6	893	1	AY494645	Unculture
143	23.4	93.6	537	15	AY943209	Mycobacte	216	23.4	93.6	979	15	AY561573	Actinobac
144	23.4	93.6	540	15	AF547892	Mycobacte	217	23.4	93.6	989	15	AY561574	Actinobac
145	23.4	93.6	540	15	AF547895	Mycobacte	218	23.4	93.6	1012	15	AY163341	Mycobacte
146	23.4	93.6	540	15	AF547909	Mycobacte	219	23.4	93.6	1013	15	AY163338	Mycobacte
147	23.4	93.6	540	15	AF547910	Mycobacte	220	23.4	93.6	1014	1	AJ863363	Unculture
148	23.4	93.6	540	15	AF547911	Mycobacte	221	23.4	93.6	1014	1	AJ863364	Unculture
149	23.4	93.6	540	15	AF547912	Mycobacte	222	23.4	93.6	1019	15	AY163339	Mycobacte
150	23.4	93.6	540	15	AF547916	Mycobacte	223	23.4	93.6	1024	15	AY163335	Mycobacte
151	23.4	93.6	540	15	AF547920	Mycobacte	224	23.4	93.6	1025	1	AJ863315	Unculture
152	23.4	93.6	540	15	AF547921	Mycobacte	225	23.4	93.6	1036	1	AJ863365	Unculture
153	23.4	93.6	540	15	AF547923	Mycobacte	226	23.4	93.6	1049	15	MSP441306	Mycobacte
154	23.4	93.6	540	15	AF547924	Mycobacte	227	23.4	93.6	1276	15	MFO416915	Mycobacte
155	23.4	93.6	540	15	AF547925	Mycobacte	228	23.4	93.6	1317	15	RC16RNAL	Mycobacte
156	23.4	93.6	540	15	AF547929	Mycobacte	229	23.4	93.6	1325	15	DQ083240	Mycobacte
157	23.4	93.6	540	15	AF547936	Mycobacte	230	23.4	93.6	1331	15	AF054278	Mycobacte
158	23.4	93.6	540	15	AF547944	Mycobacte	231	23.4	93.6	1331	15	AY943386	Mycobacte
159	23.4	93.6	540	15	AF547949	Mycobacte	232	23.4	93.6	1360	15	MSGRDQ	Mycobacte
160	23.4	93.6	540	15	AF547950	Mycobacte	233	23.4	93.6	1362	1	AY897829	Unculture
161	23.4	93.6	540	15	AF547951	Mycobacte	234	23.4	93.6	1368	1	AY897828	Unculture
162	23.4	93.6	540	15	AF547954	Mycobacte	235	23.4	93.6	1372	15	AJ833917	Mycobacte
163	23.4	93.6	540	15	AF547955	Mycobacte	236	23.4	93.6	1374	1	AY897827	Unculture
164	23.4	93.6	540	15	AF547956	Mycobacte	237	23.4	93.6	1374	1	AY897830	Unculture

238 23.4 93.6 1374 1 AY921741  
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## ALIGNMENTS

RESULT 1  
AR438653  
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 21 from patent US 6664081.  
ACCESSION AR438653

AY921741 Unculture  
AY162040 Actinobac  
AY897826 Unculture  
AJ416910 Mycobacte  
AF513815 Mycobacte  
DQ137412 Mycobacte  
AM056053 Mycobacte  
DQ145802 Mycobacte  
AF387803 Mycobacte  
AF408960 Mycobacte  
AF177352 Mycobacte  
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AF408993 Mycobacte  
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AY234735 Bacterium  
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AF408955 Mycobacte  
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DQ372734 Mycobacte  
AF479359 Glacial i  
X81996 M.gilvum 16  
X81891 Mycobacteri  
AB010912 Mycobacte  
AF408984 Mycobacte  
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DQ370009 Mycobacte  
AY255478 Mycobacte  
AF480585 Mycobacte  
DQ372733 Mycobacte  
AF480591 Mycobacte  
DQ372728 Mycobacte  
AF130308 Mycobacte  
AY012579 Mycobacte  
AF436799 Mycobacte  
AF480592 Mycobacte  
AF480594 Mycobacte  
AJ234702 Mycobacte  
AJ245702 Mycobacte  
AJ245704 Mycobacte  
AF489137 Mycobacte  
U90876 Mycobacteri  
X77780 Rhodococcus  
AF480587 Mycobacte  
U90877 Mycobacteri  
DQ372731 Mycobacte  
DQ372732 Mycobacte  
X52921 Mycobacteri  
AF480582 Mycobacte  
X52933 Mycobacteri  
Y15709 Mycobacteri  
AF264700 Mycobacte  
AF480590 Mycobacte  
AB009578 Mycobacte  
AF387804 Mycobacte  
AF494537 Mycobacte

VERSION AR438653.1 GI:42663577  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 21 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source  
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Query Match 100.0%; Score 25; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
|||||  
Db 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
|||||  
RESULT 2  
LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 21 from Patent WO0144510.  
ACCESSION AX166855  
VERSION AX166855.1 GI:14596458  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
FEATURES  
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/note="primer oligonucleotide"  
ORIGIN  
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Best Local Similarity 100.0%; Pred.No. 2.9e+02;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
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Db 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
|||||  
RESULT 3  
AF547926 541 bp DNA linear BCT 24-JAN-2006  
LOCUS AF547926  
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.  
ACCESSION AF547926  
VERSION AF547926.1 GI:27337350  
KEYWORDS  
SOURCE Mycobacterium gadium  
ORGANISM Mycobacterium gadium  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus  
 JOURNAL Mycobacterium as a model  
 PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)  
 REFERENCE 15853890  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,  
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,  
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

FEATURES  
 source Location/Qualifiers  
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 /organism="Mycobacterium gadium"  
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 /db\_xref="taxon:1794"  
 /note="type strain of Mycobacterium gadium"  
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 /product="16S ribosomal RNA"

rRNA

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||||||  
 Db 14 GCAAGTCGAACGGAAGGCCTTTCG 38

RESULT 4  
 MGAD16S  
 LOCUS MGAD16S 1456 bp DNA linear BCT 06-JUN-2003  
 DEFINITION M.gadium 16S ribosomal RNA, part.  
 ACCESSION X55594  
 VERSION X55594.1 GI:44291  
 KEYWORDS 16S ribosomal RNA.  
 SOURCE Mycobacterium gadium  
 ORGANISM Mycobacterium gadium  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1456)  
 AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.  
 TITLE Phylogeny of rapidly growing members of the genus Mycobacterium  
 JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)  
 PUBMED 1380284  
 REFERENCE 2 (bases 1 to 1456)  
 AUTHORS Wolters,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine  
 Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen  
 Garten 1-9, 2300 Kiel 1

FEATURES  
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 /strain="ATCC 27726"  
 /db\_xref="taxon:1794"  
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 /product="16S ribosomal RNA"

rRNA

ORIGIN  
 Query Match 100.0%; Score 25; DB 15; Length 1456;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||||||  
 Db 58 GCAAGTCGAACGGAAGGCCTTTCG 82

RESULT 5  
 MCO16S  
 LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003  
 DEFINITION Mycobacterium cookii partial 16S rRNA.  
 ACCESSION X53896  
 VERSION X53896.1 GI:44201  
 KEYWORDS 16S ribosomal RNA; ribosomal RNA.  
 SOURCE Mycobacterium cookii  
 ORGANISM Mycobacterium cookii  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1225)  
 AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,  
 Parlett,J.H. and Pitulle,C.  
 TITLE Mycobacterium cookii sp. nov.  
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)  
 PUBMED 1697763  
 REFERENCE 2 (bases 1 to 1459)  
 AUTHORS Stackebrandt,E.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E

FEATURES  
 source Location/Qualifiers  
 1..1459  
 /organism="Mycobacterium cookii"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 49103 (T) = NZ2."  
 /db\_xref="taxon:1775"  
 1..>1459  
 /product="16S ribosomal RNA"

rRNA

ORIGIN  
 Query Match 100.0%; Score 25; DB 15; Length 1459;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||||||  
 Db 58 GCAAGTCGAACGGAAGGCCTTTCG 82

RESULT 6  
 AR438654  
 LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 22 from patent US 6664081.  
 ACCESSION AR438654  
 VERSION AR438654.1 GI:42663578  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
 Rodrigue,M.  
 TITLE Nucleic acid amplification and detection of mycobacterium species  
 JOURNAL Patent: US 6664081-A 22 16-DEC-2003;  
 Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
 source Location/Qualifiers  
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 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 96.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||  
 Db 1 CAAGTCGAACGGAAGGCCTTTCG 24

RESULT 7  
 AX166856  
 LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001  
 DEFINITION Sequence 22 from Patent WO0144510.

MCO16S  
 LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003  
 DEFINITION Mycobacterium cookii partial 16S rRNA.  
 ACCESSION X53896  
 VERSION X53896.1 GI:44201  
 KEYWORDS 16S ribosomal RNA; ribosomal RNA.  
 SOURCE Mycobacterium cookii  
 ORGANISM Mycobacterium cookii  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1225)  
 AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,  
 Parlett,J.H. and Pitulle,C.  
 TITLE Mycobacterium cookii sp. nov.  
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)  
 PUBMED 1697763  
 REFERENCE 2 (bases 1 to 1459)  
 AUTHORS Stackebrandt,E.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E

FEATURES  
 source Location/Qualifiers  
 1..1459  
 /organism="Mycobacterium cookii"  
 /mol\_type="genomic DNA"  
 /strain="ATCC 49103 (T) = NZ2."  
 /db\_xref="taxon:1775"  
 1..>1459  
 /product="16S ribosomal RNA"

rRNA

ORIGIN  
 Query Match 100.0%; Score 25; DB 15; Length 1459;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||||||  
 Db 58 GCAAGTCGAACGGAAGGCCTTTCG 82

RESULT 6  
 AR438654  
 LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 22 from patent US 6664081.  
 ACCESSION AR438654  
 VERSION AR438654.1 GI:42663578  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
 Rodrigue,M.  
 TITLE Nucleic acid amplification and detection of mycobacterium species  
 JOURNAL Patent: US 6664081-A 22 16-DEC-2003;  
 Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
 source Location/Qualifiers  
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 /organism="unknown"  
 /mol\_type="genomic DNA"

ORIGIN  
 Query Match 96.0%; Score 24; DB 2; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25  
 ||||||||||||||||||||||||  
 Db 1 CAAGTCGAACGGAAGGCCTTTCG 24

RESULT 7  
 AX166856  
 LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001  
 DEFINITION Sequence 22 from Patent WO0144510.

```

ACCESSION  AX166856
VERSION     AX166856.1  GI:14596459
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   other sequences; artificial sequences.
REFERENCE  1
AUTHORS    Bretano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
           Rodrigue,M.
TITLE      Nucleic acid amplification and detection of mycobacterium species
JOURNAL    Patent: WO 0144510-A 22 JUN-2001;
           Gen-Probe incorporated (US) ; Biomerieux S.A. (FR)
FEATURES   Location/Qualifiers
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             /db_xref="taxon:32630"
             /note="primer oligonucleotide"
ORIGIN
Query Match      96.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2  CAAAGTCGACGGAAGGCGCTTTTCG 25
      |||||
DB   1  CAAAGTCGACGGAAGGCGCTTTTCG 24
      |||||

RESULT 8
MSGRGDSA  MSRGDSEA 1460 bp DNA linear BCT 21-SEP-1993
LOCUS     Mycobacterium celatum 16S ribosomal RNA gene.
DEFINITION
ACCESSION L08169
VERSION   L08169.1 GI:293249
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium celatum
ORGANISM  Mycobacterium celatum
REFERENCE 1 (bases 1 to 1460)
AUTHORS   Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
           Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
           Vadney,F.S. and Gross,W.M.
TITLE     Mycobacterium celatum sp. nov
JOURNAL   Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
COMMENT   Original source text: Mycobacterium celatum (library: ATCC 51131)
DNA.
FEATURES   Location/Qualifiers
            1..1460
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             /mol_type="genomic DNA"
             /db_xref="taxon:28045"
             /tissue_lib="ATCC 51131"
             <1..>1460
             /product="16S ribosomal RNA"
             /note="putative"
rRNA
ORIGIN
Query Match      96.0%; Score 24; DB 15; Length 1460;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   8  GCAAGTCGAACGGAAGGCGCTTTTCG 32
      |||||

RESULT 9
MSGRGDSB  MSGRGDSB 1479 bp DNA linear BCT 21-SEP-1993
LOCUS     Mycobacterium celatum 16S ribosomal RNA gene.
DEFINITION
ACCESSION L08170
VERSION   L08170.1 GI:293250
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium celatum
ORGANISM  Mycobacterium celatum
REFERENCE 1 (bases 1 to 1479)
AUTHORS   Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
           Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
           Vadney,F.S. and Gross,W.M.
TITLE     Mycobacterium celatum sp. nov
JOURNAL   Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
COMMENT   Original source text: Mycobacterium celatum (library: ATCC 51130)
DNA.
FEATURES   Location/Qualifiers
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             /db_xref="taxon:28045"
             /tissue_lib="ATCC 51130"
             <1..>1479
             /product="16S ribosomal RNA"
             /note="putative"
rRNA
ORIGIN
Query Match      96.0%; Score 24; DB 15; Length 1479;
Best Local Similarity 96.0%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   29  GCAAGTCGAACGGAAGGCGCTTTTCG 53
      |||||

RESULT 10
MSGRR16S  MSGRR16S 268 bp rRNA linear BCT 27-APR-1993
LOCUS     Mycobacterium kansasii 16S ribosomal RNA.
DEFINITION
ACCESSION M95469
VERSION   M95469.1 GI:175317
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium kansasii
ORGANISM  Mycobacterium kansasii
REFERENCE 1 (bases 1 to 268)
AUTHORS   Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.
           Identification of a genetically distinct sub-species of
           Mycobacterium kansasii
TITLE     Unpublished (1992)
JOURNAL
PUBMED
COMMENT   Original source text: Mycobacterium kansasii rRNA.
DNA.
FEATURES   Location/Qualifiers
            1..268
             /organism="Mycobacterium kansasii"
             /mol_type="rRNA"
             /db_xref="taxon:1768"
             1..250
             /gene="16S rRNA"
             /gene="16S rRNA"
             /product="16S ribosomal RNA"
gene
rRNA
ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 268;
Best Local Similarity 96.0%; Pred. No. 5.9e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GCAAGTCGAACGGAAGGCGCTTTTCG 25
      |||||
DB   38  GCAAGTCGAACGGAAGGCGCTTTTCG 62
      |||||

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RESULT 11  
 MSP404591 293 bp DNA linear ENV 06-JUN-2003  
 LOCUS Uncultured Mycobacterium MB1 partial 16S rRNA gene.  
 DEFINITION  
 ACCESSION AJ404591  
 VERSION  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
 SOURCE uncultured Mycobacterium MB1

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental  
 samples.

REFERENCE 1  
 AUTHORS Kempell,K.E., Cox,C.J., Hurle,M., Wong,A., Wilkie,S.,  
 Zanders,E.D., Gaston,J. and Crowe,J.

TITLE Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA  
 for Detection and Characterisation of Bacterial Species in  
 Arthritis Synovial Tissue

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 293)  
 AUTHORS Cox,C.J.

TITLE Direct Submission

JOURNAL Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,  
 Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,  
 Cambridgeshire, CB10 1SA, UNITED KINGDOM

FEATURES

source  
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 Location/Qualifiers  
 /organism="uncultured Mycobacterium MB1"  
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 /db\_xref="taxon:129682"  
 /clone="MB1"  
 /tissue\_type="Synovium"  
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 /gene="16S rRNA"  
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 /gene="16S rRNA"  
 /product="16S ribosomal RNA"

ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 293;  
 Best Local Similarity 96.0%; Pred. No. 5.7e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCGCTTCG 25

Db 20 GCAAGTCGACGGAAGGCGCTTCG 44

RESULT 12  
 MF16SRRN 316 bp DNA linear BCT 14-NOV-1996  
 LOCUS M.Fortuitum 16S rRNA gene, partial.  
 DEFINITION  
 ACCESSION Y09325

VERSION Y09325.1 GI:1669698

KEYWORDS 16S ribosomal RNA; rrr gene.

SOURCE Mycobacterium fortuitum

ORGANISM Mycobacterium fortuitum

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1  
 AUTHORS De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 316)

AUTHORS De Smet,K.A.L.

TITLE Direct Submission

JOURNAL Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical  
 School at St Marys, Medical Microbiology, Norfolk Place, London, W2  
 1PG, UK

FEATURES

source  
 1..316  
 Location/Qualifiers  
 /organism="Mycobacterium fortuitum"  
 /mol\_type="genomic DNA"

gene  
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 /isolate="36718"  
 /db\_xref="taxon:1766"

rRNA  
 <1..316  
 /gene="rrn"

/product="16S ribosomal RNA"

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 316;  
 Best Local Similarity 96.0%; Pred. No. 5.6e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCGCTTCG 25

Db 45 GCAAGTCGACGGAAGGCGCTTCG 69

RESULT 13

AY395145

LOCUS

DEFINITION

AY395145

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..388

Location/Qualifiers

/organism="uncultured bacterium"

/mol\_type="genomic DNA"

/isolation\_source="forest soil"

/db\_xref="taxon:77133"

/clone="D29ST"

/environmental\_sample

<1..388

/product="16S ribosomal RNA"

ORIGIN

Query Match

Best Local Similarity

Matches

24; Conservative

0; Mismatches

1; Indels

0; Gaps

0;

Qy 1

GCAAGTCGACGGAAGGCGCTTCG

25

Db 50

GCAAGTCGACGGAAGGCGCTTCG

74

RESULT 14

BSSMK23

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1

Schuppler,M., Mertens,F.,

Schon,G. and Gobel,U.B.

ENV 22-FEB-1995



TITLE Molecular characterization of nocardioform actinomycetes in  
activated sludge by 16S rRNA analysis  
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)  
PUBMED 7704280  
REFERENCE 2 (bases 1 to 393)  
AUTHORS Schuppler,M.  
TITLE Direct Submission  
JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.  
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.  
11, 79104 Freiburg, FRG

FEATURES  
source  
1..393  
Location/Qualifiers

/organism="unidentified bacterium"  
/mol\_type="genomic DNA"  
/isolate="SMKN23"  
/db\_xref="taxon:2338"  
1..393  
/product="16S ribosomal RNA"

rRNA  
ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 393;  
Best Local Similarity 96.0%; Pred. No. 5.3e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
|||||  
Db 7 GCAAGTCGAACGGAAGGCTTTTCG 31

RESULT 15  
AY395154  
LOCUS 394 bp DNA linear ENV 07-SEP-2004  
DEFINITION Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene,  
partial sequence.  
ACCESSION AY395154  
VERSION AY395154.1 GI:37595669  
KEYWORDS ENV.  
SOURCE uncultured actinobacterium  
ORGANISM uncultured actinobacterium  
Bacteria; Actinobacteria; environmental samples.  
REFERENCE 1 (bases 1 to 394)  
AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
TITLE Comparison of diversities and compositions of bacterial populations  
inhabiting natural forest soils  
JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)  
PUBMED 15345382

REFERENCE 2 (bases 1 to 394)  
AUTHORS Hackl,E. and Sessitsch,A.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC  
Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES  
source

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Location/Qualifiers  
/organism="uncultured actinobacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="forest soil"  
/db\_xref="taxon:152507"  
/clone="E02ST"  
/environmental\_sample  
<1..>394  
/product="16S ribosomal RNA"

rRNA  
ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 394;  
Best Local Similarity 96.0%; Pred. No. 5.3e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
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Db 50 GCAAGTCGAACGGAAGGCTTTTCG 74

RESULT 16

AY043901  
LOCUS 395 bp DNA linear ENV 05-MAY-2004  
DEFINITION Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene,  
partial sequence.  
ACCESSION AY043901  
VERSION AY043901.1 GI:22267274  
KEYWORDS ENV.  
SOURCE uncultured actinobacterium  
ORGANISM uncultured actinobacterium  
Bacteria; Actinobacteria; environmental samples.  
REFERENCE 1 (bases 1 to 395)  
AUTHORS Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and  
Davies,J.  
TITLE Molecular characterization of bacterial diversity from British  
Columbia forest soils subjected to disturbance  
JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)  
PUBMED 12224564  
REFERENCE 2 (bases 1 to 395)  
AUTHORS Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and  
Davies,J.  
TITLE Direct Submission  
JOURNAL Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,  
Vancouver, BC V6S 2L2, Canada  
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Location/Qualifiers  
/organism="uncultured actinobacterium"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:152507"  
/clone="SMS9.49WL"  
/environmental\_sample  
/note="from forest cut-block mineral soil from the British  
Columbia Ministry of Forests Long-Term Soil Productivity  
(LTSP) installation near Williams Lake, BC, Canada"  
<1..>395  
/product="16S ribosomal RNA"

rRNA  
ORIGIN

Query Match 93.6%; Score 23.4; DB 1; Length 395;  
Best Local Similarity 96.0%; Pred. No. 5.3e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
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Db 20 GCAAGTCGAACGGAAGGCTTTTCG 44

RESULT 17  
AY395151

LOCUS 395 bp DNA linear ENV 07-SEP-2004  
DEFINITION Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial  
sequence.  
ACCESSION AY395151  
VERSION AY395151.1 GI:37595666  
KEYWORDS ENV.  
SOURCE uncultured bacterium  
ORGANISM uncultured bacterium  
Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 395)  
AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
TITLE Comparison of diversities and compositions of bacterial populations  
inhabiting natural forest soils

JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)  
PUBMED 15345382  
REFERENCE 2 (bases 1 to 395)  
AUTHORS Hackl,E. and Sessitsch,A.  
TITLE Direct Submission  
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC  
Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES  
source

1..395  
Location/Qualifiers  
/organism="uncultured bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="forest soil"

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/db_xref="taxon:77133"
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/environmental_sample
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/product="16S ribosomal RNA"

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 395;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 18
BSSMKN14
LOCUS      BSSMKN14          396 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION Bacterium sp.(SMKN14) DNA.
ACCESSION  X78655
VERSION     X78655.1 GI:509724
KEYWORDS   16S ribosomal RNA.
SOURCE     unidentified bacterium
ORGANISM   Bacteria; environmental samples.

REFERENCE 1 Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
AUTHORS   Molecular characterization of nocardiform actinomycetes in
TITLE     activated sludge by 16S rRNA analysis
JOURNAL   Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED    7704280
REFERENCE 2 (bases 1 to 396)
AUTHORS   Schuppler,M.
TITLE     Direct Submission
JOURNAL   Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
          Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
          11, 79104 Freiburg, FRG

FEATURES   source
            Location/Qualifiers
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            /mol_type="genomic DNA"
            /isolate="SMKN14"
            /db_xref="taxon:2338"
            1..396
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 396;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 7 GCAAGTCGAACGGAAGGCGCTTCG 31

RESULT 19
DQ221681
LOCUS      DQ221681          400 bp      DNA      linear      ENV 12-NOV-2005
DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  DQ221681
VERSION     DQ221681.1 GI:80978382
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   uncultured bacterium
            Bacteria; environmental samples.
            1 (bases 1 to 400)
REFERENCE 1 Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
AUTHORS   Bacterial diversity on leaf surfaces of the Brazilian Atlantic
TITLE     Forest
JOURNAL   Unpublished

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2 (bases 1 to 400)
Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
Direct Submission
Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade
de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil
Location/Qualifiers
1..400
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="phylosphere"
/specific_host="Campomanesia xanthocarpa"
/db_xref="taxon:77133"
/clone="BPH3088"
/environmental_sample
<1..>400
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 400;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 15 GCAAGTCGAACGGAAGGCGCTTCG 39

RESULT 20
AY234665
LOCUS      AY234665          403 bp      DNA      linear      BCT 08-DEC-2003
DEFINITION Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234665
VERSION     AY234665.1 GI:37961822
KEYWORDS   Bacterium Ellin6013
ORGANISM   Bacterium Ellin6013
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.

REFERENCE 1 (bases 1 to 403)
AUTHORS   Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE     Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL   Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED    14660368
REFERENCE 2 (bases 1 to 403)
AUTHORS   Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
Location/Qualifiers
1..403
/organism="bacterium Ellin6013"
/mol_type="genomic DNA"
/isolate="Ellin6013"
/db_xref="taxon:234120"
<1..>403
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 403;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 21
AY792017/c
LOCUS      AY792017          407 bp      DNA      linear      BCT 20-NOV-2004

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DEFINITION Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792017
VERSION AY792017.1 GI:55740316
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. 5BR6
Mycobacterium sp. 5BR6
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 407)
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
TITLE Bioremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 407)
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
AUTHORS Direct Submission
TITLE Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales,
JOURNAL Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES
Location/Qualifiers
source
1..407
/organism="Mycobacterium sp. 5BR6"
/mol_type="genomic DNA"
/isolate="5BR6"
/isolation_source="radioactive water"
/db_xref="taxon:300866"
<1..>407
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 407;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 366 GCAAGTCGAACGGAAGGCGCTTTCG 342

RESULT 22
BSSMKN12
LOCUS Bacterium sp. (SMKN12) DNA. 410 bp DNA linear ENV 22-FEB-1995
DEFINITION
ACCESSION X78654
VERSION X78654.1 GI:509723
KEYWORDS 16S ribosomal RNA.
SOURCE unidentified bacterium
ORGANISM unidentified bacterium
Bacteria; environmental samples.
REFERENCE
1
Schuppler M., Mertens, F., Schon, G. and Gobel, U.B.
AUTHORS Molecular characterization of nocardiform actinomycetes in
TITLE activated sludge by 16S rRNA analysis
JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED 7704280
REFERENCE
2 (bases 1 to 410)
Schuppler, M.
AUTHORS Direct Submission
TITLE Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
JOURNAL Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG
FEATURES
Location/Qualifiers
source
1..410
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/isolate="SMKN12"
/db_xref="taxon:2338"
1..410
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 410;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;

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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 2 GCAAGTCGAACGGAAGGCGCTTTCG 26

RESULT 23
DQ063154
LOCUS Actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063154
VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE
ORGANISM
actinobacterium BAL218
actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 411)
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
AUTHORS Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
JOURNAL by cultivation and molecular-based methods
REFERENCE
2 (bases 1 to 411)
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
AUTHORS Hagstrom, A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39211, Sweden
FEATURES
Location/Qualifiers
source
1..411
/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 411;
Best Local Similarity 96.0%; Pred. No. 5.3e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
|||||
Db 10 GCAAGTCGAACGGAAGGCGCTTTCG 34

RESULT 24
DQ063199
LOCUS Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE
ORGANISM
actinobacterium BAL263
actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 411)
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
AUTHORS Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
JOURNAL by cultivation and molecular-based methods
REFERENCE
2 (bases 1 to 411)
Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
AUTHORS Hagstrom, A.
TITLE Direct Submission

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JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
KEYWORDS University of Kalmar, Barlasgatan 11, Kalmar 39231, Sweden
SOURCE Location/Qualifiers
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      /strain="BAL263"
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BY31, Zobel/R2A media"
/db_xref="taxon:331810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
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  Best Local Similarity 96.0%; Pred. No. 5.3e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 11 GCAAGTCGACGGAAGGCCCTTCG 35

RESULT 25
AY792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
SOURCE
  ORGANISM
    Mycobacterium sp. 4BR14
    Mycobacterium sp. 4BR14
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  1 (bases 1 to 411)
  Sarro.M.I., Garcia.A.M., Moreno.D.A. and Montero.F.
  Direct Submission
  Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
  Escuela Tecnica Superior de Ingenieros Industriales, Universidad
  Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
  28006, Spain
  Location/Qualifiers
  1. 411
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    /isolate="4BR14"
    /isolation_source="radioactive water"
    /db_xref="taxon:300864"
    <1..>411
    /product="16S ribosomal RNA"

rRNA

ORIGIN
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  Best Local Similarity 96.0%; Pred. No. 5.3e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 51 GCAAGTCGACGGAAGGCCCTTCG 75

RESULT 26
AM085786 416 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION
ACCESSION AM085786

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VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
  ORGANISM
    uncultured Mycobacterium sp.
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
    samples.
  1
  Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
  Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
  Springael,D.
  Distribution of the Mycobacterium sp. community and polycyclic
  aromatic hydrocarbons (PAHs) among different size fractions of a
  weathered PAH-contaminated soil
  Unpublished
  2 (bases 1 to 416)
  Uyttebroek,M.
  Direct Submission
  Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
  Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
  B-3001 Leuven, BELGIUM
  Location/Qualifiers
  1. .416
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    /isolation_source="PAH-contaminated soil"
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    /clone="K11"
    /environmental_sample
    /country="Denmark"
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    /gene="16S rRNA"
    <1..>416
    /gene="16S rRNA"
    /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
  Query Match 93.6%; Score 23.4; DB 1; Length 416;
  Best Local Similarity 96.0%; Pred. No. 5.3e+02;
  Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCCTTCG 25
    |||||
Db 3 GCAAGTCGACGGAAGGCCCTTCG 27

RESULT 27
AM085788 418 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION
ACCESSION AM085788
VERSION AM085788.1 GI:75754611
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
  ORGANISM
    uncultured Mycobacterium sp.
    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
    Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
    samples.
  1
  Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
  Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
  Springael,D.
  Distribution of the Mycobacterium sp. community and polycyclic
  aromatic hydrocarbons (PAHs) among different size fractions of a
  weathered PAH-contaminated soil
  Unpublished
  2 (bases 1 to 418)
  Uyttebroek,M.
  Direct Submission
  Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
  Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
  B-3001 Leuven, BELGIUM
  Location/Qualifiers

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source
1. .418
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
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/environmental_sample
/country="Denmark"
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Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
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Db 3 GCAAGTCGAACGGAAGGCGCTTTCG 27
| | | | | | | | | | | | | | | | | | | |

RESULT 28
AY673261 418 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673261
VERSION AY673261.1 GI:56683118
KEYWORDS
SOURCE
ORGANISM Mycobacteriaceae bacterium Ellin7095
Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 418)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .418
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/mol_type="genomic DNA"
/isolate="Ellin7095"
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/db_xref="taxon:305281"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 418;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
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Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54
| | | | | | | | | | | | | | | | | | | |

RESULT 29
AM085770 421 bp DNA linear ENV 21-SEP-2005
LOCUS
DEFINITION Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION AM085770

source
1. .418
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
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/clone="K13"
/environmental_sample
/country="Denmark"
<1. .>418
/gene="16S rRNA"
<1. .>418
/product="16S ribosomal RNA"

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 418;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
| | | | | | | | | | | | | | | | | | | |
Db 3 GCAAGTCGAACGGAAGGCGCTTTCG 27
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RESULT 28
AY673261 418 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY673261
VERSION AY673261.1 GI:56683118
KEYWORDS
SOURCE
ORGANISM Mycobacteriaceae bacterium Ellin7095
Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 Davis,K.E., Joseph,S.J. and Janssen,P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE
2 (bases 1 to 418)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .418
/organism="Mycobacteriaceae bacterium Ellin7095"
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/isolate="Ellin7095"
/isolation_source="soil"
/db_xref="taxon:305281"
<1. .>418
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 418;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
| | | | | | | | | | | | | | | | | | | |
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54
| | | | | | | | | | | | | | | | | | | |

RESULT 29
AM085770 421 bp DNA linear ENV 21-SEP-2005
LOCUS
DEFINITION Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION AM085770

source
1. .418
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
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/environmental_sample
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/gene="16S rRNA"
<1. .>418
/product="16S ribosomal RNA"

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 421;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
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Db 9 GCAAGTCGAACGGAAGGCGCTTTCG 33
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RESULT 30
AJ786807 422 bp DNA linear BCT 29-OCT-2004
LOCUS
DEFINITION Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION AJ786807
VERSION AJ786807.1 GI:54897545
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Mycobacterium sp. R-22838
ORGANISM Mycobacterium sp. R-22838
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
Verstraete,W. and De Vos,P.
The microbial community composition of a commercial nitrifying
inoculum
Unpublished
JOURNAL 2 (bases 1 to 422)
REFERENCE Vanparrys,B.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
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/country="Belgium"
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    Best Local Similarity         96.0%; Pred. No. 5.2e+02;  
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Db 30 GCAAGTCGAACGGAAGGCCTTTCG 54  
    |||||  
  
RESULT 31  
AY673205                  423 bp DNA linear BCT 20-MAY-2005  
LOCUS Mycobacteriaceae bacterium Ellin7039 16S ribosomal RNA gene,  
DEFINITION partial sequence.  
ACCESSION AY673205  
VERSION AY673205.1 GI:56683062  
KEYWORDS  
SOURCE Mycobacteriaceae bacterium Ellin7039  
ORGANISM Mycobacteriaceae bacterium Ellin7039  
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
          Corynebacterineae; Mycobacteriaceae.  
REFERENCE 1 (bases 1 to 423)  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.  
TITLE Effects of growth medium, inoculum size, and incubation time on  
          culturability and isolation of soil bacteria  
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
PUBMED 15691937  
REFERENCE 2 (bases 1 to 423)  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
          University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
          Australia  
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    Best Local Similarity         96.0%; Pred. No. 5.2e+02;  
    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
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Db 30 GCAAGTCGAACGGAAGGCCTTTCG 54  
    |||||  
  
RESULT 32  
AY673206                  423 bp DNA linear BCT 20-MAY-2005  
LOCUS Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,  
DEFINITION partial sequence.  
ACCESSION AY673206  
VERSION AY673206.1 GI:56683063  
KEYWORDS  
SOURCE Mycobacteriaceae bacterium Ellin7040  
ORGANISM Mycobacteriaceae bacterium Ellin7040  
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
          Corynebacterineae; Mycobacteriaceae.  
REFERENCE 1 (bases 1 to 423)  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.

TITLE Effects of growth medium, inoculum size, and incubation time on  
JOURNAL culturability and isolation of soil bacteria  
PUBMED Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
REFERENCE 15691937  
AUTHORS 2 (bases 1 to 423)  
TITLE Davis, K.E., Joseph, S.J. and Janssen, P.H.  
JOURNAL Direct Submission  
          Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
          University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
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    Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
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Db 30 GCAAGTCGAACGGAAGGCCTTTCG 54  
    |||||  
  
RESULT 33  
AY673207                  423 bp DNA linear BCT 20-MAY-2005  
LOCUS Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,  
DEFINITION partial sequence.  
ACCESSION AY673207  
VERSION AY673207.1 GI:56683064  
KEYWORDS  
SOURCE Mycobacteriaceae bacterium Ellin7041  
ORGANISM Mycobacteriaceae bacterium Ellin7041  
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
          Corynebacterineae; Mycobacteriaceae.  
REFERENCE 1 (bases 1 to 423)  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.  
TITLE Effects of growth medium, inoculum size, and incubation time on  
          culturability and isolation of soil bacteria  
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
PUBMED 15691937  
REFERENCE 2 (bases 1 to 423)  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
          University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
          Australia  
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RESULT 34
DQ063156
LOCUS actinobacterium BAL220 424 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063156
VERSION DQ063156.1 GI:68139194
KEYWORDS
SOURCE actinobacterium BAL220
ORGANISM actinobacterium BAL220
REFERENCE 1 (bases 1 to 424)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
location/Qualifiers
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/db_xref="taxon:331797"
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rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 424;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCTTTTCG 25
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RESULT 35
AY673287
LOCUS Streptoporangiaceae bacterium Ellin7121
DEFINITION Streptoporangiaceae bacterium Ellin7121 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673287
VERSION AY673287.1 GI:56683144
KEYWORDS
SOURCE Streptoporangiaceae bacterium Ellin7121
ORGANISM Streptoporangiaceae bacterium Ellin7121
REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 424)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES
source
location/Qualifiers
1..424

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/db_xref="taxon:305348"
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rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 15; Length 424;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCTTTTCG 25
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Db 30 GCAAGTCGACGGAAGGCTTTTCG 54

RESULT 36
AY394635
LOCUS Uncultured Mycobacterium sp. clone W1-11 425 bp DNA linear ENV 20-OCT-2003
DEFINITION Uncultured Mycobacterium sp. clone W1-11 16S ribosomal RNA gene, partial sequence.
ACCESSION AY394635
VERSION AY394635.1 GI:37677560
KEYWORDS ENV.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
REFERENCE 1 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Intracellular symbionts and other bacteria associated with deer ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod, Massachusetts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Molecular & Cell Biology, University of Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125, USA
FEATURES
source
location/Qualifiers
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/mol_type="genomic DNA"
/specific_host="Ixodes scapularis"
/db_xref="taxon:171292"
/clones="W1-11"
/environmental_sample
/country="USA; Massachusetts, Cape Cod, Nantucket, Wellfleet"
<1..>425
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.6%; Score 23.4; DB 1; Length 425;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCTTTTCG 25
|||||
Db 30 GCAAGTCGACGGAAGGCTTTTCG 54

RESULT 37
AY673136
LOCUS Mycobacteriaceae bacterium Ellin5409 426 bp DNA linear BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673136
VERSION AY673136.1 GI:56683290

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KEYWORDS      .
SOURCE         Mycobacteriaceae bacterium Ellin5409
ORGANISM       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae.
REFERENCE      1 (bases 1 to 426)
AUTHORS        Osborne,C.A. and Janssen,P.H.
TITLE          Direct Submission
JOURNAL        Submitted (30-JUN-2004) Department of Microbiology and Immunology,
                University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                Australia
FEATURES       Location/Qualifiers
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                        /organism="Mycobacteriaceae bacterium Ellin5409"
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                        /product="16S ribosomal RNA"
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                Best Local Similarity 96.0%; Pred. No. 5.2e+02;
                Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
                Qy      1 GCAAGTCGACGGAAGGCCCTTCG 25
                        |||
                        30 GCAAGTCGACGGAAGGCCCTTCG 54
                RESULT 38
                AB106918      428 bp DNA linear BCT 09-SEP-2003
                LOCUS        Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
                DEFINITION    sequence.
                ACCESSION    AB106918
                VERSION       AB106918.1 GI:29421132
                KEYWORDS      Gram-positive bacterium 1-6
                SOURCE        Gram-positive bacterium 1-6
                ORGANISM      Bacteria.
                REFERENCE      1
                        Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
                        Fujii,T. and Muramatsu,Y.
                TITLE          Microbial participation in iodine volatilization from soils
                JOURNAL        Environ. Sci. Technol. 37, 3885-3890 (2003)
                REFERENCE      2 (bases 1 to 428)
                        Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
                        Fujii,T. and Muramatsu,Y.
                TITLE          Direct Submission
                JOURNAL        Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
                Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
                (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
                Fax:81-47-308-8866)
                FEATURES       Location/Qualifiers
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                Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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                        30 GCAAGTCGACGGAAGGCCCTTCG 54
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                DQ063058      428 bp DNA linear BCT 27-JUN-2005
                LOCUS        Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
                DEFINITION    Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
                ACCESSION    DQ063058
                VERSION       DQ063058.1 GI:68139087
                KEYWORDS      actinobacterium BAL118
                SOURCE        actinobacterium BAL118
                ORGANISM      Bacteria; Actinobacteria.
                REFERENCE      1 (bases 1 to 428)
                        Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                        Hagstrom,A.
                AUTHORS        Bacterial community composition in the central Baltic Sea analyzed
                TITLE          by cultivation and molecular-based methods
                JOURNAL        Unpublished
                REFERENCE      2 (bases 1 to 428)
                        Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                        Hagstrom,A.
                AUTHORS        Direct Submission
                TITLE          Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
                JOURNAL        University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
                FEATURES       Location/Qualifiers
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                        /country="Sweden"
                        /latlon="60.42.726N, 05.05.595E"
                        /collection_date="2 July 2003"
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                Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
                Qy      1 GCAAGTCGACGGAAGGCCCTTCG 25
                        |||
                        8 GCAAGTCGACGGAAGGCCCTTCG 32
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                RESULT 40
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                LOCUS        Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
                DEFINITION    Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
                ACCESSION    AJ786822
                VERSION       AJ786822.1 GI:54887560
                KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
                SOURCE        Mycobacterium sp. R-23262
                ORGANISM      Mycobacterium sp. R-23262
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                REFERENCE      1
                        Vanparys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
                        Verstraete,W. and De Vos,P.
                AUTHORS        The microbial community composition of a commercial nitrifying
                TITLE          inoculum
                JOURNAL        Unpublished
                REFERENCE      2 (bases 1 to 430)
                        Vanparys,B.
                AUTHORS        Direct Submission
                TITLE          Submitted (30-JUL-2004) Vanparys B., Laboratory of Microbiology,
                JOURNAL        University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
                FEATURES       Location/Qualifiers
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/product="16S ribosomal RNA"

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Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 41
AY673202          430 bp DNA linear BCT 20-MAY-2005
LOCUS
DEFINITION
Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673202.1 GI:56683059
VERSION
KEYWORDS
ORGANISM
Mycobacteriaceae bacterium Ellin7036
Mycobacteriaceae bacterium Ellin7036
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 430)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
EFFECTS OF growth medium, inoculum size, and incubation time on
Culturable and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 430)
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
Direct Submission
AUTHORS
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
JOURNAL
PUBMED
KEYWORDS
AUTHORS
TITLE
JOURNAL
DEFINITION
Location/Qualifiers
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 42
AB106919          431 bp DNA linear BCT 09-SEP-2003
LOCUS
DEFINITION
Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
sequence.
ACCESSION
AB106919
VERSION
KEYWORDS
SOURCE
Gram-positive bacterium 2-1

/isolate="R-23262"
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/db_xref="taxon:289008"
/country="Belgium"
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/gene="16S rRNA"
<1..>430
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 430;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 43
AF078232          432 bp DNA linear ENV 10-MAY-2004
LOCUS
DEFINITION
Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION
AF078232.1 GI:4590103
VERSION
KEYWORDS
ENV.
SOURCE
grassland soil clone saf2_117
grassland soil clone saf2_117
Bacteria; environmental samples.
1 (bases 1 to 432)
McCaig, A.E., Glover, L.A. and Prosser, J.I.
Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
10103273
2 (bases 1 to 432)
McCaig, A.E., Prosser, J.I. and Glover, L.A.
Direct Submission
AUTHORS
Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
JOURNAL
PUBMED
KEYWORDS
AUTHORS
TITLE
JOURNAL
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 1; Length 432;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25

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ORGANISM
Gram-positive bacterium 2-1
Bacteria.
REFERENCE
1
AUTHORS
Amachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,
Fujii, T. and Muramatsu, Y.
TITLE
Microbial participation in iodine volatilization from soils
JOURNAL
Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE
2 (bases 1 to 431)
Amachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,
Fujii, T. and Muramatsu, Y.
TITLE
Direct Submission
JOURNAL
Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail: amachi@faculty.chiba-u.jp, Tel: 81-47-308-8868,
Fax: 81-47-308-8866)
FEATURES
Location/Qualifiers
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rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 431;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
    |||||
Db 30 GCAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 43
AF078232          432 bp DNA linear ENV 10-MAY-2004
LOCUS
DEFINITION
Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION
AF078232.1 GI:4590103
VERSION
KEYWORDS
ENV.
SOURCE
grassland soil clone saf2_117
grassland soil clone saf2_117
Bacteria; environmental samples.
1 (bases 1 to 432)
McCaig, A.E., Glover, L.A. and Prosser, J.I.
Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
10103273
2 (bases 1 to 432)
McCaig, A.E., Prosser, J.I. and Glover, L.A.
Direct Submission
AUTHORS
Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
JOURNAL
PUBMED
KEYWORDS
AUTHORS
TITLE
JOURNAL
DEFINITION
Location/Qualifiers
1..432
/organism="grassland soil clone saf2_117"
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/db_xref="taxon:80202"
/clone_lib="unimproved grassland soil SAF2"
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rRNA

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Query Match          93.6%; Score 23.4; DB 1; Length 432;
Best Local Similarity 96.0%; Pred. No. 5.2e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25

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ORGANISM bacterium Ellin6040  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae.  
 REFERENCE 1 (bases 1 to 435)  
 AUTHORS Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and Janssen,P.H.  
 TITLE Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria  
 JOURNAL Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)  
 PUBMED 14660368  
 REFERENCE 2 (bases 1 to 435)  
 AUTHORS Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and Janssen,P.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-FEB-2003) Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria 3010, Australia  
 FEATURES  
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 1..435  
 /organism="bacterium Ellin6040"  
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 /isolate="Ellin6040"  
 /db\_xref="taxon:234122"  
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 /product="16S ribosomal RNA"  
 rRNA  
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 Query Match 93.6%; Score 23.4; DB 15; Length 435;  
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
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 DB 30 GCAAGTCGACGGAAGGCGCTTTCG 54  
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 RESULT 48  
 AY673233  
 LOCUS 435 bp DNA linear BCT 20-MAY-2005  
 DEFINITION Mycobacteriaceae bacterium Ellin7067  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae.  
 ACCESSION AY673233  
 VERSION AY673233.1 GI:56683090  
 KEYWORDS  
 ORGANISM Mycobacteriaceae bacterium Ellin7067  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae.  
 REFERENCE 1 (bases 1 to 435)  
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.  
 TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria  
 JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
 PUBMED 15691937  
 REFERENCE 2 (bases 1 to 435)  
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia  
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 /isolate="Ellin7067"  
 /isolation\_sources="soil"  
 /db\_xref="taxon:305274"  
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 rRNA  
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 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
 |||||  
 DB 30 GCAAGTCGACGGAAGGCGCTTTCG 54  
 |||||  
 RESULT 49  
 DQ063046  
 LOCUS 436 bp DNA linear BCT 27-JUN-2005  
 DEFINITION Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.  
 ACCESSION DQ063046  
 VERSION DQ063046.1 GI:68139075  
 KEYWORDS  
 SOURCE actinobacterium BAL106  
 ORGANISM actinobacterium BAL106  
 Bacteria; Actinobacteria.  
 REFERENCE 1 (bases 1 to 436)  
 AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.  
 TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 436)  
 AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Bariasgatan 11, Kalmar 39231, Sweden  
 FEATURES  
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 /organism="actinobacterium BAL106"  
 /mol\_type="genomic DNA"  
 /strain="BAL106"  
 /isolation\_source="Baltic Sea, 3m depth, Landsort deep St. By31, Zobell/R2A media"  
 /db\_xref="taxon:331778"  
 /country="Sweden"  
 /lat\_lon="60.42.726N, 05.05.595E"  
 /collection\_dates="2 July 2003"  
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 rRNA  
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 Query Match 93.6%; Score 23.4; DB 15; Length 436;  
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGACGGAAGGCGCTTTCG 25  
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 DB 19 GCAAGTCGACGGAAGGCGCTTTCG 43  
 |||||  
 RESULT 50  
 AY673199  
 LOCUS 436 bp DNA linear BCT 20-MAY-2005  
 DEFINITION Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AY673199  
 VERSION AY673199.1 GI:56683056  
 KEYWORDS  
 SOURCE Mycobacteriaceae bacterium Ellin7033  
 ORGANISM Mycobacteriaceae bacterium Ellin7033  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae.  
 REFERENCE 1 (bases 1 to 436)  
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.  
 TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria  
 JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
 PUBMED 15691937  
 REFERENCE 2 (bases 1 to 436)  
 AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.  
 TITLE Direct Submission

JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
Australia

FEATURES  
source Location/Qualifiers  
1. .436  
/organism="Mycobacteriaceae bacterium Ellin7033"  
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/db\_xref="taxon:305286"  
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/product="16S ribosomal RNA"

rRNA

ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 436;  
Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25  
|||||  
Db 30 GCAAGTCGACGGAAGGCCCTTCG 54  
|||||

RESULT 51  
AY673304 436 bp DNA linear BCT 20-MAY-2005  
LOCUS Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene,  
partial sequence.  
DEFINITION AY673304  
VERSION AY673304.1 GI:56683161  
KEYWORDS  
SOURCE Mycobacteriaceae bacterium Ellin7138  
ORGANISM Mycobacteriaceae bacterium Ellin7138  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae.

REFERENCE  
1 (bases 1 to 436)  
Davis,K.E., Joseph,S.J. and Janssen,P.H.  
Effects of growth medium, inoculum size, and incubation time on  
culturability and isolation of soil bacteria  
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
15691937

JOURNAL PUBLISHED 2 (bases 1 to 436)  
REFERENCE 2 (bases 1 to 436)  
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.  
Direct Submission  
AUTHORS  
TITLE Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
Australia

FEATURES  
source Location/Qualifiers  
1. .436  
/organism="Mycobacteriaceae bacterium Ellin7138"  
/mol\_type="genomic DNA"  
/isolate="Ellin7138"  
/isolation\_source="soil"  
/db\_xref="taxon:305288"  
<1. .>436  
/product="16S ribosomal RNA"

rRNA

ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 436;  
Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25  
|||||  
Db 30 GCAAGTCGACGGAAGGCCCTTCG 54  
|||||

RESULT 52  
AF078419 437 bp DNA linear ENV 10-MAY-2004  
LOCUS Grassland soil clone sl3\_612 16S ribosomal RNA gene, partial  
DEFINITION AF078419  
VERSION AF078419  
KEYWORDS  
SOURCE Grassland soil clone sl3\_612  
ORGANISM Bacteria; environmental samples.  
1 (bases 1 to 437)  
McCaig,A.E., Glover,L.A. and Prosser,J.I.  
Molecular analysis of bacterial community structure and diversity  
in unimproved and improved upland grass pastures  
Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)  
10103273

REFERENCE 2 (bases 1 to 437)  
McCaig,A.E., Prosser,J.I. and Glover,L.A.  
Direct Submission  
AUTHORS  
TITLE Submitted (16-JUL-1998) Institute of Medical Sciences, Department  
of Molecular and Cell Biology, University of Aberdeen,  
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

FEATURES  
source Location/Qualifiers  
1. .437  
/organism="grassland soil clone sl3\_612"  
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/db\_xref="taxon:80115"  
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/environmental\_sample  
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rRNA

ORIGIN  
Query Match 93.6%; Score 23.4; DB 1; Length 437;  
Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCCTTCG 25  
|||||  
Db 8 GCAAGTCGACGGAAGGCCCTTCG 32  
|||||

RESULT 53  
AB232370 441 bp DNA linear BCT 25-JAN-2006  
LOCUS Mycobacterium kansasii gene for 16S rRNA, partial sequence,  
strain:SA-10.  
DEFINITION AB232370  
VERSION AB232370.1 GI:73589607  
KEYWORDS  
SOURCE Mycobacterium kansasii  
ORGANISM Mycobacterium kansasii  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1  
Iwamoto,T. and Saito,H.  
Comparative study of two typing methods, hsp65 PRA and ITS  
sequencing, revealed a possible evolutionary link between  
Mycobacterium kansasii type I and II isolates  
FEMS Microbiol. Lett. 254, 129-133 (2006)

JOURNAL PUBLISHED 2 (bases 1 to 441)  
REFERENCE 2 (bases 1 to 441)  
Iwamoto,T.  
Direct Submission  
AUTHORS  
TITLE Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,  
Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,  
Hyogo 6500046, Japan [E-mail: kx2t-iwmt@asahi-net.or.jp,  
URL: http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-  
top, Tel:81-78-302-6251, Fax:81-78-302-0894]

FEATURES  
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1. .441  
/organism="Mycobacterium kansasii"  
/mol\_type="genomic DNA"  
/strain="SA-10"  
/db\_xref="taxon:1768"  
/note="type II"  
<1. .>441  
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 441;  
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 |||||  
 Db 4 GCAAGTCGAACGGAAGGCGCTTCG 28

RESULT 54  
 AY306201  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mycobacterium sp. 1351  
 Mycobacterium sp. 1351  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 1 (bases 1 to 442)  
 Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.  
 A High Proportion of Novel Mycobacteria Species Identified by 16S  
 rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a  
 Clinical Setting  
 Unpublished  
 2 (bases 1 to 442)  
 Turenne,C.Y.  
 Direct Submission  
 TITLE  
 JOURNAL  
 MYCOBACTERIUM SP. 1351  
 1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada  
 Location/Qualifiers  
 1. .442  
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 /mol\_type="genomic DNA"  
 /strain="1351"  
 /isolation\_source="mouth ulcer"  
 /specific\_host="Homo sapiens"  
 /db\_xref="taxon:235254"  
 <1. .>442  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 442;  
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 |||||  
 Db 4 GCAAGTCGAACGGAAGGCGCTTCG 28

RESULT 55  
 AY306205  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mycobacterium sp. HSC507  
 Mycobacterium sp. HSC507  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 1 (bases 1 to 444)  
 Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.  
 A High Proportion of Novel Mycobacteria Species Identified by 16S  
 rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a  
 Clinical Setting  
 Unpublished  
 2 (bases 1 to 444)  
 Turenne,C.Y.

TITLE  
 JOURNAL  
 Direct Submission  
 Submitted (26-MAY-2003) National Reference Centre for  
 Mycobacteriology, National Microbiology Laboratory, Health Canada,  
 1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada  
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 1. .444  
 /organism="Mycobacterium sp. HSC507"  
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 /strain="HSC507"  
 /isolation\_source="sputum"  
 /specific\_host="Homo sapiens"  
 /db\_xref="taxon:235258"  
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 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 444;  
 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 |||||  
 Db 4 GCAAGTCGAACGGAAGGCGCTTCG 28

RESULT 56  
 AB106917  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Gram-positive bacterium 1-3  
 Gram-positive bacterium 1-3  
 Bacteria.  
 1  
 Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,  
 Fujii,T. and Muramatsu,Y.  
 Microbial participation in iodine volatilization from soils  
 Environ. Sci. Technol. 37, 3885-3890 (2003)  
 2 (bases 1 to 445)  
 Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,  
 Fujii,T. and Muramatsu,Y.  
 Direct Submission  
 Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of  
 Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan  
 (E-mail:amachi@faculty.chiba-u.jp, tel:81-47-308-8868,  
 Fax:81-47-308-8866)  
 Location/Qualifiers  
 1. .445  
 /organism="Gram-positive bacterium 1-3"  
 /mol\_type="genomic DNA"  
 /strain="1-3"  
 /db\_xref="taxon:226199"  
 <1. .>445  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

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 Best Local Similarity 96.0%; Pred. No. 5.2e+02;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 |||||  
 Db 30 GCAAGTCGAACGGAAGGCGCTTCG 54

RESULT 57  
 DQ067466  
 LOCUS  
 DEFINITION  
 ACCESSION  
 Mycobacterium sp. FI05167 16S ribosomal RNA gene, partial sequence.  
 DQ067466  
 DQ067466

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VERSION
KEYWORDS
SOURCE
ORGANISM
  DQ067466.1 GI:67528039
  Mycobacterium sp. F105167
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
  1 (bases 1 to 445)
  Tortoli, E., Mariottini, A. and Mazzarelli, G.
  Unusual mycobacteria isolated from clinical samples
  Unpublished
  2 (bases 1 to 445)
  Tortoli, E., Mariottini, A. and Mazzarelli, G.
  Direct Submission
  TITLE
  Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
  Careggi Hospital, Piasra dei Servizi, Ospedale Careggi, v.le
  Morgagni 85, Firenze, FI 50134, Italy
  Location/Qualifiers
  FEATURES
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        /mol_type="genomic DNA"
        /strain="F105167"
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        <1..>445
        /product="16S ribosomal RNA"
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    ORIGIN
      Query Match 93.6%; Score 23.4; DB 15; Length 445;
      Best Local Similarity 96.0%; Pred. No. 5.2e+02;
      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 8 GCAAGTCGAACGGAAGGCCTTTCG 32

RESULT 58
MS91016SR 450 bp DNA linear BCT 01-AUG-1997
LOCUS
DEFINITION
  Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
ACCESSION
  Y08205
VERSION
  Y08205.1 GI:2292948
KEYWORDS
  16S ribosomal RNA; 16S rRNA.
SOURCE
  Mycobacterium sp.
ORGANISM
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
  1
  Hagenau, C., Behringer, K., Naumann, L., Kaiser, R. and
  Schulze-Roebecke, R.
  Unpublished
  2 (bases 1 to 450)
  Hagenau, C.
  Direct Submission
  TITLE
  Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
  of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
  Related sequence: M95469.
  Location/Qualifiers
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        /map="E.coli 38-503"
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        /gene="16S rRNA"
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        /genes="16S rRNA"
        /product="16S ribosomal RNA"
    gene
    rRNA
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      Query Match 93.6%; Score 23.4; DB 15; Length 450;
      Best Local Similarity 96.0%; Pred. No. 5.1e+02;
      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTTCG 44

RESULT 60
AY358002 450 bp DNA linear BCT 19-AUG-2005
LOCUS
DEFINITION
  Actinobacterium iri17 16S ribosomal RNA gene, partial sequence.
ACCESSION
  AY358002
VERSION
  AY358002.1 GI:34500643
KEYWORDS
  actinobacterium iri17
  actinobacterium iri17
  Bacteria; Actinobacteria.
  1 (bases 1 to 450)
  Idris, R., Trifonova, R., Puschenreiter, M., Wenzel, W.W. and
  Sessitsch, A.
  Bacterial Communities Associated with Flowering Plants of the Ni
  Hyperaccumulator Thlaspi goesingense
  Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
  15128517
  2 (bases 1 to 450)
  Idris, R. and Sessitsch, A.
  Direct Submission
  TITLE
  Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
  Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
  Location/Qualifiers
  FEATURES
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        /mol_type="genomic DNA"
        /isolate="BN910"
        /db_xref="taxon:1785"
        /map="E.coli position 38-503"
        1..450
        /gene="16S rRNA"
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        /product="16S ribosomal RNA"
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    rRNA
    ORIGIN
      Query Match 93.6%; Score 23.4; DB 15; Length 450;
      Best Local Similarity 96.0%; Pred. No. 5.1e+02;
      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTTCG 44

RESULT 59
MSP16SR 450 bp DNA linear BCT 01-AUG-1997
LOCUS
DEFINITION
  Mycobacterium sp. 16S rRNA gene.
ACCESSION
  Y07954
VERSION
  Y07954.1 GI:2292951
KEYWORDS
  16S ribosomal RNA; 16S rRNA gene.
SOURCE
  Mycobacterium sp.
ORGANISM
  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
  1
  Hagenau, C., Behringer, K., Naumann, L., Kaiser, R. and
  Schulze-Roebecke, R.
  Unpublished
  2 (bases 1 to 450)
  Hagenau, C.
  Direct Submission
  TITLE
  Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
  of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
  Related sequence: M95469.
  Location/Qualifiers
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        /mol_type="genomic DNA"
        /isolate="BN737"
        /db_xref="taxon:1785"
        /map="E.coli 38-503"
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        /gene="16S rRNA"
        <1..>450
        /genes="16S rRNA"
        /product="16S ribosomal RNA"
    gene
    rRNA
    ORIGIN
      Query Match 93.6%; Score 23.4; DB 15; Length 450;
      Best Local Similarity 96.0%; Pred. No. 5.1e+02;
      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTTCG 44

RESULT 60
AY358002 450 bp DNA linear BCT 19-AUG-2005
LOCUS
DEFINITION
  Actinobacterium iri17 16S ribosomal RNA gene, partial sequence.
ACCESSION
  AY358002
VERSION
  AY358002.1 GI:34500643
KEYWORDS
  actinobacterium iri17
  actinobacterium iri17
  Bacteria; Actinobacteria.
  1 (bases 1 to 450)
  Idris, R., Trifonova, R., Puschenreiter, M., Wenzel, W.W. and
  Sessitsch, A.
  Bacterial Communities Associated with Flowering Plants of the Ni
  Hyperaccumulator Thlaspi goesingense
  Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
  15128517
  2 (bases 1 to 450)
  Idris, R. and Sessitsch, A.
  Direct Submission
  TITLE
  Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
  Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
  Location/Qualifiers
  FEATURES
    source
      1..450
        /organism="Mycobacterium sp."
        /mol_type="genomic DNA"
        /isolate="BN910"
        /db_xref="taxon:1785"
        /map="E.coli position 38-503"
        1..450
        /gene="16S rRNA"
        <1..>450
        /genes="16S rRNA"
        /product="16S ribosomal RNA"
    gene
    rRNA
    ORIGIN
      Query Match 93.6%; Score 23.4; DB 15; Length 450;
      Best Local Similarity 96.0%; Pred. No. 5.1e+02;
      Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 20 GCAAGTCGAACGGAAGGCCTTTCG 44

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source
1. .450
/organism="actinobacterium iRII17"
/mol_type="genomic DNA"
/strain="iRII17"
/db_xref="taxon:244182"
<1..>450
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 450;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGAAAGGCGCTTTCG 25
    |||||
Db 52 GCAAGTCGAACGAAAGGCGCTTTCG 76

RESULT 61
AJ746062
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
1 Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
and Lalucat,J.
Identification of culturable bacteria present in haemodialysis
water and fluid
FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
2 (bases 1 to 454)
Gomila,M.
Direct Submission
Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA, Microbiologia,
Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
Palma de Mallorca, SPAIN
Location/Qualifiers
1. .454
/organism="Mycobacterium sp. MG5"
/mol_type="genomic DNA"
/isolate="MG5"
/isolation_source="haemodialysis water distribution
system"
/db_xref="taxon:280864"
/country="Spain:Mallorca"
<1..>454
/gene="16S rRNA"
<1..>454
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 454;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGAAAGGCGCTTTCG 25
    |||||
Db 23 GCAAGTCGAACGAAAGGCGCTTTCG 47

RESULT 62
AY358001
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

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actinobacterium iRII16
actinobacterium iRII16
Bacteria; Actinobacteria.
1 (bases 1 to 456)
Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
Sessitsch,A.
Bacterial Communities Associated with Flowering Plants of the NI
Hyperaccumulator Thlaspi goesingense
Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
15128517
2 (bases 1 to 456)
Idris,R. and Sessitsch,A.
Direct Submission
TITLE
Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
Location/Qualifiers
1. .456
/organism="actinobacterium iRII16"
/mol_type="genomic DNA"
/strain="iRII16"
/db_xref="taxon:244181"
<1..>456
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.6%; Score 23.4; DB 15; Length 456;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGAAAGGCGCTTTCG 25
    |||||
Db 52 GCAAGTCGAACGAAAGGCGCTTTCG 76

RESULT 63
AJ609008
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bacteria; environmental samples.

REFERENCE
1 Schneider,B.A., Huettl,R.F. and Schneider,B.U.
Evidence for a diverse bacterial consortium specialized to the
degradation of aliphatic and aromatic hydrocarbons in lignite
matter of a forest reclamation site
Unpublished
2 (bases 1 to 459)
Schneider,B.A.
Direct Submission
Submitted (20-NOV-2003) Schneider B.A., Soil Protection and
Reclamation, Brandenburg Technical University,
Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
Location/Qualifiers
1. .459
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="lignite matter from the subsurface soil
of a 20 year old Black pine forest"
/db_xref="taxon:77133"
/clone="24-9"
/environmental_sample
/country="Germany:North-eastern Germany, Lusatian lignite
mining area"
1. .459
/gene="16S rRNA"
<1..>459
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN

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Query Match      93.6%; Score 23.4; DB 1; Length 459;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGGCCCTTTCG 25
    |||||
Db 8 GCAAGTCGAACGGTAAGGCCCTTTCG 32
    |||||

RESULT 64
AY754884
LOCUS      Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
DEFINITION
ACCESSION  AY754884
VERSION     AY754884.1 GI:54065968
KEYWORDS   .
SOURCE     Mycobacterium vaccae
ORGANISM   Mycobacterium vaccae
REFERENCE  1 (bases 1 to 459)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Unusual mycobacteria isolated from clinical samples
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 459)
AUTHORS    Tortoli,E.
TITLE      Direct Submission
JOURNAL    Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES   Location/Qualifiers
            source
                1..459
                /organism="Mycobacterium vaccae"
                /mol_type="genomic DNA"
                /strain="FI04098"
                /db_xref="taxon:1810"
                <1..>459
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 459;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGGCCCTTTCG 25
    |||||
Db 24 GCAAGTCGAACGGAAAGGCCCTTTCG 48
    |||||

RESULT 65
AY754885
LOCUS      Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION  AY754885
VERSION     AY754885.1 GI:54065976
KEYWORDS   .
SOURCE     Mycobacterium sp. FI02139
ORGANISM   Mycobacterium sp. FI02139
REFERENCE  1 (bases 1 to 459)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Unusual mycobacteria isolated from clinical samples
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 459)
AUTHORS    Tortoli,E.
TITLE      Direct Submission
JOURNAL    Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES   Location/Qualifiers
            source
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                /organism="Mycobacterium sp. FI02139"

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/mol_type="genomic DNA"
/strain="FI02139"
/db_xref="taxon:296718"
<1..>459
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 459;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGGCCCTTTCG 25
    |||||
Db 23 GCAAGTCGAACGGAAAGGCCCTTTCG 47
    |||||

RESULT 66
AB118817
LOCUS      Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
DEFINITION
ACCESSION  AB118817
VERSION     AB118817.1 GI:66841148
KEYWORDS   .
SOURCE     denitrifying bacterium W67a
ORGANISM   denitrifying bacterium W67a
REFERENCE  1
AUTHORS    Hashimoto,T., Whang,K.S. and Nagaoka,K.
TITLE      A Quantitative Evaluation and Phylogenetic Characterization of
            Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
            Soil Using Improved Culturability
JOURNAL    Biol. Fertil. Soils (2005) In press
REFERENCE  2 (bases 1 to 464)
AUTHORS    Hashimoto,T. and Whang,K.
TITLE      Direct Submission
JOURNAL    Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
            Research Center for Kyushu Okinawa Region, Department of
            Agro-Environmental Research; Nishigoushi-cho Suyu 2421,
            Kikuchi-gun, Kumamoto, 861-1192, Japan
            (E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
            Location/Qualifiers
            source
                1..464
                /organism="denitrifying bacterium W67a"
                /mol_type="genomic DNA"
                /isolate="W67a"
                /db_xref="taxon:245681"
                /country="Japan"
                <1..>464
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 464;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGGCCCTTTCG 25
    |||||
Db 46 GCAAGTCGAACGGAAAGGCCCTTTCG 70
    |||||

RESULT 67
DQ142669
LOCUS      Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION  DQ142669
VERSION     DQ142669.1 GI:71912648
KEYWORDS   .
SOURCE     Mycobacterium sp. FI03023
ORGANISM   Mycobacterium sp. FI03023
REFERENCE  1 (bases 1 to 464)

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AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Unusual mycobacteria isolated from clinical specimens  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Direct Submission  
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy  
FEATURES  
source  
1. .464  
/organism="Mycobacterium sp. FI03023"  
/mol\_type="genomic DNA"  
/strain="FI03023"  
/db\_xref="taxon:339672"  
<1. .>464  
/product="16S ribosomal RNA"  
ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 464;  
Best Local Similarity 96.0%; Pred. No. 5.1e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
DB 23 GCAAGTCGAACGGAAGGCGCTTTCG 47  
RESULT 68  
DQ142672  
LOCUS DQ142672 464 bp DNA linear BCT 13-AUG-2005  
DEFINITION Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.  
ACCESSION DQ142672  
VERSION DQ142672.1 GI:71912651  
KEYWORDS  
SOURCE Mycobacterium sp. FI05244  
ORGANISM Mycobacterium sp. FI05244  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Unusual mycobacteria isolated from clinical specimens  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Direct Submission  
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy  
FEATURES  
source  
1. .464  
/organism="Mycobacterium sp. FI05244"  
/mol\_type="genomic DNA"  
/strain="FI05244"  
/db\_xref="taxon:339674"  
<1. .>464  
/product="16S ribosomal RNA"  
ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 464;  
Best Local Similarity 96.0%; Pred. No. 5.1e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
DB 23 GCAAGTCGAACGGAAGGCGCTTTCG 47  
RESULT 69  
DQ067465  
LOCUS DQ067465 466 bp DNA linear BCT 05-JAN-2006  
DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.  
ACCESSION DQ067465  
VERSION DQ067465.1 GI:67528030  
KEYWORDS

SOURCE Mycobacterium sp. FI05038  
ORGANISM Mycobacterium sp. FI05038  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS Tortoli,E., Mantella,A., Mariottini,A., Mazzarelli,G., Pecile,P., Rogasi,P.G., Sterrantino,G., Fantoni,E. and Leoncini,F.  
TITLE Successfully treated spondylodiscitis due to a previously unreported mycobacterium  
JOURNAL J. Med. Microbiol. 55 (PT 1), 119-121 (2006)  
PUBMED 16388040  
REFERENCE 2 (bases 1 to 466)  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Direct Submission  
JOURNAL Submitted (18-MAY-2005) Reg. Reference Center for Mycobacteria, Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le Morgagni 85, Firenze, FI 50134, Italy  
FEATURES  
source  
1. .466  
/organism="Mycobacterium sp. FI05038"  
/mol\_type="genomic DNA"  
/strain="FI05038"  
/db\_xref="taxon:332012"  
<1. .>466  
/product="16S ribosomal RNA"  
ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 466;  
Best Local Similarity 96.0%; Pred. No. 5.1e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
DB 27 GCAAGTCGAACGGAAGGCGCTTTCG 51  
RESULT 70  
AY524839  
LOCUS AY524839 466 bp DNA linear BCT 03-FEB-2004  
DEFINITION Mycobacterium sp. FI02027 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY524839  
VERSION AY524839.1 GI:41387175  
KEYWORDS  
SOURCE Mycobacterium sp. FI02027  
ORGANISM Mycobacterium sp. FI02027  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Unusual mycobacteria isolated from clinical samples  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 466)  
AUTHORS Tortoli,E.  
TITLE Direct Submission  
JOURNAL Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale Morgagni 85, Firenze, FI 50134, Italy  
FEATURES  
source  
1. .466  
/organism="Mycobacterium sp. FI02027"  
/mol\_type="genomic DNA"  
/strain="FI02027"  
/db\_xref="taxon:262002"  
<1. .>466  
/product="16S ribosomal RNA"  
ORIGIN  
Query Match 93.6%; Score 23.4; DB 15; Length 466;  
Best Local Similarity 96.0%; Pred. No. 5.1e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
DB 27 GCAAGTCGAACGGAAGGCGCTTTCG 51

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RESULT 71
DQ154332
LOCUS      DQ154332          468 bp      DNA      linear      BCT 27-AUG-2005
DEFINITION Soil bacterium RFS-II28 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ154332
VERSION    DQ154332.1  GI:73672122
KEYWORDS   soil bacterium RFS-II28
SOURCE     soil bacterium RFS-II28
ORGANISM   soil bacterium RFS-II28
            Bacteria.
REFERENCE  1 (bases 1 to 468)
AUTHORS   Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
TITLE     Low nutrient fluxes result in high cultivation efficiencies of soil
          bacteria
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 468)
AUTHORS   Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
TITLE     Direct Submission
JOURNAL   Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
          West State Street, West Lafayette, IN 47907-2054, USA
FEATURES   Location/Qualifiers
            source
              1..468
              /organism="soil bacterium RFS-II28"
              /mol_type="genomic DNA"
              /isolate="RFS-II28"
              /isolation_source="Ross Forest soil"
              /db_xref="taxon:341515"
              <1..>468
              /product="16S ribosomal RNA"
            rRNA
            ORIGIN
Query Match      93.6%; Score 23.4; DB 15; Length 468;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCAAGTCGACGGAAGGCGCTTTCG 25
      |||||
Db  19  GCAAGTCGACGGAAGGCGCTTTCG 43
      |||||

RESULT 72
AY043719
LOCUS      AY043719          473 bp      DNA      linear      ENV 05-MAY-2004
DEFINITION Uncultured actinobacterium clone NOW2.35WL 16S ribosomal RNA gene,
          partial sequence.
ACCESSION  AY043719
VERSION    AY043719.1  GI:22267092
KEYWORDS   ENV.
SOURCE     uncultured actinobacterium
ORGANISM   uncultured actinobacterium
REFERENCE  1 (bases 1 to 473)
AUTHORS   Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
          Davies, J.
TITLE     Molecular characterization of bacterial diversity from British
          Columbia forest soils subjected to disturbance
JOURNAL   Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED    12224564
REFERENCE  2 (bases 1 to 473)
AUTHORS   Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
          Davies, J.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,
          Vancouver, BC V6S 2L2, Canada
FEATURES   Location/Qualifiers
            source
              1..473
              /organism="uncultured actinobacterium"
              /mol_type="genomic DNA"
              /db_xref="taxon:152507"
              /clone="NOW2.35WL"
              /environmental_sample

/Note="from forest cut-block surface organic matter from
the British Columbia Ministry of Forests Long-Term Soil
Productivity (LTSP) Installation near Williams Lake, BC,
Canada"
<1..>473
/product="16S ribosomal RNA"

Query Match      93.6%; Score 23.4; DB 1; Length 473;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCAAGTCGACGGAAGGCGCTTTCG 25
      |||||
Db  20  GCAAGTCGACGGAAGGCGCTTTCG 44
      |||||

RESULT 73
DQ136108
LOCUS      DQ136108          474 bp      DNA      linear      ENV 13-AUG-2005
DEFINITION Uncultured bacterium clone SC27 16S ribosomal RNA gene, partial
          sequence.
ACCESSION  DQ136108
VERSION    DQ136108.1  GI:71905197
KEYWORDS   ENV.
SOURCE     uncultured bacterium
ORGANISM   uncultured bacterium
REFERENCE  1 (bases 1 to 474)
AUTHORS   Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
TITLE     Microbiological remediation studies on diesel-contaminated soil of
          Baekun Mountain
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 474)
AUTHORS   Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
TITLE     Direct Submission
JOURNAL   Submitted (19-JUL-2005) School of Applied Biology and Chemistry,
          Seoul National University, San 56-1 Silmdong Kwanakgu 151-921,
          Korea
FEATURES   Location/Qualifiers
            source
              1..474
              /organism="uncultured bacterium"
              /mol_type="genomic DNA"
              /isolation_source="diesel-contaminated soil"
              /db_xref="taxon:77133"
              /clone="SC27"
              /environmental_sample
              <1..>474
              /product="16S ribosomal RNA"
            rRNA
            ORIGIN
Query Match      93.6%; Score 23.4; DB 1; Length 474;
Best Local Similarity 96.0%; Pred. No. 5.1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GCAAGTCGACGGAAGGCGCTTTCG 25
      |||||
Db  40  GCAAGTCGACGGAAGGCGCTTTCG 64
      |||||

RESULT 74
AY792024
LOCUS      AY792024          474 bp      DNA      linear      BCT 20-NOV-2004
DEFINITION Mycobacterium sp. 6BR15 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY792024
VERSION    AY792024.1  GI:55740323
KEYWORDS   .
SOURCE     Mycobacterium sp. 6BR15
ORGANISM   Mycobacterium sp. 6BR15
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 474)
AUTHORS   Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
```

TITLE	Biorremediation of radioactive water with metallic materials									
JOURNAL	Unpublished									
REFERENCE	2 (bases 1 to 474)									
AUTHORS	Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.									
TITLE	Direct Submission									
JOURNAL	Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain									
FEATURES	Location/Qualifiers									
source	1..474									
	/organism="Mycobacterium sp. 6BR15"									
	/mol_type="genomic DNA"									
	/isolate="6BR15"									
	/isolation_source="radioactive water"									
	/db_xref="taxon:300870"									
	<1..>474									
	/product="16S ribosomal RNA"									
rRNA										
ORIGIN										
Query Match	93.6%; Score 23.4; DB 15; Length 474;									
Best Local Similarity	96.0%; Pred. No. 5.1e+02;									
Matches	24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	1 GCAAGTCGAACGGGAAGCCCTTCG 25									
Db	29 GCAAGTCGAACGGGAAGCCCTTCG 53									
RESULT 75										
AY559492										
LOCUS	AY559492 476 bp DNA linear BCT 22-MAR-2004									
DEFINITION	Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial sequence.									
ACCESSION	AY559492									
VERSION	AY559492.1 GI:45511545									
KEYWORDS										
SOURCE	Mycobacterium porcinum									
ORGANISM	Mycobacterium porcinum									
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.									
AUTHORS	1 (bases 1 to 476)									
TITLE	Hontzas,N., Belimov,A., Safronova,V. and Glick,B.									
JOURNAL	Characterization of various plant growth-promoting bacteria									
REFERENCE	Unpublished									
AUTHORS	2 (bases 1 to 476)									
TITLE	Hontzas,N., Belimov,A., Safronova,V. and Glick,B.									
JOURNAL	Direct Submission									
	Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada									
FEATURES	Location/Qualifiers									
source	1..476									
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Matches	24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;									
Qy	1 GCAAGTCGAACGGGAAGCCCTTCG 25									
Db	30 GCAAGTCGAACGGGAAGCCCTTCG 54									
RESULT 76										
AY251205										
LOCUS	AY251205 478 bp DNA linear ENV 20-APR-2003									
DEFINITION	Uncultured actinobacterium clone 1B 5 16S ribosomal RNA gene,									

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Query Match      93.6%; Score 23.4; DB 15; Length 481;
Best Local Similarity 96.0%; Pred. No. 5, 1e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25
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Db 432 GCAAGTCGAACGGAAAGCCCTTCG 408

RESULT 78
AY943206
LOCUS      495 bp      DNA      linear      BCT 20-MAR-2005
DEFINITION Mycobacterium brisbanense strain CIP 107830 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY943206
VERSION     AY943206.1 GI:61200493
KEYWORDS   .
SOURCE     Mycobacterium brisbanense
ORGANISM   Mycobacterium brisbanense
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 495)
AUTHORS    Pichat,C. and Flandrois,J.P.
TITLE      Direct Submission
JOURNAL    Submitted (24-FEB-2005) Dynamique Des Populations Bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,
            Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
            Location/Qualifiers
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rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 495;
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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25
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RESULT 79
DQ154344
LOCUS      496 bp      DNA      linear      ENV 27-AUG-2005
DEFINITION Uncultured soil bacterium clone RFS-Cl4 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  DQ154344
VERSION     DQ154344.1 GI:73672134
KEYWORDS   ENV
SOURCE     uncultured soil bacterium
            uncultured soil bacterium
            Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 496)
AUTHORS    Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE      Low nutrient fluxes result in high cultivation efficiencies of soil
            bacteria
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 496)
AUTHORS    Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915
            West State Street, West Lafayette, IN 47907-2054, USA
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/db_xref="taxon:164851"
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rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 1; Length 496;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25
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Db 50 GCAAGTCGAACGGAAAGCCCTTCG 74

RESULT 80
AY215287
LOCUS      498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium mucogenicum isolate N241 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY215287
VERSION     AY215287.1 GI:28274541
KEYWORDS   .
SOURCE     Mycobacterium mucogenicum
ORGANISM   Mycobacterium mucogenicum
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of
            Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
            J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
            12682128
REFERENCE  2 (bases 1 to 498)
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
            Location/Qualifiers
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rRNA

ORIGIN

Query Match      93.6%; Score 23.4; DB 15; Length 498;
Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25
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Db 53 GCAAGTCGAACGGAAAGCCCTTCG 77

RESULT 81
AY215324
LOCUS      498 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N141 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY215324
VERSION     AY215324.1 GI:28274578
KEYWORDS   .
SOURCE     Mycobacterium sp. N141
ORGANISM   Mycobacterium sp. N141
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 498)
AUTHORS    Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE      Evaluation of the MicroSeq System for Identification of

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Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)

## JOURNAL

PUBMED

12682128

2 (bases 1 to 498)

## REFERENCE

Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.

## AUTHORS

Direct Submission

## JOURNAL

Submitted (08-JAN-2003) Department of Laboratory Medicine and Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

## FEATURES

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|||||

53 GCAAGTCGAACGGAAGGCGCTTCG 77

## RESULT 82

AY215336

## LOCUS

Mycobacterium sp. N1772T 16S ribosomal RNA gene, partial sequence.  
AY215336.1 GI:28274590

## DEFINITION

ACCESSION

VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Mycobacterium sp. N1772T

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Corynebacterineae; Mycobacteriaceae; Mycobacterium.

## REFERENCE

AUTHORS

TITLE

Evaluation of the MicroSeq System for Identification of Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)

## JOURNAL

PUBMED

12682128

2 (bases 1 to 498)

## REFERENCE

AUTHORS

TITLE

Submitted (08-JAN-2003) Department of Laboratory Medicine and Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

## FEATURES

Location/Qualifiers

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53 GCAAGTCGAACGGAAGGCGCTTCG 77

Uncultured soil bacterium clone RFS-C252 16S ribosomal RNA gene, partial sequence.  
DQ154566.1 GI:73672356

## ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Low nutrient fluxes result in high cultivation efficiencies of soil bacteria  
Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.  
1 (bases 1 to 499)

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Location/Qualifiers

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50 GCAAGTCGAACGGAAGGCGCTTCG 74

## RESULT 84

DQ154328

## LOCUS

Soil bacterium RFS-I117 16S ribosomal RNA gene, partial sequence.  
DQ154328.1 GI:73672118

## DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Low nutrient fluxes result in high cultivation efficiencies of soil bacteria  
Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.  
1 (bases 1 to 499)

JOURNAL

REFERENCE

AUTHORS

TITLE

Low nutrient fluxes result in high cultivation efficiencies of soil bacteria  
Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.  
2 (bases 1 to 499)

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

Location/Qualifiers

source

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/organism="soil bacterium RFS-I117"

/mol\_type="genomic DNA"

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## ORIGIN

Query Match

Best Local Similarity 93.6%; Score 23.4; DB 15; Length 499;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V., Mattes,T.E., Gossett,J.M. and Spain,J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl
chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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Qy 1 GCAAGTCGACGGAAGGCCCTTTCG 25
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Db 53 GCAAGTCGACGGAAGGCCCTTTCG 77

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AY162027
LOCUS Mycobacterium rhodesiae 500 bp DNA linear BCT 01-OCT-2003
DEFINITION Mycobacterium rhodesiae 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162027
VERSION AY162027.1 GI:24850312
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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Db 53 GCAAGTCGACGGAAGGCCCTTTCG 77

RESULT 91
AY215218
LOCUS Mycobacterium sp. N661 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N661 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215218
VERSION AY215218.1 GI:28274472
KEYWORDS
SOURCE Mycobacterium sp. N661
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
    avium complex (MAC).
REFERENCE 1 (bases 1 to 500)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.I. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.I.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V., Mattes,T.E., Gossett,J.M. and Spain,J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl
chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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Db 53 GCAAGTCGACGGAAGGCCCTTTCG 77

RESULT 90
AY162030
LOCUS Mycobacterium mageritense 500 bp DNA linear BCT 01-OCT-2003
DEFINITION Mycobacterium mageritense 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162030
VERSION AY162030.1 GI:24850315
KEYWORDS
SOURCE Mycobacterium mageritense
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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Qy 1 GCAAGTCGACGGAAGGCCCTTTCG 25
    |||||
Db 53 GCAAGTCGACGGAAGGCCCTTTCG 77

RESULT 91
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LOCUS Mycobacterium sp. N661 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N661 16S ribosomal RNA gene, partial sequence.
ACCESSION AY215218
VERSION AY215218.1 GI:28274472
KEYWORDS
SOURCE Mycobacterium sp. N661
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
    avium complex (MAC).
REFERENCE 1 (bases 1 to 500)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.I. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
JOURNAL J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.I.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 500;  
Best Local Similarity 96.0%; Pred. No. 5e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
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Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 92  
AV215228 500 bp DNA linear BCT 08-APR-2003  
LOCUS Mycobacterium sp. N110 16S ribosomal RNA gene, partial sequence.  
DEFINITION  
ACCESSION AV215228  
VERSION AV215228.1 GI:28274482  
KEYWORDS  
SOURCE Mycobacterium sp. N110  
ORGANISM Mycobacterium sp. N110  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128

REFERENCE 2 (bases 1 to 500)  
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.  
TITLE Direct Submission  
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
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rRNA

ORIGIN

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Best Local Similarity 96.0%; Pred. No. 5e+02;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
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Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 93  
AV215234 500 bp DNA linear BCT 08-APR-2003  
LOCUS Mycobacterium abscessus isolate N019 16S ribosomal RNA gene,  
partial sequence.  
DEFINITION  
ACCESSION AV215234  
VERSION AV215234.1 GI:28274488  
KEYWORDS  
SOURCE Mycobacterium abscessus  
ORGANISM Mycobacterium abscessus  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128

2 (bases 1 to 500)  
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.  
TITLE Direct Submission  
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
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rRNA

ORIGIN

Query Match 93.6%; Score 23.4; DB 15; Length 500;  
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Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
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Db 53 GCAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 94  
AV215235 500 bp DNA linear BCT 08-APR-2003  
LOCUS Mycobacterium abscessus isolate N416 16S ribosomal RNA gene,  
partial sequence.  
DEFINITION  
ACCESSION AV215235  
VERSION AV215235.1 GI:28274489  
KEYWORDS  
SOURCE Mycobacterium abscessus  
ORGANISM Mycobacterium abscessus  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 500)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128

REFERENCE 2 (bases 1 to 500)  
AUTHORS Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.  
TITLE Direct Submission  
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
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rRNA

ORIGIN

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LOCUS Mycobacterium sp. N570 16S ribosomal RNA gene, partial sequence.  
DEFINITION  
ACCESSION AV215237  
VERSION AV215237.1 GI:28274491



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Mycobacterium sp. N570  
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS  
TITLE  
Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL  
PUBMED  
12682128  
REFERENCE  
AUTHORS  
TITLE  
Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
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REFERENCE  
AUTHORS  
TITLE  
Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
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JOURNAL  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS  
TITLE  
Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL  
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REFERENCE  
AUTHORS  
TITLE  
Roberts, G.D., Hall, L., Doerr, K.A. and Wohlfiel, S.L.  
Direct Submission  
JOURNAL  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
AUTHORS  
TITLE  
Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
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Direct Submission  
JOURNAL  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

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Best Local Similarity 96.0%; Pred. No. 5e+02;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25
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Db 53 GCAAGTCGAACGGAAGGCCCTTCG 77

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VERSION    AY215252.1 GI:28274506
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REFERENCE  1 (bases 1 to 500)
AUTHORS   Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE     Evaluation of the MicroSeq System for Identification of
            Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
            J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL    12682128
PUBMED
REFERENCE  2 (bases 1 to 500)
AUTHORS   Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE     Direct Submission
            Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
JOURNAL
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VERSION    AY215266.1 GI:28274520
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ORGANISM      Mycobacterium immunogenum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE  1 (bases 1 to 500)
AUTHORS   Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE     Evaluation of the MicroSeq System for Identification of
            Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
            J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL    12682128
PUBMED
REFERENCE  2 (bases 1 to 500)
AUTHORS   Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE     Direct Submission
            Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
JOURNAL
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Searched: 6366136 seqs, 31973710525 residues

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Minimum DB seq length: 0  
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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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136	22.4	93.3	512	15	AF215272	Mycobacte	209	22.4	93.3	810	15	AJ746058	Mycobacte
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## ALIGNMENTS

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RESULT 1
AR438654 AR438654 linear PAT 20-FEB-2004
LOCUS Sequence 22 from patent US 6664081.
DEFINITION
ACCESSION
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VERSION AR438654.1 GI:42663578
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
ORIGIN
Query Match 100.0%; Score 24; DB 2; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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AX166856 24 bp DNA linear PAT 04-JUL-2001
LOCUS
DEFINITION Sequence 22 from Patent WO0144510.
ACCESSION AX166856
VERSION AX166856.1 GI:14596459
KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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source
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Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
Nucleic acid amplification and detection of mycobacterium species
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JOURNAL      Patent: US 6664081-A 21 16-DEC-2003;
FEATURES      Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
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Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25

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DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION  AX166855
VERSION     AX166855.1 GI:14596458
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL     Patent: WO 0144510-A 21 21-JUN-2001;
            Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES    source
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DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AF547926
VERSION     AF547926.1 GI:27733750
KEYWORDS   .
SOURCE      Mycobacterium gadium
            Mycobacterium gadium
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 541)
AUTHORS     Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE       A multigene approach to phylogenetic analysis using the genus
            Mycobacterium as a model
JOURNAL     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED     15653890
REFERENCE   2 (bases 1 to 541)
AUTHORS     Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE       Direct Submission
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

JOURNAL      Patent: US 6664081-A 21 16-DEC-2003;
FEATURES      Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
source        Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 2 CAAGTCGAACGGAAGGCGCTTTTCG 25

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DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION  AX166855
VERSION     AX166855.1 GI:14596458
KEYWORDS   .
SOURCE      synthetic construct
            other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
            Rodrigue,M.
TITLE       Nucleic acid amplification and detection of mycobacterium species
JOURNAL     Patent: WO 0144510-A 21 21-JUN-2001;
            Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES    source
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RESULT 5
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DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AF547926
VERSION     AF547926.1 GI:27733750
KEYWORDS   .
SOURCE      Mycobacterium gadium
            Mycobacterium gadium
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 541)
AUTHORS     Devulder,G., de Montclos,M.P. and Flandrois,J.P.
TITLE       A multigene approach to phylogenetic analysis using the genus
            Mycobacterium as a model
JOURNAL     Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)
PUBMED     15653890
REFERENCE   2 (bases 1 to 541)
AUTHORS     Devulder,G., Pichat,C. and Flandrois,J.P.
TITLE       Direct Submission
JOURNAL     Submitted (20-SEP-2002) Dynamique des populations bacteriennes,
            Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

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Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France
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Db 15 CAAGTCGAACGGAAGGCGCTTTTCG 38

RESULT 6
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LOCUS      MGAD16S                1456 bp      DNA      linear      BCT 06-JUN-2003
DEFINITION M.gadium 16S ribosomal RNA, part.
ACCESSION  X55594
VERSION     X55594.1 GI:44291
KEYWORDS   16S ribosomal RNA.
SOURCE      Mycobacterium gadium
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            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 1456)
AUTHORS     Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.
TITLE       Phylogeny of rapidly growing members of the genus Mycobacterium
JOURNAL     Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)
PUBMED     1380284
REFERENCE   2 (bases 1 to 1456)
AUTHORS     Wolters,J.
TITLE       Direct Submission
JOURNAL     Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine
            Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen
            Garten 1-9, 2300 Kiel 1

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rRNA
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RESULT 7
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LOCUS      MCO16S                1459 bp      DNA      linear      BCT 11-JUN-2003
DEFINITION Mycobacterium cookii partial 16S rRNA.
ACCESSION  X53896
VERSION     X53896.1 GI:44201
KEYWORDS   16S ribosomal RNA; ribosomal RNA.
SOURCE      Mycobacterium cookii
            Mycobacterium cookii
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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REFERENCE 1 (bases 1 to 1225)
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,
          Parlett,J.H. and Pitulle,C.
TITLE    Mycobacterium cookii sp. nov
JOURNAL  Int.J. Syst. Bacteriol. 40 (3), 217-223 (1990)
PUBMED   1697763
REFERENCE 2 (bases 1 to 1459)
AUTHORS Stackebrandt,E.
TITLE    Direct Submission
JOURNAL  Submitted (01-AUG-1990) Stackebrandt E
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Db 59 CAACTCGAACGGAAGGCGCTTTTCG 82

RESULT 8
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DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08169
VERSION   L08169.1 GI:293249
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium celatum
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE 1 (bases 1 to 1460)
AUTHORS  Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
          Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
          Vadney,F.S. and Gross,W.M.
TITLE    Mycobacterium celatum sp. nov
JOURNAL  Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
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Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 9 CAACTCGAACGGAAGGCGCTTTTCG 32

RESULT 9
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LOCUS    Mycobacterium celatum 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.

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L08170
ACCESSION L08170.1 GI:293250
VERSION   16S ribosomal RNA.
KEYWORDS  Mycobacterium celatum
SOURCE    Mycobacterium celatum
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE 1 (bases 1 to 1479)
AUTHORS  Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
          Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
          Vadney,F.S. and Gross,W.M.
TITLE    Mycobacterium celatum sp. nov
JOURNAL  Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED   8102246
COMMENT   Original source text: Mycobacterium celatum (library: ATCC 51130)
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Best Local Similarity 95.8%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 30 CAACTCGAACGGAAGGCGCTTTTCG 53

RESULT 10
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LOCUS    Mycobacterium kansasii 268 bp rRNA linear BCT 27-APR-1993
DEFINITION Mycobacterium kansasii 16S ribosomal RNA.
ACCESSION M95469
VERSION   M95469.1 GI:175317
KEYWORDS  16S ribosomal RNA.
SOURCE    Mycobacterium kansasii
ORGANISM  Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 268)
AUTHORS  Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.
TITLE    Identification of a genetically distinct sub-species of
          Mycobacterium kansasii
JOURNAL  Unpublished (1992)
COMMENT   Original source text: Mycobacterium kansasii rRNA.
          DNA.
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                /db_xref="taxon:1768"
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                /gene="16S rRNA"
            1..250
                /gene="16S rRNA"
                /product="16S ribosomal RNA"
    gene
    rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 268;
Best Local Similarity 95.8%; Pred. No. 4.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 39 CAACTCGAACGGAAGGCGCTTTTCG 62

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RESULT 11
MSP404591      MSP404591      293 bp      DNA      linear      ENV 06-JUN-2003
LOCUS          Uncultured Mycobacterium MB1 partial 16S rRNA gene.
DEFINITION
ACCESSION     AJ404591
VERSION       AJ404591.1 GI:8926769
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE        uncultured Mycobacterium MB1
ORGANISM      uncultured Mycobacterium MB1
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
               samples.
REFERENCE     1
AUTHORS      Kempell,K.E., Cox,C.J., Hurlie,M., Wong,A., Wilkie,S.,
               Zanders,E.D., Gaston,J. and Crowe,J.
TITLE        Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA
               for Detection and Characterisation of Bacterial Species in
               Arthritis Synovial Tissue
JOURNAL
AUTHORS
TITLE        Direct Submission
JOURNAL
AUTHORS      Cox,C.J.
TITLE        Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
               Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
               Cambridgeshire, CB10 1SA, UNITED KINGDOM
FEATURES     Location/Qualifiers
               source
               1..293
               /organism="uncultured Mycobacterium MB1"
               /mol_type="genomic DNA"
               /db_xref="taxon:129682"
               /clone="MB1"
               /tissue_type="Synovium"
               1..293
               /gene="16S rRNA"
               <1..293
               /gene="16S rRNA"
               /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 293;
Best Local Similarity 95.8%; Pred. No. 4e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTTCG 24
      |||||||||||||||||||||||||
Db      21 CAAGTCGAACGGAAGGCGCTTTCG 44

RESULT 12
MF16SRRN
LOCUS          MF16SRRN      316 bp      DNA      linear      BCT 14-NOV-1996
DEFINITION     M.fortuitum 16S rRNA gene, partial.
ACCESSION     Y09325
VERSION       Y09325.1 GI:1669698
KEYWORDS      16S ribosomal RNA; rsn gene.
SOURCE        Mycobacterium fortuitum
ORGANISM      Mycobacterium fortuitum
               Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
               Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE     1
AUTHORS      De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 316)
AUTHORS      De Smet,K.A.L.
TITLE        Direct Submission
JOURNAL      Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
               School at St Marys, Medical Microbiology, Norfolk Place, London, W2
               1PG, UK
               Location/Qualifiers
               source
               1..316
               /organism="Mycobacterium fortuitum"
               /mol_type="genomic DNA"

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/isolate="36718"
/db_xref="taxon:1766"
1..316
/gene="rrn"
<1..316
/gene="rrn"
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 316;
Best Local Similarity 95.8%; Pred. No. 3.9e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTTCG 24
      |||||||||||||||||||||||||
Db      46 CAAGTCGAACGGAAGGCGCTTTCG 69

RESULT 13
AY395145
LOCUS          AY395145      388 bp      DNA      linear      ENV 07-SEP-2004
DEFINITION     Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
               sequence.
ACCESSION     AY395145
VERSION       AY395145.1 GI:37595660
KEYWORDS      ENV.
SOURCE        uncultured bacterium
ORGANISM      Bacteria; environmental samples.
REFERENCE     1 (bases 1 to 388)
AUTHORS      Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE        Comparison of diversities and compositions of bacterial populations
               inhabiting natural forest soils
JOURNAL      Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED       15345382
REFERENCE     2 (bases 1 to 388)
AUTHORS      Hackl,E. and Sessitsch,A.
TITLE        Direct Submission
JOURNAL      Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
               Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES     Location/Qualifiers
               source
               1..388
               /organism="uncultured bacterium"
               /mol_type="genomic DNA"
               /isolation_source="forest soil"
               /db_xref="taxon:77133"
               /clone="D29ST"
               /environmental_sample
               <1..388
               /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 388;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAGTCGAACGGAAGGCGCTTTCG 24
      |||||||||||||||||||||||||
Db      51 CAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 14
BSSMKN23
LOCUS          BSSMKN23      393 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION     Bacterium sp. (SMKN23) DNA.
ACCESSION     X78659
VERSION       X78659.1 GI:509728
KEYWORDS      16S ribosomal RNA.
SOURCE        unidentified bacterium
ORGANISM      Bacteria; environmental samples.
REFERENCE     1
AUTHORS      Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.

```



**TITLE** Molecular characterization of nocardioform actinomycetes in activated sludge by 16S rRNA analysis  
**JOURNAL** Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)  
**PUBMED** 7704280  
**REFERENCE** 2 (bases 1 to 393)  
**AUTHORS** Schuppler,M.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med. Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St. 11, 79104 Freiburg, FRG

**FEATURES** Location/Qualifiers  
 source  
 1..393  
 /organism="unidentified bacterium"  
 /mol\_type="genomic DNA"  
 /isolate="SMKN23"  
 /db\_xref="taxon:2338"  
 1..393  
 /product="16S ribosomal RNA"

**ORIGIN**

**Query Match** 93.3%; Score 22.4; DB 1; Length 393;  
**Best Local Similarity** 95.8%; Pred. No. 3.7e+02;  
**Matches** 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 |||||  
**Db** 8 CAAGTCGAACGGAAGGCGCTTTCG 31

**RESULT 15**

**AY395154** 394 bp DNA linear ENV 07-SEP-2004  
**LOCUS** Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene, partial sequence.  
**DEFINITION**  
**ACCESSION** AY395154  
**VERSION** AY395154.1 GI:37595669  
**KEYWORDS** ENV.  
**SOURCE** uncultured actinobacterium  
**ORGANISM** uncultured actinobacterium  
**REFERENCE** 1 (bases 1 to 394)  
**AUTHORS** Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
**TITLE** Bacteria; Actinobacteria; environmental samples.  
**TITLE** Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
**AUTHORS** Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils  
**TITLE** Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

**JOURNAL** Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

**PUBMED** 15345382

**REFERENCE** 2 (bases 1 to 394)

**AUTHORS** Hackl,E. and Sessitsch,A.

**TITLE** Direct Submission

**JOURNAL** Submitted (19-SEP-2003) Environmental and Life Sciences, ARC Seibersdorf research GmbH, Seibersdorf A-2444, Austria

**FEATURES** Location/Qualifiers

source  
 1..394  
 /organism="uncultured actinobacterium"  
 /mol\_type="genomic DNA"  
 /isolation\_source="forest soil"  
 /db\_xref="taxon:152507"  
 /clone="E02ST"  
 /environmental\_sample  
 <1..>394  
 /product="16S ribosomal RNA"

**ORIGIN**

**Query Match** 93.3%; Score 22.4; DB 1; Length 394;  
**Best Local Similarity** 95.8%; Pred. No. 3.7e+02;  
**Matches** 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 |||||  
**Db** 51 CAAGTCGAACGGAAGGCGCTTTCG 74

**RESULT 16**

**AY043901**

**LOCUS**

**DEFINITION** Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene, partial sequence.  
**ACCESSION** AY043901  
**VERSION** AY043901.1 GI:22267274  
**KEYWORDS** ENV.  
**SOURCE** uncultured actinobacterium  
**ORGANISM** uncultured actinobacterium  
**REFERENCE** 1 (bases 1 to 395)  
**AUTHORS** Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.  
**TITLE** Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance  
**JOURNAL** Can. J. Microbiol. 48 (7), 655-674 (2002)  
**PUBMED** 12224564  
**REFERENCE** 2 (bases 1 to 395)  
**AUTHORS** Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall, Vancouver, BC V6S 2L2, Canada  
**FEATURES** Location/Qualifiers  
 source  
 1..395  
 /organism="uncultured actinobacterium"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:152507"  
 /clone="SMS9.49WL"  
 /environmental\_sample  
 /note="from forest cut-block mineral soil from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) installation near Williams Lake, BC, Canada"  
 <1..>395  
 /product="16S ribosomal RNA"

**ORIGIN**

**Query Match** 93.3%; Score 22.4; DB 1; Length 395;  
**Best Local Similarity** 95.8%; Pred. No. 3.7e+02;  
**Matches** 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 |||||  
**Db** 21 CAAGTCGAACGGAAGGCGCTTTCG 44

**RESULT 17**

**AY395151**

**LOCUS**

**DEFINITION** Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial sequence.  
**ACCESSION** AY395151  
**VERSION** AY395151.1 GI:37595666  
**KEYWORDS** ENV.  
**SOURCE** uncultured bacterium  
**ORGANISM** uncultured bacterium  
**REFERENCE** 1 (bases 1 to 395)  
**AUTHORS** Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
**TITLE** Bacteria; environmental samples.  
**TITLE** Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
**AUTHORS** Comparison of diversities and compositions of bacterial populations inhabiting natural forest soils  
**TITLE** Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

**JOURNAL** Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)

**PUBMED** 15345382

**REFERENCE** 2 (bases 1 to 395)

**AUTHORS** Hackl,E. and Sessitsch,A.

**TITLE** Direct Submission

**JOURNAL** Submitted (19-SEP-2003) Environmental and Life Sciences, ARC Seibersdorf research GmbH, Seibersdorf A-2444, Austria

**FEATURES** Location/Qualifiers

source  
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 /organism="uncultured bacterium"  
 /mol\_type="genomic DNA"  
 /isolation\_source="forest soil"  
 /db\_xref="taxon:152507"  
 /clone="D36ST"  
 /environmental\_sample  
 <1..>395  
 /product="16S ribosomal RNA"

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/db xref="taxon:77133"
/clone="D36ST"
/environmental_sample
<1..395
/product="16S ribosomal RNA"

rRNA
ORIGIN
    Query Match      93.3%; Score 22.4; DB 1; Length 395;
    Best Local Similarity 95.8%; Pred. No. 3.7e+02;
    Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 51 CAACTCGAACGGAAGGCGCTTTCG 74

RESULT 18
BSSMKN14
LOCUS      BSSMKN14      396 bp      DNA      linear      ENV 22-FEB-1995
DEFINITION Bacterium sp.(SMKN14) DNA.
ACCESSION  X78655
VERSION     X78655.1 GI:509724
KEYWORDS   16S ribosomal RNA.
SOURCE      unidentified bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE       Molecular characterization of nocardioform actinomycetes in
            activated sludge by 16S rRNA analysis
JOURNAL     Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED     7704280
REFERENCE   2 (bases 1 to 396)
AUTHORS     Schuppler,M.
TITLE       Direct Submission
JOURNAL     Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
            Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
            11, 79104 Freiburg, FRG
FEATURES   Location/Qualifiers
            source      1..396
                        /organism="unidentified bacterium"
                        /mol_type="genomic DNA"
                        /isolate="SMKN14"
                        /db_xref="taxon:2338"
rRNA       1..395
            /product="16S ribosomal RNA"

ORIGIN
    Query Match      93.3%; Score 22.4; DB 1; Length 396;
    Best Local Similarity 95.8%; Pred. No. 3.7e+02;
    Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 8 CAACTCGAACGGAAGGCGCTTTCG 31

RESULT 19
DQ221681
LOCUS      DQ221681      400 bp      DNA      linear      ENV 12-NOV-2005
DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  DQ221681
VERSION     DQ221681.1 GI:80978382
KEYWORDS   uncultured bacterium
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1 (bases 1 to 400)
AUTHORS     Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
TITLE       Bacterial diversity on leaf surfaces of the Brazilian Atlantic
            forest
JOURNAL     Unpublished

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REFERENCE   2 (bases 1 to 400)
AUTHORS     Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.
TITLE       Direct Submission
JOURNAL     Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade
            de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil
            Location/Qualifiers
            source      1..400
                        /organism="uncultured bacterium"
                        /mol_type="genomic DNA"
                        /isolation_source="phyllosphere"
                        /specific_host="Campomanesia xanthocarpa"
                        /db_xref="taxon:77133"
                        /clone="BPH3088"
                        /environmental_sample
                        <1..>400
                        /product="16S ribosomal RNA"

rRNA       <1..>400
            /product="16S ribosomal RNA"

ORIGIN
    Query Match      93.3%; Score 22.4; DB 1; Length 400;
    Best Local Similarity 95.8%; Pred. No. 3.7e+02;
    Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 16 CAACTCGAACGGAAGGCGCTTTCG 39

RESULT 20
DQ063065
LOCUS      DQ063065      401 bp      DNA      linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063065
VERSION     DQ063065.1 GI:68139094
KEYWORDS   actinobacterium BAL125
SOURCE      actinobacterium BAL125
ORGANISM    Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 401)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 401)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
            Location/Qualifiers
            source      1..401
                        /organism="actinobacterium BAL125"
                        /mol_type="genomic DNA"
                        /strain="BAL125"
                        /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                        BV31, Zobel/R2A media"
                        /db_xref="taxon:331783"
                        /country="Sweden"
                        /lat_lon="60.42.726N, 05.05.595E"
                        /collection_date="2 July 2003"
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                        /product="16S ribosomal RNA"

rRNA       <1..>401
            /product="16S ribosomal RNA"

ORIGIN
    Query Match      93.3%; Score 22.4; DB 15; Length 401;
    Best Local Similarity 95.8%; Pred. No. 3.7e+02;
    Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 1 CAACTCGAACGGAAGGCGCTTTCG 24

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RESULT 21
AY234665
LOCUS      Bacterium Ellin6013 403 bp DNA linear BCT 08-DEC-2003
DEFINITION Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234665
VERSION     AY234665.1 GI:37961822
KEYWORDS
SOURCE      bacterium Ellin6013
ORGANISM    Bacterium Ellin6013
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1 (bases 1 to 403)
AUTHORS     Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE       Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL     Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED     14860368
REFERENCE   2 (bases 1 to 403)
AUTHORS     Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES   Location/Qualifiers
            source      1..403
                        /organism="Bacterium Ellin6013"
                        /mol_type="genomic DNA"
                        /isolate="Ellin6013"
                        /db_xref="taxon:234120"
                        <1..>403
                        /product="16S ribosomal RNA"
            rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 403;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAAGTCGAACGGAAGGCGCTTTTCG 24
        |||||
Db      31 CAAAGTCGAACGGAAGGCGCTTCG 54

RESULT 22
AY792017/c
LOCUS      Mycobacterium sp. 5BR6 407 bp DNA linear BCT 20-NOV-2004
DEFINITION Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY792017
VERSION     AY792017.1 GI:55740316
KEYWORDS
SOURCE      Mycobacterium sp. 5BR6
ORGANISM    Mycobacterium sp. 5BR6
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 407)
AUTHORS     Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE       Bioremediation of radioactive water with metallic materials
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 407)
AUTHORS     Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE       Direct Submission
JOURNAL     Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
            Escuela Tecnica Superior de Ingenieros Industriales, Universidad
            Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
            28006, Spain
FEATURES   Location/Qualifiers
            source      1..407
                        /organism="Mycobacterium sp. 5BR6"
                        /mol_type="genomic DNA"
                        /isolate="5BR6"
                        /isolation_source="radioactive water"
                        /db_xref="taxon:300866"
                        <1..>407
            rRNA

RESULT 23
BSSMKN12
LOCUS      Bacterium sp.(SMKN12) DNA.
DEFINITION Bacterium sp.(SMKN12) DNA.
ACCESSION  X78654
VERSION     X78654.1 GI:509723
KEYWORDS    16S ribosomal RNA.
SOURCE      unidentified bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE       Molecular characterization of nocardioform actinomycetes in
            activated sludge by 16S rRNA analysis
JOURNAL     Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED     7704280
REFERENCE   2 (bases 1 to 410)
AUTHORS     Schuppler,M.
TITLE       Direct Submission
JOURNAL     Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
            Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
            11, 79104 Freiburg, FRG
FEATURES   Location/Qualifiers
            source      1..410
                        /organism="unidentified bacterium"
                        /mol_type="genomic DNA"
                        /isolate="SMKN12"
                        /db_xref="taxon:2338"
                        1..410
                        /product="16S ribosomal RNA"
            rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 410;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAAGTCGAACGGAAGGCGCTTTTCG 24
        |||||
Db      3  CAAAGTCGAACGGAAGGCGCTTCG 26

RESULT 24
DQ063154
LOCUS      actinobacterium BAL218 411 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL218
ACCESSION  DQ063154
VERSION     DQ063154.1 GI:68139192
KEYWORDS
SOURCE      actinobacterium BAL218
ORGANISM    actinobacterium BAL218
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 411)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 411)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Direct Submission
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ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 407;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAAGTCGAACGGAAGGCGCTTTTCG 24
        |||||
Db      365 CAAAGTCGAACGGAAGGCGCTTCG 342

RESULT 23
BSSMKN12
LOCUS      Bacterium sp.(SMKN12) DNA.
DEFINITION Bacterium sp.(SMKN12) DNA.
ACCESSION  X78654
VERSION     X78654.1 GI:509723
KEYWORDS    16S ribosomal RNA.
SOURCE      unidentified bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE       Molecular characterization of nocardioform actinomycetes in
            activated sludge by 16S rRNA analysis
JOURNAL     Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED     7704280
REFERENCE   2 (bases 1 to 410)
AUTHORS     Schuppler,M.
TITLE       Direct Submission
JOURNAL     Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
            Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
            11, 79104 Freiburg, FRG
FEATURES   Location/Qualifiers
            source      1..410
                        /organism="unidentified bacterium"
                        /mol_type="genomic DNA"
                        /isolate="SMKN12"
                        /db_xref="taxon:2338"
                        1..410
                        /product="16S ribosomal RNA"
            rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 410;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CAAAGTCGAACGGAAGGCGCTTTTCG 24
        |||||
Db      3  CAAAGTCGAACGGAAGGCGCTTCG 26

RESULT 24
DQ063154
LOCUS      actinobacterium BAL218 411 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL218
ACCESSION  DQ063154
VERSION     DQ063154.1 GI:68139192
KEYWORDS
SOURCE      actinobacterium BAL218
ORGANISM    actinobacterium BAL218
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 411)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 411)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE       Direct Submission
```

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JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..411
/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:3311796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGACGGAAGGCGCTTTCG 24
|||||
Db 11 CAAGTCGACGGAAGGCGCTTTCG 34
|||||

RESULT 25
DQ063199 411 bp DNA linear BCT 27-JUN-2005
LOCUS
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
Bacteria; Actinobacteri-
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..411
/organism="actinobacterium BAL263"
/mol_type="genomic DNA"
/strain="BAL263"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:3311810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGACGGAAGGCGCTTTCG 24
|||||
Db 12 CAAGTCGACGGAAGGCGCTTTCG 35
|||||

RESULT 26
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AY792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS
DEFINITION Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
SOURCE Mycobacterium sp. 4BR14
ORGANISM Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biotremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES
source
1..411
/organism="Mycobacterium sp. 4BR14"
/mol_type="genomic DNA"
/strain="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 411;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGACGGAAGGCGCTTTCG 24
|||||
Db 52 CAAGTCGACGGAAGGCGCTTTCG 75
|||||

RESULT 27
AM085773 414 bp DNA linear ENV 21-SEP-2005
LOCUS
DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone T6.
ACCESSION AM085773
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Rynjaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uytendaele,M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
source
1..414
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="T6"
/environmental_sample
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gene /country="Belgium"
<1..>414
rRNA /gene="16S rRNA"
<1..>414
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match 93.3%; Score 22.4; DB 1; Length 414;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 28
DQ063108 415 bp DNA linear BCT 27-JUN-2005
LOCUS Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
DEFINITION DQ063108
ACCESSION DQ063108
VERSION DQ063108.1 GI:68139141
KEYWORDS actinobacterium BAL168
SOURCE actinobacterium BAL168
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 415)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
Location/Qualifiers
1..415
/organism="actinobacterium BAL168"
/mol_type="genomic DNA"
/strain="BAL168"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel1/R2A media"
/db_xref="taxon:331762"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="8 October 2003"
<1..>415
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 415;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 29
AM085786 416 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION AM085786
ACCESSION AM085786
VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.

1
REFERENCE
AUTHORS Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B., Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and Springael,D.
TITLE Distribution of the Mycobacterium sp. community and polycyclic aromatic hydrocarbons (PAHs) among different size fractions of a weathered PAH-contaminated soil
Unpublished
2 (bases 1 to 416)
Uyttebroek,M.
Direct Submission
TITLE Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water Management, Catholic University of Leuven, Kasteelpark Arenberg 20, B-3001 Leuven, BELGIUM
JOURNAL Location/Qualifiers
1..416
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="K11"
/environmental_sample
/country="Denmark"
<1..>416
/gene="16S rRNA"
<1..>416
/product="16S ribosomal RNA"

ORIGIN
Query Match 93.3%; Score 22.4; DB 1; Length 416;
Best Local Similarity 95.8%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAATCGAACGGAAGGCGCTTTCG 24
|||||
Db 4 CAAATCGAACGGAAGGCGCTTTCG 27

RESULT 30
AM085788 418 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION AM085788
ACCESSION AM085788
VERSION AM085788.1 GI:75754611
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.

1
REFERENCE
AUTHORS Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B., Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and Springael,D.
TITLE Distribution of the Mycobacterium sp. community and polycyclic aromatic hydrocarbons (PAHs) among different size fractions of a weathered PAH-contaminated soil
Unpublished
2 (bases 1 to 418)
Uyttebroek,M.
Direct Submission
TITLE Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water Management, Catholic University of Leuven, Kasteelpark Arenberg 20, B-3001 Leuven, BELGIUM
JOURNAL Location/Qualifiers
1..418
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
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/clone="K13"
/environmental_sample
/country="Denmark"
<1..>418
/gene="16S rRNA"
<1..>418
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.3%; Score 22.4; DB 1; Length 418;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 4 CAAGTCGAACGGAAGGCCCTTTCG 27

RESULT 31
AY673261          418 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION      Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
ACCESSION      AY673261
VERSION        AY673261.1 GI:56683118
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7095
ORGANISM      Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source      Location/Qualifiers
1..418
/mol_type="genomic DNA"
/isolate="Ellin7095"
/isolation_source="soil"
/db_xref="taxon:305281"
<1..>418
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          93.3%; Score 22.4; DB 15; Length 418;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCCCTTTCG 54

RESULT 32
AM085770
LOCUS      AM085770          421 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION      Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION      AM085770
VERSION        AM085770.1 GI:75754591
KEYWORDS      ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
ORGANISM      Bacteria; environmental samples.

REFERENCE
AUTHORS      Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE      Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
Unpublished
JOURNAL
REFERENCE
AUTHORS      Uytendaele,M.
TITLE      Direct Submission
JOURNAL
Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
source      Location/Qualifiers
1..421
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:77133"
/clone="T3"
/environmental sample
/country="Belgium"
<1..>421
/gene="16S rRNA"
<1..>421
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          93.3%; Score 22.4; DB 1; Length 421;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 10 CAAGTCGAACGGAAGGCCCTTTCG 33

RESULT 33
AJ786807
LOCUS      AJ786807          422 bp      DNA      linear      BCT 29-OCT-2004
DEFINITION      Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION      AJ786807
VERSION        AJ786807.1 GI:54887545
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. R-22838
ORGANISM      Mycobacterium sp. R-22838
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS      Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
Verstraete,W. and De Vos,P.
TITLE      The microbial community composition of a commercial nitrifying
inoculum
JOURNAL      Unpublished
REFERENCE
AUTHORS      Vanparrys,B.
TITLE      Direct Submission
JOURNAL      Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES
source      Location/Qualifiers
1..422
/organism="Mycobacterium sp. R-22838"
/mol_type="genomic DNA"
/isolate="R-22838"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:28999"
/country="Belgium"
1..422
/gene="16S rRNA"
<1..>422
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN

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Davis, K.E.R., Joseph, S.J. and Janssen, P.H.  
 Direct Submission  
 Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
 University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
 Australia

**FEATURES**  
 source 1..423 Location/Qualifiers  
 /organism="Mycobacteriaceae bacterium Ellin7039"  
 /mol\_type="genomic DNA"  
 /isolate="Ellin7039"  
 /isolation\_source="soil"  
 /db\_xref="taxon:305258"  
 <1..>423  
 /product="16S ribosomal RNA"

**rRNA**

**ORIGIN**  
 Query Match 93.3%; Score 22.4; DB 15; Length 423;  
 Best Local Similarity 95.8%; Pred. No. 3.6e+02;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAAGCCCTTCG 24  
 |||||  
 Db 31 CAAAGTCGAACGGAAAGCCCTTCG 54

**RESULT 36**  
 AY673206 423 bp DNA linear BCT 20-MAY-2005  
**LOCUS** Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,  
**DEFINITION** partial sequence.  
**ACCESSION** AY673206  
**VERSION** AY673206.1 GI:56683063  
**KEYWORDS** Mycobacteriaceae bacterium Ellin7040  
**SOURCE** Mycobacteriaceae bacterium Ellin7040  
**ORGANISM** Mycobacteriaceae bacterium Ellin7040  
**REFERENCE** Davis, K.E.R., Joseph, S.J. and Janssen, P.H.  
**AUTHORS** Effects of growth medium, inoculum size, and incubation time on  
**TITLE** culturability and isolation of soil bacteria  
**JOURNAL** Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
**PUBMED** 15691937  
**REFERENCE** 2 (bases 1 to 423)  
**AUTHORS** Davis, K.E.R., Joseph, S.J. and Janssen, P.H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
 University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
 Australia

**FEATURES**  
 source 1..423 Location/Qualifiers  
 /organism="Mycobacteriaceae bacterium Ellin7040"  
 /mol\_type="genomic DNA"  
 /isolate="Ellin7040"  
 /isolation\_source="soil"  
 /db\_xref="taxon:305259"  
 <1..>423  
 /product="16S ribosomal RNA"

**rRNA**

**ORIGIN**  
 Query Match 93.3%; Score 22.4; DB 15; Length 423;  
 Best Local Similarity 95.8%; Pred. No. 3.6e+02;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAAGCCCTTCG 24  
 |||||  
 Db 31 CAAAGTCGAACGGAAAGCCCTTCG 54

**RESULT 37**  
 AY673207 423 bp DNA linear BCT 20-MAY-2005  
**LOCUS** Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,  
**DEFINITION**

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partial sequence.
ACCESSION      AY673207
VERSION        AY673207.1  GI:56683064
KEYWORDS
SOURCE
ORGANISM       Mycobacteriaceae bacterium Ellin7041
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae.
REFERENCE
AUTHORS        Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE          Effects of growth medium, inoculum size, and incubation time on
                culturability and isolation of soil bacteria
JOURNAL        Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED         15691937
REFERENCE
AUTHORS        Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE          Direct Submission
JOURNAL        Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                Australia
FEATURES       Location/Qualifiers
                1..423
                /organism="Mycobacteriaceae bacterium Ellin7041"
                /mol_type="genomic DNA"
                /isolate="Ellin7041"
                /isolation_source="soil"
                /db_xref="Taxon:305260"
                <1..>423
                /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 423;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGCCCTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGCCCTTTCG 54

RESULT 38
DQ063156
LOCUS          actinobacterium BAL220 424 bp DNA linear BCT 27-JUN-2005
DEFINITION    actinobacterium BAL220
ACCESSION     DQ063156
VERSION       DQ063156.1  GI:68139194
KEYWORDS
SOURCE        actinobacterium BAL220
ORGANISM      Bacteria; Actinobacteria.
REFERENCE
AUTHORS       Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                Hagstrom,A.
TITLE         Bacterial community composition in the central Baltic Sea analyzed
                by cultivation and molecular-based methods
JOURNAL       Unpublished
REFERENCE
AUTHORS       Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                Hagstrom,A.
TITLE         Direct Submission
JOURNAL       Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
                University of Kalmar, Barlastgatan 11, Kalmar 39031, Sweden
FEATURES       Location/Qualifiers
                1..424
                /organism="actinobacterium BAL220"
                /mol_type="genomic DNA"
                /strain="BAL220"
                /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                BY31, Zobel1/R2A media"
                /db_xref="taxon:331797"
                /country="Sweden"
                /lat_lon="60.42.726N, 05.05.595E"
                /collection_date="17 May 2004"

partial sequence.
ACCESSION      AY673287
VERSION        AY673287.1  GI:56683144
KEYWORDS
SOURCE
ORGANISM       Streptosporangiaceae bacterium Ellin7121
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Streptosporangiaceae.
REFERENCE
AUTHORS        Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE          Effects of growth medium, inoculum size, and incubation time on
                culturability and isolation of soil bacteria
JOURNAL        Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED         15691937
REFERENCE
AUTHORS        Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE          Direct Submission
JOURNAL        Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                Australia
FEATURES       Location/Qualifiers
                1..424
                /organism="Streptosporangiaceae bacterium Ellin7121"
                /mol_type="genomic DNA"
                /isolate="Ellin7121"
                /isolation_source="soil"
                /db_xref="taxon:305348"
                <1..>424
                /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 424;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGCCCTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGCCCTTTCG 54

RESULT 40
AY756031
LOCUS          Unidentified bacterium TMB805 424 bp DNA linear BCT 08-APR-2005
DEFINITION    Unidentified bacterium TMB805
ACCESSION     AY756031
VERSION       AY756031.1  GI:54299184
KEYWORDS
SOURCE        Unidentified bacterium TMB805
ORGANISM      Bacteria.
REFERENCE
AUTHORS       Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
                Christen,R., Chevenet,F. and Heulin,T.
TITLE         Diversity of Bacteria and Archaea in the arid desert of Tataouine
                Unpublished

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REFERENCE
AUTHORS      2 (bases 1 to 424)
Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
Christen,R., Chevenet,F. and Heulin,T.
TITLE        Direct Submission
JOURNAL      Submitted (21-SEP-2004) LEMIR-DEVW-DSV, CEA, Cadarache, Saint Paul
Lez Duranc 13108, France
FEATURES
source      Location/Qualifiers
1..424
/organism="Unidentified bacterium TMB805"
/mol_type="genomic DNA"
/strain="TMB805"
/isolation_source="arid soil"
/db_xref="taxon:297191"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 424;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 41
LOCUS      AV394635 425 bp DNA linear ENV 20-OCT-2003
DEFINITION Uncultured Mycobacterium sp. Clone W1-11 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AV394635
VERSION     AV394635.1 GI:37677560
KEYWORDS   ENV.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE  1 (bases 1 to 425)
Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
Intracellular symbionts and other bacteria associated with deer
ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
Massachusetts
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 425)
Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
Direct Submission
TITLE      Submitted (19-SEP-2003) Molecular & Cell Biology, University of
Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
USA
FEATURES
source      Location/Qualifiers
1..425
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/specific_host="Ixodes scapularis"
/db_xref="taxon:171292"
/clone="W1-11"
/environmental_sample
/country="USA; Massachusetts, Cape Cod, Nantucket,
Wellfleet"
<1..>425
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 425;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

REFERENCE
AUTHORS      2 (bases 1 to 424)
Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
Christen,R., Chevenet,F. and Heulin,T.
TITLE        Direct Submission
JOURNAL      Submitted (21-SEP-2004) LEMIR-DEVW-DSV, CEA, Cadarache, Saint Paul
Lez Duranc 13108, France
FEATURES
source      Location/Qualifiers
1..424
/organism="Unidentified bacterium TMB805"
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/isolation_source="arid soil"
/db_xref="taxon:297191"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 424;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24

RESULT 42
LOCUS      AV673136 426 bp DNA linear BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AV673136
VERSION     AV673136
KEYWORDS   Mycobacteriaceae bacterium Ellin5409
SOURCE     Mycobacteriaceae bacterium Ellin5409
ORGANISM   Mycobacteriaceae bacterium Ellin5409
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 426)
Osborne,C.A. and Janssen,P.H.
Direct Submission
TITLE      Submitted (30-JUN-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
JOURNAL
FEATURES
source      Location/Qualifiers
1..426
/organism="Mycobacteriaceae bacterium Ellin5409"
/mol_type="genomic DNA"
/isolate="Ellin5409"
/isolation_source="soil"
/db_xref="taxon:305244"
<1..>426
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 426;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

REFERENCE
AUTHORS      1
Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
Direct Submission
TITLE      Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8868)
JOURNAL
FEATURES
source      Location/Qualifiers
1..428
/organism="Gram-positive bacterium 1-6"
/mol_type="genomic DNA"
/strain="1-6"
/db_xref="taxon:226200"
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/product="16S ribosomal RNA"

rRNA

ORIGIN

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REFERENCE
AUTHORS      1
Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
Direct Submission
TITLE      Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8868)
JOURNAL
FEATURES
source      Location/Qualifiers
1..428
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/mol_type="genomic DNA"
/strain="1-6"
/db_xref="taxon:226200"
<1..>428
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 426;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

REFERENCE
AUTHORS      1
Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
Direct Submission
TITLE      Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8868)
JOURNAL
FEATURES
source      Location/Qualifiers
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/organism="Gram-positive bacterium 1-6"
/mol_type="genomic DNA"
/strain="1-6"
/db_xref="taxon:226200"
<1..>428
/product="16S ribosomal RNA"

rRNA

ORIGIN

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Query Match      93.3%; Score 22.4; DB 15; Length 428;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTTCG 54

RESULT 44
DQ063058
LOCUS actinobacterium BAL118 428 bp DNA linear BCT 27-JUN-2005
DEFINITION actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063058
VERSION DQ063058.1 GI:68139087
KEYWORDS .
SOURCE actinobacterium BAL118
ORGANISM actinobacterium BAL118
REFERENCE 1 (bases 1 to 428)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hegstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 428)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hegstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source 1..428
/organism="actinobacterium BAL118"
/mol_type="genomic DNA"
/strain="BAL118"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel/R2A media"
/db_xref="taxon:331781"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="2 July 2003"
<1..>428
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 428;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 9 CAACTCGAACGGAAGGCGCTTTTCG 32

RESULT 45
AJ786822
LOCUS Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
DEFINITION Mycobacterium sp. R-23262 partial 16S rRNA gene.
ACCESSION AJ786822
VERSION AJ786822.1 GI:54887560
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Mycobacterium sp. R-23262
ORGANISM Mycobacterium sp. R-23262
REFERENCE 1
AUTHORS Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L., Verstraete,W. and De Vos,P.
TITLE The microbial community composition of a commercial nitrifying inoculum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 430)

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AUTHORS Vanparrys,B.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology, University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES
source 1..430
/organism="Mycobacterium sp. R-23262"
/mol_type="genomic DNA"
/isolate="R-23262"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:289008"
/country="Belgium"
1..430
/gene="16S rRNA"
<1..>430
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 430;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTTCG 54

RESULT 46
AY673202
LOCUS Mycobacteriaceae bacterium Ellin7036 430 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673202
VERSION AY673202.1 GI:56683059
KEYWORDS .
ORGANISM Mycobacteriaceae bacterium Ellin7036
Mycobacteriaceae bacterium Ellin7036
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 430)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 430)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES
source 1..430
/organism="Mycobacteriaceae bacterium Ellin7036"
/mol_type="genomic DNA"
/isolate="Ellin7036"
/isolation_source="soil"
/db_xref="taxon:305257"
<1..>430
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 430;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 31 CAACTCGAACGGAAGGCGCTTTTCG 54

RESULT 47

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AB106919      431 bp      DNA      linear      BCT 09-SEP-2003
LOCUS      Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
DEFINITION      sequence.
ACCESSION      AB106919
VERSION      AB106919.1 GI:29421133
KEYWORDS
SOURCE      Gram-positive bacterium 2-1
ORGANISM      Gram-positive bacterium 2-1
REFERENCE      1
AUTHORS      Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
              Fujii,T. and Muramatsu,Y.
TITLE      Microbial participation in iodine volatilization from soils
JOURNAL      Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE      2 (bases 1 to 431)
AUTHORS      Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
              Fujii,T. and Muramatsu,Y.
TITLE      Direct Submission
JOURNAL      Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
              Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
              (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
              Fax:81-47-308-8866)
FEATURES
source      Location/Qualifiers
              1..431
              /organism="Gram-positive bacterium 2-1"
              /mol_type="genomic DNA"
              /strain="2-1"
              /db_xref="taxon:226201"
              <1..>431
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 431;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTTCG 24
      |||
Db      31 CAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 48
AF078232
LOCUS      Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF078232
VERSION      AF078232.1 GI:4590103
KEYWORDS      ENV.
SOURCE      grassland soil clone saf2_117
ORGANISM      grassland soil clone saf2_117
REFERENCE      1 (bases 1 to 432)
AUTHORS      McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE      Molecular analysis of bacterial community structure and diversity
              in unimproved and improved upland grass pastures
JOURNAL      Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED      10103273
REFERENCE      2 (bases 1 to 432)
AUTHORS      McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE      Direct Submission
JOURNAL      Submitted (16-JUL-1998) Institute of Medical Sciences, Department
              of Molecular and Cell Biology, University of Aberdeen,
              Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES
source      Location/Qualifiers
              1..432
              /organism="grassland soil clone saf2_117"
              /mol_type="genomic DNA"
              /db_xref="taxon:80202"
              /clone_lib="unimproved grassland soil SAF2"
              /environmental_sample
              <1..>432

rRNA

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ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 432;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTTCG 24
      |||
Db      9 CAAGTCGAACGGAAGGCGCTTTTCG 32

RESULT 49
AY673198
LOCUS      Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673198
VERSION      AY673198.1 GI:56683055
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7032
ORGANISM      Mycobacteriaceae bacterium Ellin7032
REFERENCE      1 (bases 1 to 433)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
              culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE      2 (bases 1 to 433)
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
              University of Melbourne, Grattan Street, Parkville, Victoria 3010,
              Australia
FEATURES
source      Location/Qualifiers
              1..433
              /organism="Mycobacteriaceae bacterium Ellin7032"
              /mol_type="genomic DNA"
              /isolate="Ellin7032"
              /isolation_source="soil"
              /db_xref="taxon:305255"
              <1..>433
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 433;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTTCG 24
      |||
Db      31 CAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 50
AY673266
LOCUS      Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
DEFINITION      partial sequence.
ACCESSION      AY673266
VERSION      AY673266.1 GI:56683123
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7100
ORGANISM      Mycobacteriaceae bacterium Ellin7100
REFERENCE      1 (bases 1 to 433)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
              culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

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PUBMED 15691937
REFERENCE 2 (bases 1 to 433)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
    source      Location/Qualifiers
                1..433
                /organism="Mycobacteriaceae bacterium Ellin7100"
                /mol_type="genomic DNA"
                /isolate="Ellin7100"
                /isolation_source="soil"
                /db_xref="taxon:305283"
                <1..>433
                /product="16S ribosomal RNA"
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 433;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54
    |||||

RESULT 51
DQ0631195
LOCUS actinobacterium BAL259 435 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ0631195
VERSION DQ0631195.1 GI:68139233
SOURCE actinobacterium BAL259
ORGANISM actinobacterium BAL259
REFERENCE 1 (bases 1 to 435)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 435)
AUTHORS Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source      Location/Qualifiers
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                /organism="actinobacterium BAL259"
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                /strain="BAL259"
                /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                BY31, Zobell/R2A media"
                /db_xref="taxon:331808"
                /country="Sweden"
                /lat_lon="60.42.726N, 05.05.595E"
                /collection_dates="17 May 2004"
                <1..>435
                /product="16S ribosomal RNA"
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Query Match      93.3%; Score 22.4; DB 15; Length 435;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 16 CAAGTCGAACGGAAGGCGCTTTCG 39
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RESULT 52
AY234692
LOCUS Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
DEFINITION Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
ACCESSION AY234692
VERSION AY234692.1 GI:37961849
KEYWORDS
SOURCE Bacterium Ellin6040
ORGANISM Bacterium Ellin6040
REFERENCE 1 (bases 1 to 435)
AUTHORS Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
Janssen,P.H.
TITLE Laboratory Cultivation of Widespread and Previously Uncultured Soil
Bacteria
JOURNAL Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED 14660368
REFERENCE 2 (bases 1 to 435)
AUTHORS Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2003) Department of Microbiology and Immunology,
University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES
    source      Location/Qualifiers
                1..435
                /organism="bacterium Ellin6040"
                /mol_type="genomic DNA"
                /isolate="Ellin6040"
                /db_xref="taxon:234122"
                <1..>435
                /product="16S ribosomal RNA"
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 435;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54
    |||||

RESULT 53
AY673233
LOCUS Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AY673233
VERSION AY673233.1 GI:56683090
KEYWORDS
SOURCE Mycobacteriaceae bacterium Ellin7067
ORGANISM Mycobacteriaceae bacterium Ellin7067
REFERENCE 1 (bases 1 to 435)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 435)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
    source      Location/Qualifiers
                1..435
                /organism="Mycobacteriaceae bacterium Ellin7067"
                /mol_type="genomic DNA"
                /isolate="Ellin7067"
                /isolation_source="soil"

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/db_xref="taxon:305274"
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/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 435;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 54
DQ063046
LOCUS      436 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063046
VERSION DQ063046.1 GI:68139075
KEYWORDS
SOURCE      actinobacterium BAL106
ORGANISM    actinobacterium BAL106
REFERENCE   1 (bases 1 to 436)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE       Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL
REFERENCE   2 (bases 1 to 436)
AUTHORS     Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE       Direct Submission
JOURNAL     Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..436
/organism="actinobacterium BAL106"
/mol_type="genomic DNA"
/strain="BAL106"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobell/R2A media"
/db_xref="taxon:331778"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>436
/product="16S ribosomal RNA"

rRNA

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Query Match      93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 20 CAAAGTCGAACGGAAGGCGCTTTCG 43

RESULT 55
AY673199
LOCUS      436 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673199
VERSION AY673199.1 GI:56683056
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7033
ORGANISM    Mycobacteriaceae bacterium Ellin7033
REFERENCE   1 (bases 1 to 436)
Corynebacterineae; Mycobacteriaceae.

/db_xref="taxon:305274"
<1..>435
/product="16S ribosomal RNA"

AUTHORS     Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE   2 (bases 1 to 436)
AUTHORS     Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
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source
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/organism="Mycobacteriaceae bacterium Ellin7033"
/mol_type="genomic DNA"
/isolate="Ellin7033"
/isolation_source="soil"
/db_xref="taxon:305256"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 56
AY673304
LOCUS      436 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673304
VERSION AY673304.1 GI:56683161
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7138
ORGANISM    Mycobacteriaceae bacterium Ellin7138
REFERENCE   1 (bases 1 to 436)
AUTHORS     Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE   2 (bases 1 to 436)
AUTHORS     Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
FEATURES
source
1..436
/organism="Mycobacteriaceae bacterium Ellin7138"
/mol_type="genomic DNA"
/isolate="Ellin7138"
/isolation_source="soil"
/db_xref="taxon:305288"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 436;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
|||||
Db 31 CAAAGTCGAACGGAAGGCGCTTTCG 54

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RESULT 57
AF078419
LOCUS      437 bp      DNA      linear      ENV 10-MAY-2004
DEFINITION  Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078419
VERSION    AF078419.1 GI:4590290
KEYWORDS   ENV.
SOURCE     Grassland soil clone sl3_612
ORGANISM   Grassland soil clone sl3_612
           Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 437)
           McCaig,A.E., Glover,L.A. and Prosser,J.I.
           Molecular analysis of bacterial community structure and diversity
           in unimproved and improved upland grass pastures
           Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
JOURNAL    10103273
PUBMED
REFERENCE  2 (bases 1 to 437)
           McCaig,A.E., Prosser,J.I. and Glover,L.A.
           Direct Submission
           Submitted (16-JUL-1998) Institute of Medical Sciences, Department
           of Molecular and Cell Biology, University of Aberdeen,
           Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
           Location/Qualifiers
FEATURES   1..437
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           /mol_type="genomic DNA"
           /db_xref="taxon:80115"
           /clone_lib="improved grassland soil SL3"
           /environmental_sample
           <1..>437
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 437;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
    |||||
Db 9 CAAGTCGAGCGGAAGGCGCTTTCG 32
    |||||

RESULT 58
AB232370
LOCUS      441 bp      DNA      linear      BCT 25-JAN-2006
DEFINITION  Mycobacterium kansasii gene for 16S rRNA, partial sequence,
strain:SA-10.
ACCESSION  AB232370
VERSION    AB232370.1 GI:73589607
KEYWORDS   Mycobacterium kansasii
SOURCE     Mycobacterium kansasii
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1
           Iwamoto,T. and Saito,H.
           Comparative study of two typing methods, hsp65 PRA and ITS
           sequencing, revealed a possible evolutionary link between
           Mycobacterium kansasii type I and II isolates
           FEMS Microbiol. Lett. 254, 129-133 (2006)
JOURNAL    2 (bases 1 to 441)
PUBMED
REFERENCE  Iwamoto,T.
           Direct Submission
           Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
           Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
           Hyogo 6500046, Japan [E-mail:kw2t-iwmt@asahi-net.or.jp,
           URL:http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
           top, Tel:81-78-302-6251, Fax:81-78-302-0894]
           Location/Qualifiers
FEATURES   1..441
           source
           /organism="Mycobacterium kansasii"
           /mol_type="genomic DNA"
           /strain="SA-10"
           /isolation_source="mouth ulcer"
           /specific_host="Homo sapiens"
           /db_xref="taxon:235254"
           <1..>442
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 442;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
    |||||
Db 5 CAAGTCGACGGAAGGCGCTTTCG 28
    |||||

RESULT 60
AY306205
LOCUS      444 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION  Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION    AY306205.1 GI:32250954
KEYWORDS   Mycobacterium sp. HSC507
SOURCE     Mycobacterium sp. HSC507
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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/organism="Mycobacterium kansasii"
/mol_type="genomic DNA"
/strain="SA-10"
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/notes="type II"
<1..>441
/product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 441;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
    |||||
Db 5 CAAGTCGACGGAAGGCGCTTTCG 28
    |||||

RESULT 59
AY306201
LOCUS      442 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION  Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306201
VERSION    AY306201.1 GI:32250950
KEYWORDS   Mycobacterium sp. 1351
SOURCE     Mycobacterium sp. 1351
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1 (bases 1 to 442)
           Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
           A High Proportion of Novel Mycobacteria Species Identified by 16S
           rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
           Clinical Setting
           Unpublished
           2 (bases 1 to 442)
           Turenne,C.Y.
           Direct Submission
           Submitted (26-MAY-2003) National Reference Centre for
           Mycobacteriology, National Microbiology Laboratory, Health Canada,
           1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
           Location/Qualifiers
FEATURES   1..442
           source
           /organism="Mycobacterium sp. 1351"
           /mol_type="genomic DNA"
           /strain="1351"
           /isolation_source="mouth ulcer"
           /specific_host="Homo sapiens"
           /db_xref="taxon:235254"
           <1..>442
           /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 442;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCGCTTTCG 24
    |||||
Db 5 CAAGTCGACGGAAGGCGCTTTCG 28
    |||||

RESULT 60
AY306205
LOCUS      444 bp      DNA      linear      BCT 25-JUN-2003
DEFINITION  Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION    AY306205.1 GI:32250954
KEYWORDS   Mycobacterium sp. HSC507
SOURCE     Mycobacterium sp. HSC507
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Corynebacterineae; Mycobacteriaceae; Mycobacterium.

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REFERENCE 1 (bases 1 to 444)
AUTHORS Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE A High Proportion of Novel Mycobacteria Species Identified by 16S
rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
Clinical Setting
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 444)
AUTHORS Turenne,C.Y.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-2003) National Reference Centre for
Mycobacteriology, National Microbiology Laboratory, Health Canada,
1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
LOCATION/Qualifiers
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1. .444
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/mol_type="genomic DNA"
/strains="HSC507"
/isolation_sources="sputum"
/specific_host="Homo sapiens"
/db_xref="taxon:235258"
<1. .>444
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 444;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
|||||
Db 5 CAAGTCGAACGGAAGGCGCTTCG 28
|||||
RESULT 61
LOCUS AB106917 445 bp DNA linear BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial
sequence.
ACCESSION AB106917
VERSION AB106917.1 GI:29421131
KEYWORDS
SOURCE Gram-positive bacterium 1-3
ORGANISM Gram-positive bacterium 1-3
Bacteria.
REFERENCE 1
AUTHORS Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE Microbial participation in iodine volatilization from soils
JOURNAL Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE 2 (bases 1 to 445)
AUTHORS Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE Direct Submission
JOURNAL Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
LOCATION/Qualifiers
FEATURES
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1. .445
/organism="Gram-positive bacterium 1-3"
/mol_type="genomic DNA"
/strains="1-3"
/db_xref="taxon:226199"
<1. .>445
/product="16S ribosomal RNA"
rRNA
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Query Match 93.3%; Score 22.4; DB 15; Length 445;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
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Db 31 CAAGTCGAACGGAAGGCGCTTCG 54
RESULT 62
LOCUS DQ067466 445 bp DNA linear BCT 18-JUL-2005
DEFINITION Mycobacterium sp. FI05167 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ067466
VERSION DQ067466.1 GI:67528039
KEYWORDS
SOURCE Mycobacterium sp. FI05167
ORGANISM Mycobacterium sp. FI05167
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 445)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 445)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy
LOCATION/Qualifiers
FEATURES
source
1. .445
/organism="Mycobacterium sp. FI05167"
/mol_type="genomic DNA"
/strains="FI05167"
/db_xref="taxon:332013"
<1. .>445
/product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 445;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
|||||
Db 9 CAAGTCGAACGGAAGGCGCTTCG 32
|||||
RESULT 63
LOCUS MS91016SR 450 bp DNA linear BCT 01-AUG-1997
DEFINITION Mycobacterium sp.16S rRNA gene, isolate BN910, partial.
ACCESSION Y08205
VERSION Y08205.1 GI:2292948
KEYWORDS 16S ribosomal RNA; 16S rRNA.
SOURCE Mycobacterium sp.
ORGANISM Mycobacterium sp.
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
AUTHORS Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
Schulze-Roebecke,R.
TITLE Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 450)
AUTHORS Hagenau,C.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT Related sequence M95469.
LOCATION/Qualifiers
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source
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/organism="Mycobacterium sp."
/mol_type="genomic DNA"
/isolate="BN910"
/db_xref="taxon:1785"
/map="E.coli position 38-503"
<1. .>450
/gene="16S rRNA"
gene

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rRNA      <1..>450
           /gene="16S rRNA"
           /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 450;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 21 CAAGTCGAACGGAAGGCCCTTTCG 44

RESULT 64
MSP16SR      MSP16SR      450 bp      DNA      linear      BCT 01-AUG-1997
LOCUS      Mycobacterium sp. 16S rRNA gene.
DEFINITION
ACCESSION      Y07954
VERSION      Y07954.1 GI:2292951
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp.
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1 Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
              Schulze-Roebecke,R.
              Unpublished
REFERENCE      2 (bases 1 to 450)
AUTHORS      Hagenau,C.
TITLE      Direct Submission
JOURNAL      Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
              of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT      Related sequence: M95469.
FEATURES
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               /mol_type="genomic DNA"
               /isolate="BN737"
               /db_xref="taxon:1785"
               /map="E.coli 38-503"
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               /gene="16S rRNA"
             rRNA
               <1..>450
               /gene="16S rRNA"
               /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 450;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 21 CAAGTCGAACGGAAGGCCCTTTCG 44

RESULT 65
AY358002      AY358002      450 bp      DNA      linear      BCT 19-AUG-2005
LOCUS      Actinobacterium irIII7 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION      AY358002
VERSION      AY358002.1 GI:34500643
KEYWORDS      actinobacterium irIII7
SOURCE      actinobacterium irIII7
ORGANISM      Bacteria; Actinobacteria.
REFERENCE      1 (bases 1 to 450)
AUTHORS      Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
              Sessitsch,A.
              Bacterial Communities Associated with Flowering Plants of the Ni
              Hyperaccumulator Thlaspi goesingense


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JOURNAL      Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED      15128517
REFERENCE      2 (bases 1 to 450)
AUTHORS      Idris,R. and Sessitsch,A.
TITLE      Direct Submission
JOURNAL      Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
              Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES
             Location/Qualifiers
             source
               1..450
               /organism="actinobacterium irIII7"
               /mol_type="genomic DNA"
               /strain="irIII7"
               /db_xref="taxon:244182"
               <1..>450
               /product="16S ribosomal RNA"

             rRNA
               <1..>450
               /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 450;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 53 CAAGTCGAACGGAAGGCCCTTTCG 76

RESULT 66
AJ746062      AJ746062      454 bp      DNA      linear      BCT 11-MAR-2005
LOCUS      Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MGS.
DEFINITION
ACCESSION      AJ746062
VERSION      AJ746062.1 GI:161097518
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. MG5
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1 Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
              and Lalucat,J.
              Identification of culturable bacteria present in haemodialysis
              water and fluid
JOURNAL      FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
REFERENCE      2 (bases 1 to 454)
AUTHORS      Gomila,M.
TITLE      Direct Submission
JOURNAL      Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia,
              Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
              Palma de Mallorca, SPAIN
FEATURES
             Location/Qualifiers
             source
               1..454
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               /mol_type="genomic DNA"
               /isolate="MGS"
               /isolation_source="haemodialysis water distribution
               system"
               /db_xref="taxon:280864"
               /country="Spain:Mallorca"
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               /gene="16S rRNA"
             rRNA
               <1..>454
               /gene="16S rRNA"
               /product="16S ribosomal RNA"

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 454;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
    |||||
Db 24 CAAGTCGAACGGAAGGCCCTTTCG 47


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RESULT 67
AY358001
LOCUS      Actinobacterium irIII6 456 bp DNA linear BCT 19-AUG-2005
DEFINITION Actinobacterium irIII6 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358001
VERSION     AY358001.1 GI:34500642
KEYWORDS   actinobacterium irIII6
SOURCE     actinobacterium irIII6
ORGANISM   actinobacterium irIII6
REFERENCE   1 (bases 1 to 456)
AUTHORS    Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE      Bacterial Communities Associated with Flowering Plants of the Ni
JOURNAL    Hyperaccumulator Thlaspi goesingense
PUBMED     15128517
REFERENCE   2 (bases 1 to 456)
AUTHORS    Idris,R. and Sessitsch,A.
TITLE      Direct Submission
JOURNAL    Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES   .
            Location/Qualifiers
            source
            1..456
            /organism="actinobacterium irIII6"
            /mol_type="genomic DNA"
            /strain="irIII6"
            /db_xref="taxon:244181"
            <1..>456
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 456;
Best Local Similarity 95.8%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 53 CAACTCGAACGGAAGGCGCTTCG 76

RESULT 68
AJ609008
LOCUS      Uncultured bacterium partial 16S rRNA gene, clone 24-9.
DEFINITION Uncultured bacterium partial 16S rRNA gene, clone 24-9.
ACCESSION  AJ609008
VERSION     AJ609008.1 GI:41033549
KEYWORDS   ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE   1
AUTHORS    Schneider,B.A., Huettl,R.F. and Schneider,B.U.
TITLE      Evidence for a diverse bacterial consortium specialized to the
            degradation of aliphatic and aromatic hydrocarbons in lignite
            matter of a forest reclamation site
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 459)
AUTHORS    Schneider,B.A.
TITLE      Direct Submission
JOURNAL    Submitted (20-NOV-2003) Schneider B.A., Soil Protection and
            Reclamation, Brandenburg Technical University,
            Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
FEATURES   .
            Location/Qualifiers
            source
            1..459
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="lignite matter from the subsurface soil
            of a 20 year old Black pine forest"
            /db_xref="taxon:77133"
            /clone="24-9"
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ACTINOBACTERIUM irIII6 456 bp DNA linear BCT 19-AUG-2005
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ORIGIN
Query Match      93.3%; Score 22.4; DB 1; Length 459;
Best Local Similarity 95.8%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 9 CAACTCGAACGGAAGGCGCTTCG 32

RESULT 69
AY754884
LOCUS      Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION  AY754884
VERSION     AY754884.1 GI:54065968
KEYWORDS   Mycobacterium vaccae
SOURCE     Mycobacterium vaccae
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 459)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Unusual mycobacteria isolated from clinical samples
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 459)
AUTHORS    Tortoli,E.
TITLE      Direct Submission
JOURNAL    Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
            Morgagni 85, Firenze, FI 50134, Italy
FEATURES   .
            Location/Qualifiers
            source
            1..459
            /organism="Mycobacterium vaccae"
            /mol_type="genomic DNA"
            /strain="FI04098"
            /db_xref="taxon:1810"
            <1..>459
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 459;
Best Local Similarity 95.8%; Pred. No. 3.6e+02; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 1;

Qy 1 CAACTCGAACGGAAGGCGCTTTTCG 24
    |||||
Db 25 CAACTCGAACGGAAGGCGCTTCG 48

RESULT 70
AY754885
LOCUS      Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacterium sp. FI02139
ACCESSION  AY754885
VERSION     AY754885.1 GI:54065976
KEYWORDS   Mycobacterium sp. FI02139
SOURCE     Mycobacterium sp. FI02139
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 459)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Unusual mycobacteria isolated from clinical samples
JOURNAL    Unpublished

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REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli E.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
    source      1..459
                /organism="Mycobacterium sp. FI02139"
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                /product="16S ribosomal RNA"
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 459;
Best Local Similarity 95.8%; Pred. No. 3.6e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
    |||||
Db 24 CAAGTCGAACGGAAGGCGCTTCG 47

RESULT 71
AB118817 464 bp DNA linear BCT 01-JUN-2005
LOCUS Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
DEFINITION sequence.
ACCESSION AB118817
VERSION AB118817.1 GI:66841148
KEYWORDS denitrifying bacterium W67a
SOURCE denitrifying bacterium W67a
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 Hashimoto, T., Whang, K.S. and Nagaoka, K.
AUTHORS A Quantitative Evaluation and Phylogenetic Characterization of
TITLE Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
JOURNAL Soil Using Improved Culturability
REFERENCE 2 Biol. Fertil. Soils (2005) In press
AUTHORS Hashimoto, T. and Whang, K.
TITLE Direct Submission
JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
Research Center for Kyushu Okinawa Region, Department of
Agro-Environmental Research; Nishigoushi-cho Suya 2421,
Kikuchi-gun, Kumamoto, 861-1192, Japan
(E-mail: hashimoto@affrc.go.jp, Tel: 0962427765, Fax: 0962491002)
FEATURES
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                /organism="denitrifying bacterium W67a"
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                /country="Japan"
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ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 464;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
    |||||
Db 47 CAAGTCGAACGGAAGGCGCTTCG 70

RESULT 72
DQ142669 464 bp DNA linear BCT 13-AUG-2005
LOCUS Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
DEFINITION

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ACCESSION DQ142669
VERSION DQ142669.1 GI:71912648
KEYWORDS
SOURCE Mycobacterium sp. FI03023
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli E., Mariottini, A. and Mazzarelli, G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli E., Mariottini, A. and Mazzarelli, G.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
    source      1..464
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ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 464;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
    |||||
Db 24 CAAGTCGAACGGAAGGCGCTTCG 47

RESULT 73
DQ142672 464 bp DNA linear BCT 13-AUG-2005
LOCUS Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ142672
VERSION DQ142672.1 GI:71912651
KEYWORDS
SOURCE Mycobacterium sp. FI05244
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 464)
AUTHORS Tortoli E., Mariottini, A. and Mazzarelli, G.
TITLE Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 464)
AUTHORS Tortoli E., Mariottini, A. and Mazzarelli, G.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale Morgagni 85, Firenze, FI 50134, Italy
FEATURES
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                <1..>464
                /product="16S ribosomal RNA"
ORIGIN
Query Match      93.3%; Score 22.4; DB 15; Length 464;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCGCTTCG 24
    |||||
Db 24 CAAGTCGAACGGAAGGCGCTTCG 47

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RESULT 74
DQ067465
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Tortoli, E., Mantella, A., Mariottini, A., Mazzarelli, G., Pecile, P.,
Rogasi, P. G., Sterratino, G., Pantoni, E. and Leoncini, F.
TITLE
Successfully treated spondylodiscitis due to a previously
unreported mycobacterium
JOURNAL
PUBMED
16388040
J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
REFERENCE
2 (bases 1 to 466)
Tortoli, E., Mariottini, A. and Mazzarelli, G.
Direct Submission
TITLE
Submitted (18-MAY-2005) Reg. Reference Center for Mycobacteria,
Careggi Hospital, Piasra dei Servizi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy
JOURNAL
Location/Qualifiers
FEATURES
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/db_xref="taxon:332012"
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/product="16S ribosomal RNA"
ORIGIN
Query Match
Best Local Similarity 93.3%; Score 22.4; DB 15; Length 466;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 28 CAAGTCGAACGGAAGGCCTTTCG 51
RESULT 75
AY524839
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS
Tortoli, E., Mariottini, A. and Mazzarelli, G.
TITLE
Unusual mycobacteria isolated from clinical samples
JOURNAL
REFERENCE
2 (bases 1 to 466)
Tortoli, E.
Direct Submission
TITLE
Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
JOURNAL
Location/Qualifiers
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ORIGIN
rRNA

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Query Match
Best Local Similarity 93.3%; Score 22.4; DB 15; Length 466;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 28 CAAGTCGAACGGAAGGCCTTTCG 51
RESULT 76
DQ154332
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium RFS-I128
Bacteria.
REFERENCE
1 (bases 1 to 468)
Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
AUTHORS
Low nutrient fluxes result in high cultivation efficiencies of soil
bacteria
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 468)
Becker, J.M., Nakatsu, C.H., Turco, R.F. and Konopka, A.
AUTHORS
Direct Submission
TITLE
Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
West State Street, West Lafayette, IN 47907-2054, USA
JOURNAL
Location/Qualifiers
FEATURES
source
1..468
/organism="soil bacterium RFS-I128"
/mol_type="genomic DNA"
/isolate="RFS-I128"
/isolation_source="Ross Forest soil"
/db_xref="taxon:341515"
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/product="16S ribosomal RNA"
ORIGIN
Query Match
Best Local Similarity 93.3%; Score 22.4; DB 15; Length 468;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 20 CAAGTCGAACGGAAGGCCTTTCG 43
RESULT 77
AY043719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Uncultured actinobacterium clone NOW2.35WL
Bacteria; Actinobacteria; environmental samples.
REFERENCE
1 (bases 1 to 473)
Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
Davies, J.
TITLE
Molecular characterization of bacterial diversity from British
Columbia forest soils subjected to disturbance
JOURNAL
PUBMED
12224564
Can. J. Microbiol. 48 (7), 655-674 (2002)
REFERENCE
2 (bases 1 to 473)
Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
Davies, J.
AUTHORS
Direct Submission
TITLE
Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,

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FEATURES  
source  
Vancouver, BC V6S 2L2, Canada  
Location/Qualifiers  
1. .473  
/organism="uncultured actinobacterium"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:152507"  
/clone="NOW2.35WL"  
/environmental\_sample  
/note="from forest cut-block surface organic matter from the British Columbia Ministry of Forests Long-term Soil Productivity (LTSP) Installation near Williams Lake, BC, Canada"  
<1. .>473  
/product="16S ribosomal RNA"  
rRNA  
ORIGIN  
Query Match 93.3%; Score 22.4; DB 1; Length 473;  
Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
|||||  
Db 21 CAAGTCGAACGGAAGGCGCTTTCG 44  
|||||  
RESULT 78  
DQ136108 474 bp DNA linear ENV 13-AUG-2005  
LOCUS  
DEFINITION Uncultured bacterium clone SC27 16S ribosomal RNA gene, partial sequence.  
DQ136108  
ACCESSION DQ136108.1 GI:71905197  
VERSION  
KEYWORDS ENV,  
SOURCE uncultured bacterium  
ORGANISM uncultured bacterium  
REFERENCE  
1 (bases 1 to 474)  
Ka, J.-O., Kim, M.-S. and Ahn, J.-H.  
AUTHORS Microbiological remediation studies on diesel-contaminated soil of Baekun Mountain  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 474)  
Ka, J.-O., Kim, M.-S. and Ahn, J.-H.  
AUTHORS Direct Submission  
TITLE Submitted (19-JUL-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Silmdong Kwanakgu 151-921, Korea  
JOURNAL  
FEATURES  
source  
Location/Qualifiers  
1. .474  
/organism="uncultured bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="diesel-contaminated soil"  
/db\_xref="taxon:77133"  
/clone="SC27"  
/environmental\_sample  
<1. .>474  
/product="16S ribosomal RNA"  
rRNA  
ORIGIN  
Query Match 93.3%; Score 22.4; DB 1; Length 474;  
Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
|||||  
Db 41 CAAGTCGAACGGAAGGCGCTTTCG 64  
|||||  
RESULT 79  
DQ136108 474 bp DNA linear BCT 20-NOV-2004  
LOCUS  
DEFINITION Mycobacterium sp. 6BR15 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY792024

VERSION AY792024.1 GI:55740323  
KEYWORDS  
SOURCE Mycobacterium sp. 6BR15  
ORGANISM Mycobacterium sp. 6BR15  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
1 (bases 1 to 474)  
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.  
AUTHORS Bioremediation of radioactive water with metallic materials  
TITLE Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 474)  
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.  
AUTHORS Direct Submission  
TITLE Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain  
JOURNAL  
FEATURES  
source  
Location/Qualifiers  
1. .474  
/organism="Mycobacterium sp. 6BR15"  
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/isolate="6BR15"  
/isolation\_source="radioactive water"  
/db\_xref="taxon:300870"  
<1. .>474  
/product="16S ribosomal RNA"  
rRNA  
ORIGIN  
Query Match 93.3%; Score 22.4; DB 15; Length 474;  
Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24  
|||||  
Db 30 CAAAGTCGAACGGAAGGCGCTTTCG 53  
|||||  
RESULT 80  
AY559492 476 bp DNA linear BCT 22-MAR-2004  
LOCUS  
DEFINITION Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial sequence.  
AY559492  
ACCESSION AY559492.1 GI:45511545  
VERSION  
KEYWORDS Mycobacterium porcinum  
SOURCE Mycobacterium porcinum  
ORGANISM Mycobacterium porcinum  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE  
1 (bases 1 to 476)  
Hontzas, N., Belimov, A., Safronova, V. and Glick, B.  
AUTHORS Characterization of various plant growth-promoting bacteria  
TITLE Unpublished  
JOURNAL  
REFERENCE 2 (bases 1 to 476)  
Hontzas, N., Belimov, A., Safronova, V. and Glick, B.  
AUTHORS Direct Submission  
TITLE Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada  
JOURNAL  
FEATURES  
source  
Location/Qualifiers  
1. .476  
/organism="Mycobacterium porcinum"  
/mol\_type="genomic DNA"  
/strain="M552"  
/db\_xref="taxon:39693"  
<1. .>476  
/product="16S ribosomal RNA"  
rRNA  
ORIGIN  
Query Match 93.3%; Score 22.4; DB 15; Length 476;  
Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

Db						
31	CAAGTCGAACGGAAGGCCCTTTCG	54				
RESULT 81						
AY251205	478 bp	DNA	linear	ENV 20-APR-2003		
LOCUS	Uncultured actinobacterium clone IB_5 16S ribosomal RNA gene,					
DEFINITION	partial sequence.					
ACCESSION	AY251205					
VERSION	AY251205.1	GI:30027023				
KEYWORDS	ENV.					
SOURCE	uncultured actinobacterium					
ORGANISM	Bacteria; Actinobacteria; environmental samples.					
REFERENCE	1 (bases 1 to 478)					
AUTHORS	Vanbroekhoven,K., Bastiaens,L., De mot,R. and Springael,D.					
TITLE	Microbial community changes during different bioremediation strategies in diesel fuel-contaminated laboratory microcosms unpublished					
JOURNAL	2 (bases 1 to 478)					
REFERENCE	Vanbroekhoven,K., Bastiaens,L., De mot,R. and Springael,D.					
AUTHORS	Submitted (07-MAR-2003) Environmental Technology, Flemish Institute for Technological Research, Boeretang 200, Mol 2400, Belgium					
TITLE	Location/Qualifiers					
JOURNAL	1. .478					
FEATURES	/organism="uncultured actinobacterium"					
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	/db_xref="taxon:152507"					
	/clone="IB_5"					
	/environmental_sample					
	<1. .>478					
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rRNA						
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Best Local Similarity	95.8%;	Pred. No. 3.5e+02;				
Matches	23;	Conservative	0;	Mismatches	1;	
			Indels	0;	Gaps	0;
QY	1	CAAGTCGAACGGAAGGCCCTTTCG	24			
Db	16	CAAGTCGAGCGGAAGGCCCTTTCG	39			
RESULT 82						
MSP413603/c	481 bp	DNA	linear	BCT 06-JUN-2003		
LOCUS	MSP413603					
DEFINITION	Mycobacterium sp. dtb94 partial 16S rRNA gene, strain dtb94.					
ACCESSION	AJ413603					
VERSION	AJ413603.1	GI:16151371				
KEYWORDS	16S ribosomal RNA; 16S rRNA gene.					
SOURCE	Mycobacterium sp. dtb94					
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.					
REFERENCE	1					
AUTHORS	Oravec,O.					
TITLE	Identification of cultured bacteria from the gut of the millipede Cyndrochilus boleti (Diplopoda)					
JOURNAL	Unpublished					
REFERENCE	2 (bases 1 to 481)					
AUTHORS	Oravec,O.					
TITLE	Direct Submission					
JOURNAL	Submitted (26-SEP-2001) Oravec O., Dept. of Microbiology, Eotvos Lorand University, Pazmany Peter setany 1/C, H-1117, HUNGARY					
FEATURES	Location/Qualifiers					
source	1. .481					
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	/strain="dtb94"					
	/db_xref="taxon:172993"					

Direct Submission  
Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915  
West State Street, West Lafayette, IN 47907-2054, USA  
Location/Qualifiers  
1. .496  
/organism="uncultured soil bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="Ross Forest soil"  
/db\_xref="Taxon:164851"  
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rRNA  
ORIGIN  
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAACTCGAAGCGAAGGCTTTTCG 24  
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Db 51 CAACTCGAAGCGAAGGCTTTTCG 74  
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RESULT 85  
LOCUS AY215287 498 bp DNA linear BCT 08-APR-2003  
DEFINITION Mycobacterium mucogenicum isolate N241 16S ribosomal RNA gene,  
partial sequence.  
ACCESSION AY215287  
VERSION AY215287.1 GI:28274541  
KEYWORDS  
SOURCE Mycobacterium mucogenicum  
ORGANISM Mycobacterium mucogenicum  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1 (bases 1 to 498)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128  
AUTHORS  
TITLES  
Direct Submission  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
Location/Qualifiers  
1. .498  
/organism="Mycobacterium mucogenicum"  
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/isolate="N241"  
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rRNA  
ORIGIN  
Query Match 93.3%; Score 22.4; DB 15; Length 498;  
Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CAACTCGAAGCGAAGGCTTTTCG 24  
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Db 54 CAACTCGAAGCGAAGGCTTTTCG 77  
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RESULT 86  
LOCUS AY215324 498 bp DNA linear BCT 08-APR-2003  
DEFINITION Mycobacterium sp. N141 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY215324  
VERSION AY215324.1 GI:28274578

KEYWORDS  
SOURCE Mycobacterium sp. N141  
ORGANISM Mycobacterium sp. N141  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1 (bases 1 to 498)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128  
AUTHORS  
TITLES  
Direct Submission  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
Location/Qualifiers  
1. .498  
/organism="Mycobacterium sp. N141"  
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
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QY 1 CAACTCGAAGCGAAGGCTTTTCG 24  
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Db 54 CAACTCGAAGCGAAGGCTTTTCG 77  
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RESULT 87  
LOCUS AY215336 498 bp DNA linear BCT 08-APR-2003  
DEFINITION Mycobacterium sp. N1772T 16S ribosomal RNA gene, partial sequence.  
ACCESSION AY215336  
VERSION AY215336.1 GI:28274590  
KEYWORDS  
SOURCE Mycobacterium sp. N1772T  
ORGANISM Mycobacterium sp. N1772T  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1 (bases 1 to 498)  
AUTHORS Hall, L., Doerr, K.A., Wohlfiel, S.L. and Roberts, G.D.  
TITLE Evaluation of the MicroSeq System for Identification of  
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration  
into a Routine Clinical Mycobacteriology Laboratory  
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)  
JOURNAL PUBLISHED 12682128  
AUTHORS  
TITLES  
Direct Submission  
Submitted (08-JAN-2003) Department of Laboratory Medicine and  
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA  
Location/Qualifiers  
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
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Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 88
DQ154566 499 bp DNA linear ENV 27-AUG-2005
LOCUS uncultured soil bacterium clone RFS-C252 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION DQ154566
VERSION DQ154566.1 GI:73672356
KEYWORDS ENV.
SOURCE uncultured soil bacterium
ORGANISM uncultured soil bacterium
REFERENCE 1 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Low nutrient fluxes result in high cultivation efficiencies of soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2005) Biological Sciences, Purdue University, 915
WEST State Street, West Lafayette, IN 47907-2054, USA
FEATURES
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1. 499
/organism="uncultured soil bacterium"
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/environmental_sample
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/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 93.3%; Score 22.4; DB 1; Length 499;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 51 CAAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 89
DQ154328 499 bp DNA linear BCT 27-AUG-2005
LOCUS Soil bacterium RFS-1117 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ154328
VERSION DQ154328.1 GI:73672118
KEYWORDS soil bacterium RFS-1117
SOURCE soil bacterium RFS-1117
ORGANISM Bacteria.
REFERENCE 1 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Low nutrient fluxes result in high cultivation efficiencies of soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 499)
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
WEST State Street, West Lafayette, IN 47907-2054, USA
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 51 CAAAGTCGAACGGAAGGCGCTTTCG 74

RESULT 90
AV215236 499 bp DNA linear BCT 08-APR-2003
LOCUS Mycobacterium abscessus isolate N418 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AV215236
VERSION AV215236.1 GI:28274490
KEYWORDS Mycobacterium abscessus
SOURCE Mycobacterium abscessus
ORGANISM Mycobacterium abscessus
REFERENCE 1 (bases 1 to 499)
AUTHORS Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
TITLE Evaluation of the MicroSeq System for Identification of
JOURNAL Mycobacteria by 16S Ribosomal DNA Sequencing and its Integration
PUBMED 12682128
REFERENCE 2 (bases 1 to 499)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
source
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/organism="Mycobacterium abscessus"
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rRNA

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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 91
UEU233561 500 bp DNA linear ENV 06-JUN-2003
LOCUS uncultured eubacterium 16S ribosomal RNA, clone WR169.
DEFINITION
ACCESSION UEU233561
VERSION UEU233561.1 GI:5708350
KEYWORDS 16S ribosomal RNA.
SOURCE uncultured eubacterium WR169
ORGANISM uncultured eubacterium WR169
REFERENCE 1 (bases 1 to 500)
AUTHORS Nogales,B., Moore,E.R., Abraham,W.R. and Timmis,K.N.
TITLE Identification of the metabolically active members of a bacterial
JOURNAL community in a polychlorinated biphenyl-polluted moorland soil
PUBMED 11207739

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REFERENCE 2 (bases 1 to 500)
AUTHORS Nogales B.
TITLE Direct Submission
JOURNAL Submitted (24-SEP-1998) Nogales B., GBF-National Research Centre
for Biotechnology, Mascheroder Weg, 1, D-38124 Braunschweig,
Germany
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rRNA
ORIGIN
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    Best Local Similarity 95.8%; Pred. No. 3.5e+02;
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Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
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Db 50 CAACTCGAACGGAAGGCGCTTTCG 73

RESULT 92
AF498660 500 bp DNA linear BCT 02-DEC-2002
LOCUS Mycobacterium rhodesiae strain K1 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF498660
VERSION AF498660.1 GI:21686167
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V., Mattes,T.E., Gossett,J.M. and Spain,J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl
chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
FEATURES
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                chloride"
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rRNA
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Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAACTCGAACGGAAGGCGCTTTCG 77

RESULT 93
AF498661 500 bp DNA linear BCT 02-DEC-2002
LOCUS Mycobacterium rhodesiae strain TW1 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF498661
VERSION AF498661.1 GI:21686168
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V., Mattes,T.E., Gossett,J.M. and Spain,J.C.
TITLE Phylogenetic and kinetic diversity of aerobic vinyl
chloride-assimilating bacteria from contaminated sites
JOURNAL Appl. Environ. Microbiol. 68 (12), 6162-6171 (2002)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V.
TITLE Direct Submission
JOURNAL Submitted (05-APR-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
FEATURES
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                chloride"
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rRNA
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    Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAACTCGAACGGAAGGCGCTTTCG 77

RESULT 94
AF162027 500 bp DNA linear BCT 01-OCT-2003
LOCUS Mycobacterium rhodesiae 16S ribosomal RNA gene, partial sequence.
ACCESSION AY162027
VERSION AY162027.1 GI:24850312
KEYWORDS
SOURCE Mycobacterium rhodesiae
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 500)
AUTHORS Coleman,N.V. and Spain,J.C.
TITLE Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
Ehene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
PUBMED 12450841
REFERENCE 2 (bases 1 to 500)
AUTHORS Coleman,N.V. and Henley,C.M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2002) Air Force Research Laboratory - MLQL,
Building 1117, 139 Barnes Dr., Tyndall AFB, FL 32403, USA
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ORIGIN
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    Best Local Similarity 95.8%; Pred. No. 3.5e+02;
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Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
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Db 54 CAACTCGAACGGAAGGCGCTTTCG 77

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Query Match      93.3%; Score 22.4; DB 15; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 95
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LOCUS      500 bp      DNA      linear      BCT 01-OCT-2003
DEFINITION Mycobacterium mageritense 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY162030
VERSION     AY162030.1 GI:24850315
KEYWORDS   .
SOURCE     Mycobacterium mageritense
ORGANISM   Mycobacterium mageritense
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  Coleman,N.V. and Spain,J.C.
AUTHORS    Distribution of the Coenzyme M Pathway of Epoxide Metabolism among
TITLE      Ethene- and Vinyl Chloride-Degrading Mycobacterium Strains
JOURNAL    Appl. Environ. Microbiol. 69 (10), 6041-6046 (2003)
REFERENCE  2 (bases 1 to 500)
AUTHORS    Coleman,N.V. and Henley,C.M.
TITLE      Direct Submission
JOURNAL    Submitted (10-OCT-2002) Air Force Research Laboratory - MLQI,
            Building 1117, 119 Barnes Dr., Tyndall AFB, FL 32403, USA
FEATURES   Location/Qualifiers
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rRNA

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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

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LOCUS      500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N661 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY15218
VERSION     AY15218.1 GI:28274472
KEYWORDS   .
SOURCE     Mycobacterium sp. N661
ORGANISM   Mycobacterium sp. N661
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium
            avium complex (MAC)
REFERENCE  Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
AUTHORS    Evaluation of the MicroSeq System for Identification of
TITLE      Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
JOURNAL    J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
REFERENCE  2 (bases 1 to 500)
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 97
AV15228
LOCUS      500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium sp. N110 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY15228
VERSION     AY15228.1 GI:28274482
KEYWORDS   .
SOURCE     Mycobacterium sp. N110
ORGANISM   Mycobacterium sp. N110
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
AUTHORS    Evaluation of the MicroSeq System for Identification of
TITLE      Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
            into a Routine Clinical Mycobacteriology Laboratory
JOURNAL    J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
REFERENCE  2 (bases 1 to 500)
AUTHORS    Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-JAN-2003) Department of Laboratory Medicine and
            Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
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Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 98
AV15234
LOCUS      500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium abscessus isolate N019 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY15234
VERSION     AY15234.1 GI:28274488
KEYWORDS   .
SOURCE     Mycobacterium abscessus
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rRNA

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QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24
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Db 54 CAAAGTCGAACGGAAGGCGCTTTCG 77

RESULT 99
AV15234
LOCUS      500 bp      DNA      linear      BCT 08-APR-2003
DEFINITION Mycobacterium abscessus isolate N019 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY15234
VERSION     AY15234.1 GI:28274488
KEYWORDS   .
SOURCE     Mycobacterium abscessus
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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rRNA

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Query Match 93.3%; Score 22.4; DB 15; Length 500;
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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
Db 54 CAAGTCGAACGGAAGGCCTTTCG 77

RESULT 99
AV215235
LOCUS 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium abscessus isolate N416 16S ribosomal RNA gene,
partial sequence.
AV215235
VERSION AV215235.1 GI:28274489
KEYWORDS
SOURCE Mycobacterium abscessus
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
FEATURES
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 93.3%; Score 22.4; DB 15; Length 500;
Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
Db 54 CAAGTCGAACGGAAGGCCTTTCG 77

Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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<1_>500
/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
Db 54 CAAGTCGAACGGAAGGCCTTTCG 77

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RESULT 100
AV215237
LOCUS 500 bp DNA linear BCT 08-APR-2003
DEFINITION Mycobacterium sp. N570 16S ribosomal RNA gene, partial sequence.
AV215237
VERSION AV215237.1 GI:28274491
KEYWORDS
SOURCE Mycobacterium sp. N570
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 500)
Hall,L., Doerr,K.A., Wohlfiel,S.L. and Roberts,G.D.
Evaluation of the MicroSeq System for Identification of
Mycobacteria by 16S Ribosomal DNA Sequencing and Its Integration
into a Routine Clinical Mycobacteriology Laboratory
J. Clin. Microbiol. 41 (4), 1447-1453 (2003)
JOURNAL
PUBMED 12682128
REFERENCE 2 (bases 1 to 500)
AUTHORS Roberts,G.D., Hall,L., Doerr,K.A. and Wohlfiel,S.L.
TITLE Direct Submission
JOURNAL Submitted (08-JAN-2003) Department of Laboratory Medicine and
Pathology, Mayo Clinic, 200 First St. SW, Rochester, MN 55906, USA
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rRNA

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Best Local Similarity 95.8%; Pred. No. 3.5e+02;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
Db 55 CAAGTCGAACGGAAGGCCTTTCG 78

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

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Title: US-10-665-708-23  
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Sequence: 1 gtcgaacggaagccttcgg 22  
Scoring table: IDENTITY NUC  
Gapop 10'0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : GenEmbl.\*

- 1: gb\_env.\*
- 2: gb\_pat.\*
- 3: gb\_ph.\*
- 4: gb\_pl.\*
- 5: gb\_pr.\*
- 6: gb\_ro.\*
- 7: gb\_scs.\*
- 8: gb\_sy.\*
- 9: gb\_un.\*
- 10: gb\_vi.\*
- 11: gb\_ov.\*
- 12: gb\_htg.\*
- 13: gb\_in.\*
- 14: gb\_om.\*
- 15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
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1	22	100.0	22	2	AR438655	Sequence	
2	22	100.0	22	2	AX166857	Sequence	
3	22	100.0	541	15	AF547926	Mycobacte	
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5	22	100.0	1459	15	MC016S	X53896 Mycobacteri	
6	21	95.5	24	2	AR438654	Sequence	
7	21	95.5	24	2	AX166856	Sequence	
8	21	95.5	25	2	AR438653	Sequence	
9	21	95.5	25	2	AX166855	Sequence	
10	21	95.5	1460	15	MSGRGDSA	L08169 Mycobacteri	
11	21	95.5	1479	15	MSGRGDSB	L08170 Mycobacteri	
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13	20.4	92.7	171	15	AF059783	AF059783 Mycobacte	
14	20.4	92.7	171	15	AF059795	AF059795 Mycobacte	
15	20.4	92.7	171	15	AF059797	AF059797 Mycobacte	
16	20.4	92.7	171	15	AF059808	AF059808 Mycobacte	
17	20.4	92.7	171	15	AF059812	AF059812 Mycobacte	
18	20.4	92.7	171	15	AF059833	AF059833 Mycobacte	

19	20.4	92.7	171	15	AF059834	Mycobacte	
20	20.4	92.7	171	15	AF059835	Mycobacte	
21	20.4	92.7	171	15	AF059839	Mycobacte	
22	20.4	92.7	171	15	AF059841	Mycobacte	
23	20.4	92.7	171	15	AF059851	Mycobacte	
24	20.4	92.7	171	15	AF059852	Mycobacte	
25	20.4	92.7	172	15	AF059793	Mycobacte	
26	20.4	92.7	268	15	MSGRR16S	Mycobacteri	
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29	20.4	92.7	384	15	DQ063127	Actinobac	
30	20.4	92.7	388	1	AY395145	Unculture	
31	20.4	92.7	393	1	BSSMKN23	Bacterium s	
32	20.4	92.7	394	1	AY395154	Unculture	
33	20.4	92.7	395	1	AY043901	AY043901 Unculture	
34	20.4	92.7	395	1	AY395151	Unculture	
35	20.4	92.7	396	1	BSSMKN14	Bacterium s	
36	20.4	92.7	400	1	DQ221681	Unculture	
37	20.4	92.7	401	15	DQ063085	Actinobac	
38	20.4	92.7	403	15	AY234665	Bacterium	
39	20.4	92.7	407	15	AY792017	Mycobacte	
40	20.4	92.7	410	1	BSSMKN12	Bacterium s	
41	20.4	92.7	411	15	DQ063154	Actinobac	
42	20.4	92.7	411	15	DQ063199	Actinobac	
43	20.4	92.7	411	15	AY792013	Mycobacte	
44	20.4	92.7	414	1	AM085773	Unculture	
45	20.4	92.7	414	1	DQ223051	Unculture	
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62	20.4	92.7	428	15	AB106918	Gram-posi	
63	20.4	92.7	428	15	DQ063058	Actinobac	
64	20.4	92.7	430	15	AJ786822	Mycobacte	
65	20.4	92.7	430	15	AY673202	Mycobacte	
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67	20.4	92.7	432	1	AF078232	Graessland	
68	20.4	92.7	433	15	AY673198	Mycobacte	
69	20.4	92.7	433	15	AY673266	Mycobacte	
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71	20.4	92.7	435	15	AY234692	Bacterium	
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80	20.4	92.7	445	15	AB106917	Gram-posi	
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87	20.4	92.7	456	15	AY358001	Actinobac	
88	20.4	92.7	459	1	AJ609008	AJ609008 Unculture	
89	20.4	92.7	459	15	AY754884	Mycobacte	
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92	20.4	92.7	464	15	DQ142669	DQ142669 Mycobacte	165	20.4	92.7	532	15	DQ124114	DQ124114 Mycobacte
93	20.4	92.7	464	15	DQ142672	DQ142672 Mycobacte	166	20.4	92.7	534	15	MF0416908	MF0416908 Mycobacte
94	20.4	92.7	466	15	DQ067465	DQ067465 Mycobacte	167	20.4	92.7	535	1	AY148216	AY148216 Unculture
95	20.4	92.7	466	15	AY524839	AY524839 Mycobacte	168	20.4	92.7	537	15	AY943209	AY943209 Mycobacte
96	20.4	92.7	468	15	DQ154332	DQ154332 Soil bact	169	20.4	92.7	540	15	AF547892	AF547892 Mycobacte
97	20.4	92.7	473	1	AY043719	AY043719 Unculture	170	20.4	92.7	540	15	AF547895	AF547895 Mycobacte
98	20.4	92.7	474	1	DQ136108	DQ136108 Unculture	171	20.4	92.7	540	15	AF547909	AF547909 Mycobacte
99	20.4	92.7	474	15	AY792024	AY792024 Mycobacte	172	20.4	92.7	540	15	AF547910	AF547910 Mycobacte
100	20.4	92.7	476	15	AY559452	AY559452 Mycobacte	173	20.4	92.7	540	15	AF547911	AF547911 Mycobacte
101	20.4	92.7	481	15	AY251205	AY251205 Unculture	174	20.4	92.7	540	15	AF547912	AF547912 Mycobacte
102	20.4	92.7	481	15	MSP413603	MSP413603 Mycobacte	175	20.4	92.7	540	15	AF547916	AF547916 Mycobacte
103	20.4	92.7	495	15	AY943206	AY943206 Mycobacte	176	20.4	92.7	540	15	AF547920	AF547920 Mycobacte
104	20.4	92.7	495	1	DQ154344	DQ154344 Unculture	177	20.4	92.7	540	15	AF547921	AF547921 Mycobacte
105	20.4	92.7	498	15	AY215287	AY215287 Mycobacte	178	20.4	92.7	540	15	AF547923	AF547923 Mycobacte
106	20.4	92.7	498	15	AY215334	AY215334 Mycobacte	179	20.4	92.7	540	15	AF547924	AF547924 Mycobacte
107	20.4	92.7	498	15	AY215336	AY215336 Mycobacte	180	20.4	92.7	540	15	AF547925	AF547925 Mycobacte
108	20.4	92.7	499	1	DQ154566	DQ154566 Unculture	181	20.4	92.7	540	15	AF547929	AF547929 Mycobacte
109	20.4	92.7	499	15	DQ154328	DQ154328 Soil bact	182	20.4	92.7	540	15	AF547936	AF547936 Mycobacte
110	20.4	92.7	499	15	AY215236	AY215236 Mycobacte	183	20.4	92.7	540	15	AF547944	AF547944 Mycobacte
111	20.4	92.7	500	1	UEU233561	UEU233561 unculture	184	20.4	92.7	540	15	AF547949	AF547949 Mycobacte
112	20.4	92.7	500	15	AF498660	AF498660 Mycobacte	185	20.4	92.7	540	15	AF547950	AF547950 Mycobacte
113	20.4	92.7	500	15	AF498661	AF498661 Mycobacte	186	20.4	92.7	540	15	AF547951	AF547951 Mycobacte
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115	20.4	92.7	500	15	AY162030	AY162030 Mycobacte	188	20.4	92.7	540	15	AF547955	AF547955 Mycobacte
116	20.4	92.7	500	15	AY215218	AY215218 Mycobacte	189	20.4	92.7	540	15	AF547956	AF547956 Mycobacte
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119	20.4	92.7	500	15	AY215235	AY215235 Mycobacte	192	20.4	92.7	540	15	AF547963	AF547963 Mycobacte
120	20.4	92.7	500	15	AY215237	AY215237 Mycobacte	193	20.4	92.7	540	15	AF547964	AF547964 Mycobacte
121	20.4	92.7	500	15	AY215245	AY215245 Mycobacte	194	20.4	92.7	540	15	AF547972	AF547972 Mycobacte
122	20.4	92.7	500	15	AY215247	AY215247 Mycobacte	195	20.4	92.7	540	15	AF547981	AF547981 Mycobacte
123	20.4	92.7	500	15	AY215251	AY215251 Mycobacte	196	20.4	92.7	540	15	AY438068	AY438068 Mycobacte
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126	20.4	92.7	500	15	AY215280	AY215280 Mycobacte	199	20.4	92.7	541	15	AF547943	AF547943 Mycobacte
127	20.4	92.7	500	15	AY215285	AY215285 Mycobacte	200	20.4	92.7	541	15	AY438067	AY438067 Mycobacte
128	20.4	92.7	500	15	AY215286	AY215286 Mycobacte	201	20.4	92.7	542	15	AF547897	AF547897 Mycobacte
129	20.4	92.7	500	15	AY215288	AY215288 Mycobacte	202	20.4	92.7	542	15	AF547917	AF547917 Mycobacte
130	20.4	92.7	500	15	AY215289	AY215289 Mycobacte	203	20.4	92.7	542	15	AF547918	AF547918 Mycobacte
131	20.4	92.7	500	15	AY215290	AY215290 Mycobacte	204	20.4	92.7	542	15	AF547980	AF547980 Mycobacte
132	20.4	92.7	500	15	AY215291	AY215291 Mycobacte	205	20.4	92.7	542	15	AY438079	AY438079 Mycobacte
133	20.4	92.7	500	15	AY215292	AY215292 Mycobacte	206	20.4	92.7	551	1	AY725804	AY725804 Unculture
134	20.4	92.7	500	15	AY215293	AY215293 Mycobacte	207	20.4	92.7	552	15	AY438073	AY438073 Mycobacte
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137	20.4	92.7	500	15	AY215320	AY215320 Mycobacte	210	20.4	92.7	558	15	AY367021	AY367021 Mycobacte
138	20.4	92.7	500	15	AY215323	AY215323 Mycobacte	211	20.4	92.7	576	15	AJ627393	AJ627393 Mycobacte
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298 20.4 92.7 1430 15 AF408984  
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300 20.4 92.7 1433 15 DQ370009

## ALIGNMENTS

RESULT 1  
AR438655  
LOCUS AR438655 22 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 23 from patent US 6664081.  
ACCESSION AR438655

VERSION AR438655.1 GI:42663579  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Brenkano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 23 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source location/Qualifiers  
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/mol\_type="genomic DNA"  
ORIGIN  
Query Match 100.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCGAACGGAAGGCGCTTTCGG 22  
|||||  
Db 1 GTCGAACGGAAGGCGCTTTCGG 22  
RESULT 2  
AR438657  
LOCUS AR438657 22 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 23 from Patent WO0144510.  
ACCESSION AR438657  
VERSION AR438657.1 GI:14596460  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 23 21-JUN-2001;  
Gen-Probe Incorporated (US) ; Biomerieux S.A. (FR)  
FEATURES  
source location/Qualifiers  
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/note="primer oligonucleotide"  
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GTCGAACGGAAGGCGCTTTCGG 22  
RESULT 3  
AF547926  
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006  
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.  
ACCESSION AF547926  
VERSION AF547926.1 GI:27733750  
KEYWORDS  
SOURCE Mycobacterium gadium  
ORGANISM Mycobacterium gadium  
REFERENCE 1 (bases 1 to 541)  
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.

TITLE A multigene approach to phylogenetic analysis using the genus  
 JOURNAL Mycobacterium as a model  
 PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)  
 REFERENCE 15653990  
 2 (bases 1 to 541)  
 AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,  
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,  
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France

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 source Location/Qualifiers  
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 /organism="Mycobacterium gadium"  
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 Best Local Similarity 100.0%; Pred. No. 29;  
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 Qy 1 GTCGAACGGAAGGCCCTTTGG 22  
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 Db 18 GTCGAACGGAAGGCCCTTTGG 39

RESULT 4  
 MGAD16S  
 LOCUS 1456 bp DNA linear BCT 06-JUN-2003  
 DEFINITION M.gadium 16S ribosomal RNA, part.  
 ACCESSION X55594  
 VERSION X55594.1 GI:44291  
 KEYWORDS 16S ribosomal RNA  
 SOURCE Mycobacterium gadium  
 ORGANISM Mycobacterium gadium  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1456)  
 AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.  
 TITLE Phylogeny of rapidly growing members of the genus Mycobacterium  
 JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)  
 PUBMED 1380284  
 REFERENCE 2 (bases 1 to 1456)  
 AUTHORS Wolters,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine  
 Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen  
 Garten 1-9, 2300 Kiel 1

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 /db\_xref="taxon:1794"  
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 /product="16S ribosomal RNA"

rRNA  
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 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCCCTTTGG 22  
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 Db 62 GTCGAACGGAAGGCCCTTTGG 83

RESULT 5  
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 LOCUS 1459 bp DNA linear BCT 11-JUN-2003  
 DEFINITION Mycobacterium cookii partial 16S rRNA.  
 ACCESSION X53896  
 VERSION X53896.1 GI:44201  
 KEYWORDS 16S ribosomal RNA; ribosomal RNA.  
 SOURCE Mycobacterium cookii  
 ORGANISM Mycobacterium cookii  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 1225)  
 AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M.,  
 Parlett,J.H. and Pitulle,C.  
 TITLE Mycobacterium cookii sp. nov.  
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)  
 PUBMED 1697763  
 REFERENCE 2 (bases 1 to 1459)  
 AUTHORS Stackebrandt,E.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E

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 /product="16S ribosomal RNA"

rRNA  
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 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 62 GTCGAACGGAAGGCCCTTTGG 83

RESULT 6  
 AR438654  
 LOCUS 24 bp DNA linear PAT 20-FEB-2004  
 DEFINITION Sequence 22 from patent US 6664081.  
 ACCESSION AR438654  
 VERSION AR438654.1 GI:42663578  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 24)  
 AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
 Rodrigue,M.  
 TITLE Nucleic acid amplification and detection of mycobacterium species  
 JOURNAL Patent: US 6664081-A 22 16-DEC-2003;  
 Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
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 Db 4 GTCGAACGGAAGGCCCTTTGG 24

RESULT 7  
 AX166856  
 LOCUS 24 bp DNA linear PAT 04-JUL-2001  
 DEFINITION Sequence 22 from Patent WO0144510.

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ACCESSION AX166856
VERSION AX166856.1 GI:14596459
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 22 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
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source Location/Qualifiers
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Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GTCGAACGGAAGGCGCTTTCG 24
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RESULT 8
AR438653
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 21 from patent US 6664081.
ACCESSION AR438653
VERSION AR438653.1 GI:42663577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.
TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: US 6664081-A 21 16-DEC-2003;
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA
FEATURES
source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.7e+02;
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Qy 1 GTCGAACGGAAGGCGCTTTCG 21
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Db 5 GTCGAACGGAAGGCGCTTTCG 25
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RESULT 9
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LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001
DEFINITION Sequence 21 from Patent WO0144510.
ACCESSION AX166855
VERSION AX166855.1 GI:14596458
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 other sequences; artificial sequences.
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and
Rodrigue,M.

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TITLE Nucleic acid amplification and detection of mycobacterium species
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)
FEATURES
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Db 5 GTCGAACGGAAGGCGCTTTCG 25
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RESULT 10
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LOCUS MSGRGDSA 1460 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08169
VERSION L08169.1 GI:293249
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.
TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51131)
DNA.
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source Location/Qualifiers
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rRNA

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Best Local Similarity 95.5%; Pred. No. 53;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCG 22
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RESULT 11
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LOCUS MSGRGDSB 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08170
VERSION L08170.1 GI:293250
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,

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Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,  
 Vadney,F.S. and Gross,W.M.  
 Mycobacterium celatum sp. nov  
 Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)  
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 COMMENT Original source text: Mycobacterium celatum (library: ATCC 51130)  
 DNA.

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rRNA

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RESULT 12  
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 DEFINITION Mycobacterium fortuitum isolate 92144 16S ribosomal RNA (rrs) gene,  
 partial sequence.  
 ACCESSION AF059778  
 VERSION AF059778.1 GI:3132922  
 KEYWORDS  
 SOURCE Mycobacterium fortuitum  
 ORGANISM Mycobacterium fortuitum  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 171)  
 Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,  
 Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.  
 Simultaneous genotyping and species identification using  
 hybridization pattern recognition analysis of generic Mycobacterium  
 DNA arrays  
 Genome Res. 8 (5), 435-448 (1998)  
 9582189

JOURNAL  
 PUBLISHED 9582189  
 REFERENCE 3 (bases 1 to 171)  
 Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,  
 Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.  
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 hybridization pattern recognition analysis of generic Mycobacterium  
 DNA arrays  
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 9582189

JOURNAL  
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 REFERENCE 3 (bases 1 to 171)  
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 Simultaneous genotyping and species identification using  
 hybridization pattern recognition analysis of generic Mycobacterium  
 DNA arrays  
 Genome Res. 8 (5), 435-448 (1998)  
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JOURNAL  
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 REFERENCE 3 (bases 1 to 171)  
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 Simultaneous genotyping and species identification using  
 hybridization pattern recognition analysis of generic Mycobacterium  
 DNA arrays  
 Genome Res. 8 (5), 435-448 (1998)  
 9582189

JOURNAL  
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 REFERENCE 3 (bases 1 to 171)  
 Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,  
 Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.  
 Simultaneous genotyping and species identification using  
 hybridization pattern recognition analysis of generic Mycobacterium





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/notes="originally described as Mycobacterium kansasii,
please refer to publication."
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Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
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Db 2 GTCGAACGGAAGCCCTTCGG 23
    |||||

RESULT 18
AF059833
LOCUS
DEFINITION
Mycobacterium chelonae isolate 95A8654 16S ribosomal RNA (rrs)
gene, partial sequence.
AF059833
ACCESSION
VERSION
GI:3132977
KEYWORDS
SOURCE
ORGANISM
Mycobacterium chelonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 171)
Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
Genome Res. 8 (5), 435-448 (1998)
9582189
2 (bases 1 to 171)
Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
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Genome Res. 8 (5), 435-448 (1998)
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3 (bases 1 to 171)
Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
Direct Submission
Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
Location/Qualifiers
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/isolate="95A8654"
/db_xref="taxon:1774"
<1..>171
/genes="rrs"
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/product="16S ribosomal RNA"

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Query Match          92.7%; Score 20.4; DB 15; Length 171;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 2 GTCGAACGGAAGCCCTTCGG 23
    |||||

RESULT 19
AF059834
LOCUS
DEFINITION
Mycobacterium chelonae isolate 95A0779 16S ribosomal RNA (rrs)
gene, partial sequence.
AF059834
ACCESSION
VERSION
GI:3132978
KEYWORDS
SOURCE
ORGANISM
Mycobacterium chelonae
Mycobacterium chelonae

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ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 171;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTTCGG 22
Db 2 GTCGAACGGAAGGCGCTTTCGG 23

RESULT 22
AF059841
LOCUS AF059841 171 bp rRNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium chelonae isolate 95A9151 16S ribosomal RNA (rrs)
gene, partial sequence.
ACCESSION AF059841
VERSION AF059841.1 GI:3132985
KEYWORDS
SOURCE Mycobacterium chelonae
ORGANISM Mycobacterium chelonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniowski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniowski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 3 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniowski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
source
1..171
/organism="Mycobacterium chelonae"
/mol_type="rRNA"
/strain="ATCC6841"
/db_xref="ATCC:6841"
/db_xref="taxon:1774"
<1..>171
/gene="rrs"
<1..>171
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/product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 171;
Best Local Similarity 95.5%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTTCGG 22
Db 2 GTCGAACGGAAGGCGCTTTCGG 23

RESULT 24
AF059852
LOCUS AF059852 171 bp rRNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium chelonae strain ATCC35752 16S ribosomal RNA (rrs)
gene, partial sequence.
ACCESSION AF059852
VERSION AF059852.1 GI:3132996
KEYWORDS
SOURCE Mycobacterium chelonae
ORGANISM Mycobacterium chelonae
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 171)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniowski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic Mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
PUBMED 9582189
REFERENCE 2 (bases 1 to 171)

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**AUTHORS** Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
**TITLE** Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
**JOURNAL** Genome Res. 8 (5), 435-448 (1998)  
**PUBMED** 9582189  
**REFERENCE** 3 (bases 1 to 171)  
**AUTHORS** Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA  
**FEATURES** Location/Qualifiers  
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 /mol\_type="rRNA"  
 /strain="ATCC35752"  
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 Best Local Similarity 95.5%; Pred. No. 2.8e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCGCTTTCGG 22  
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 Db 2 GTCGAACGGAAGGCGCTTTCGG 23  
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 RESULT 25  
 LOCUS AF059793 172 bp rRNA linear BCT 15-MAY-1998  
 DEFINITION Mycobacterium fortuitum isolate 60447 16S ribosomal RNA (rrs) gene, partial sequence.  
 ACCESSION AF059793  
 VERSION AF059793.1 GI:3132937  
 KEYWORDS  
 SOURCE Mycobacterium fortuitum  
 ORGANISM Mycobacterium fortuitum  
 Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
**JOURNAL** Genome Res. 8 (5), 435-448 (1998)  
**PUBMED** 9582189  
**REFERENCE** 2 (bases 1 to 172)  
**AUTHORS** Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
**TITLE** Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
**JOURNAL** Genome Res. 8 (5), 435-448 (1998)  
**PUBMED** 9582189  
**REFERENCE** 3 (bases 1 to 172)  
**AUTHORS** Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA  
**FEATURES** Location/Qualifiers  
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 /organism="Mycobacterium fortuitum"

gene /mol\_type="rRNA"  
 /isolate="60447"  
 /db\_xref="taxon:1766"  
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 /gene="rrs"  
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 /gene="rrs"  
 /product="16S ribosomal RNA"  
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 Query Match 92.7%; Score 20.4; DB 15; Length 172;  
 Best Local Similarity 95.5%; Pred. No. 2.8e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCGCTTTCGG 22  
 |||||  
 Db 2 GTCGAACGGAAGGCGCTTTCGG 23  
 |||||  
 RESULT 26  
 LOCUS MSGRR16S 268 bp rRNA linear BCT 27-APR-1993  
 DEFINITION Mycobacterium kansasii 16S ribosomal RNA.  
 ACCESSION M95469  
 VERSION M95469.1 GI:175317  
 KEYWORDS 16S ribosomal RNA.  
 SOURCE Mycobacterium kansasii  
 ORGANISM Mycobacterium kansasii  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE  
 AUTHORS Ross,B.C., Jackson,K., Yang,M., Sievers,A. and Dwyer,B.  
 TITLE Identification of a genetically distinct sub-species of Mycobacterium kansasii  
 JOURNAL Unpublished (1992)  
 COMMENT Original source text: Mycobacterium kansasii rRNA.  
 FEATURES Location/Qualifiers  
 source  
 1..268  
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 ORIGIN  
 Query Match 92.7%; Score 20.4; DB 15; Length 268;  
 Best Local Similarity 95.5%; Pred. No. 2.3e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCGCTTTCGG 22  
 |||||  
 Db 42 GTCGAACGGAAGGCGCTTTCGG 63  
 |||||  
 RESULT 27  
 LOCUS MSP404591 293 bp DNA linear ENV 06-JUN-2003  
 DEFINITION Uncultured Mycobacterium MB1 partial 16S rRNA gene.  
 ACCESSION AJ404591  
 VERSION AJ404591.1 GI:8926769  
 KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
 SOURCE uncultured Mycobacterium MB1  
 ORGANISM uncultured Mycobacterium MB1  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental samples.  
 REFERENCE  
 AUTHORS Kempell,K.E., Cox,C.J., Hurle,M., Wong,A., Wilkie,S., Zanders,E.D., Gaston,J. and Crowe,J.  
 TITLE Reverse Transcriptase-Polymerase Chain Reaction of Bacterial rRNA

```

for Detection and Characterisation of Bacterial Species in
Arthritis Synovial Tissue
JOURNAL
REFERENCE 2 (bases 1 to 293)
AUTHORS Cox, C.J.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SA, UNITED KINGDOM
FEATURES
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            /clone="MB1"
            /tissue_type="Synovium"
            1..293
            /gene="16S rRNA"
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            /product="16S ribosomal RNA"
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Query Match          92.7%;   Score 20.4;   DB 1;   Length 293;
Best Local Similarity 95.5%;   Pred. No. 2.2e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAGCCCTTCGG 22
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Db   24  GTCGAACGGAAGCCCTTCGG 45

RESULT 28
MF16SRRN
LOCUS M.fortuitum 16S rRNA gene, partial.
DEFINITION M.fortuitum 16S rRNA gene, partial.
ACCESSION Y09325
VERSION Y09325.1 GI:1669698
KEYWORDS 16S ribosomal RNA; rrrn gene.
SOURCE Mycobacterium fortuitum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 De Smet, K., Kampmann, B., Marshall, B., Kroll, S. and Levin, M.
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 316)
REFERENCE De Smet, K.A.L.
AUTHORS Direct Submission
TITLE Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
JOURNAL School at St Marys, Medical Microbiology, Norfolk Place, London, W2
1PG, UK
FEATURES
    source
        1..316
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Query Match          92.7%;   Score 20.4;   DB 15;   Length 316;
Best Local Similarity 95.5%;   Pred. No. 2.1e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAGCCCTTCGG 22
      |||||
Db   49  GTCGAACGGAAGCCCTTCGG 70

for Detection and Characterisation of Bacterial Species in
Arthritis Synovial Tissue
JOURNAL
REFERENCE 2 (bases 1 to 293)
AUTHORS Cox, C.J.
TITLE Direct Submission
JOURNAL Submitted (05-JUN-2000) Cox C.J., Cancer Research, Sanger Centre,
Wellcome Trust Genome Campus, Hinxton Hall, Hinxton,
Cambridgeshire, CB10 1SA, UNITED KINGDOM
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            /db_xref="taxon:129682"
            /clone="MB1"
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            /gene="16S rRNA"
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Query Match          92.7%;   Score 20.4;   DB 1;   Length 293;
Best Local Similarity 95.5%;   Pred. No. 2.2e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAGCCCTTCGG 22
      |||||
Db   24  GTCGAACGGAAGCCCTTCGG 45

RESULT 28
MF16SRRN
LOCUS M.fortuitum 16S rRNA gene, partial.
DEFINITION M.fortuitum 16S rRNA gene, partial.
ACCESSION Y09325
VERSION Y09325.1 GI:1669698
KEYWORDS 16S ribosomal RNA; rrrn gene.
SOURCE Mycobacterium fortuitum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 De Smet, K., Kampmann, B., Marshall, B., Kroll, S. and Levin, M.
AUTHORS Unpublished
JOURNAL 2 (bases 1 to 316)
REFERENCE De Smet, K.A.L.
AUTHORS Direct Submission
TITLE Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
JOURNAL School at St Marys, Medical Microbiology, Norfolk Place, London, W2
1PG, UK
FEATURES
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            /db_xref="taxon:1766"
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            /gene="rrrn"
            /product="16S ribosomal RNA"
ORIGIN
Query Match          92.7%;   Score 20.4;   DB 15;   Length 316;
Best Local Similarity 95.5%;   Pred. No. 2.1e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAGCCCTTCGG 22
      |||||
Db   49  GTCGAACGGAAGCCCTTCGG 70

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RESULT 29
DQ063127
LOCUS Actinobacterium BAL187 384 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL187 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063127
VERSION DQ063127.1 GI:68139160
KEYWORDS
SOURCE
ORGANISM actinobacterium BAL187
actinobacterium BAL187
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 384)
AUTHORS Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 384)
AUTHORS Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
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            /mol_type="genomic DNA"
            /strain="BAL187"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
            BY31, Zobel1/R2A media"
            /db_xref="taxon:331761"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="8 October 2003"
            <1..384
            /product="16S ribosomal RNA"
ORIGIN
Query Match          92.7%;   Score 20.4;   DB 15;   Length 384;
Best Local Similarity 95.5%;   Pred. No. 1.9e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAGCCCTTCGG 22
      |||||
Db   1  GTCGAACGGAAGCCCTTCGG 22

RESULT 30
AY395145
LOCUS Uncultured bacterium clone D29ST 388 bp DNA linear ENV 07-SEP-2004
DEFINITION Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY395145
VERSION AY395145.1 GI:37595660
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 388)
AUTHORS Hackl, E., Zechmeister-Boltenstern, S., Bodrossy, L. and Sessitsch, A.
TITLE Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED 15345382
REFERENCE 2 (bases 1 to 388)
AUTHORS Hackl, E. and Sessitsch, A.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES
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            /organism="uncultured bacterium"
            /mol_type="genomic DNA"

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JOURNAL	Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED	15345382
REFERENCE	2 (bases 1 to 394)
AUTHORS	Hackl,E. and Sessitsch,A.
TITLE	Direct Submission
JOURNAL	Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
	Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES	Location/Qualifiers
source	1..394
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	/clone="E02St"
	/environmental_sample
	<1..>394
	/product="16S ribosomal RNA"
rRNA	
ORIGIN	
Query Match	92.7%; Score 20.4; DB 1; Length 394;
Best Local Similarity	95.5%; Pred. No. 1.9e+02;
Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GTCGAACGGAAGGCCTTCGG 22
Db	54 GTCGAACGGAAGGCCTTCGG 75
RESULT 33	
AY043901	Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene, partial sequence.
LOCUS	AY043901.1 GI:22267274
DEFINITION	ENV. uncultured actinobacterium
ACCESSION	AY043901
VERSION	AY043901.1
KEYWORDS	uncultured actinobacterium
SOURCE	uncultured actinobacterium
ORGANISM	Bacteria; Actinobacteria; environmental samples.
REFERENCE	1 (bases 1 to 395)
AUTHORS	Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.
TITLE	Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance
JOURNAL	Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED	12224564
REFERENCE	2 (bases 1 to 395)
AUTHORS	Axelrood,P.E., Chow,M.L., Radomski,C.C., McDermott,J.M. and Davies,J.
TITLE	Direct Submission
JOURNAL	Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall, Vancouver, BC V6S 2L2, Canada
FEATURES	Location/Qualifiers
source	1..395
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	/mol_type="genomic DNA"
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	/clone="SMS9.49WL"
	/environmental_sample
	/note="From forest cut-block mineral soil from the British Columbia Ministry of Forests Long-Term Soil Productivity (LTSP) installation near Williams Lake, BC, Canada"
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	/product="16S ribosomal RNA"
rRNA	
ORIGIN	
Query Match	92.7%; Score 20.4; DB 1; Length 395;
Best Local Similarity	95.5%; Pred. No. 1.9e+02;
Matches	21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GTCGAACGGAAGGCCTTCGG 22
Db	24 GTCGAACGGAAGGCCTTCGG 45

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RESULT 34
AY395151
LOCUS       AY395151                395 bp    DNA        linear    ENV 07-SEP-2004
DEFINITION   Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial
sequence.
ACCESSION    AY395151
VERSION      AY395151.1  GI:37595666
KEYWORDS     ENV.
SOURCE       uncultured bacterium
ORGANISM     Bacteria; environmental samples.

REFERENCE    1 (bases 1 to 395)
AUTHORS      Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE        Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
JOURNAL      Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED       15345382
REFERENCES   2 (bases 1 to 395)
AUTHORS      Hackl,E. and Sessitsch,A.
TITLE        Direct Submission
JOURNAL      Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES     source
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             /isolation_source="Forest soil"
             /db_xref="taxon:77133"
             /clone="D36ST"
             /environmental_sample
             <1..>395
             /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 1; Length 395;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GTCGACGGAAGGCGCTTTCGG 22
    |||||||||||||||
DB  54  GTCGACGGAAGGCGCTTTCGG 75

RESULT 35
BSSMKN14
LOCUS       BSSMKN14                396 bp    DNA        linear    ENV 22-FEB-1995
DEFINITION   Bacterium sp. (SMKN14) DNA.
ACCESSION    X78655
VERSION      X78655.1  GI:509724
KEYWORDS     16S ribosomal RNA.
SOURCE       unidentified bacterium
ORGANISM     Bacteria; environmental samples.

REFERENCE    1
AUTHORS      Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.
TITLE        Molecular characterization of nocardioform actinomycetes in
activated sludge by 16S rRNA analysis
JOURNAL      Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
PUBMED       7704280
REFERENCES   2 (bases 1 to 396)
AUTHORS      Schuppler,M.
TITLE        Direct Submission
JOURNAL      Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.
11, 79104 Freiburg, FRG

FEATURES     source
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             /organism="unidentified bacterium"
             /mol_type="genomic DNA"
             /isolate="SMKN14"
             /db_xref="taxon:2338"

rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 1; Length 400;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GTCGACGGAAGGCGCTTTCGG 22
    |||||||||||||||
DB  19  GTCGACGGAAGGCGCTTTCGG 40

RESULT 37
DQ063065
LOCUS       DQ063065                401 bp    DNA        linear    BCT 27-JUN-2005
DEFINITION   Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence.
ACCESSION    DQ063065
VERSION      DQ063065.1  GI:68139094
KEYWORDS     actinobacterium BAL125
SOURCE       actinobacterium BAL125
ORGANISM     Bacteria; Actinobacteria.
REFERENCE    1 (bases 1 to 401)
AUTHORS      Riemann,L., Leitert,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE        Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 401)

```



AUTHORS Riemann, L., Leitet, C., Pommier, T., Simu, K., Holmfeldt, K. and Hagstrom, A.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Bärnäsgratan 11, Kalmar 39031, Sweden  
 FEATURES Location/Qualifiers

1..401  
 /organism="actinobacterium BAL125"  
 /mol\_type="genomic DNA"  
 /strain="BAL125"  
 /isolation\_source="Baltic Sea, 3m depth, Landsort deep St.  
 BY31, Zobel/R2A media"  
 /db\_xref="taxon:331783"  
 /country="Sweden"  
 /lat\_lon="60.42.726N, 05.05.595E"  
 /collection\_date="2 July 2003"  
 <1..>401  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 401;  
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22  
 |||||  
 Db 4 GTCGAACGGAAGGCTTTTCGG 25

RESULT 38  
 AY234665

LOCUS Bacterium Ellin6013 403 bp DNA linear BCT 08-DEC-2003  
 DEFINITION Bacterium Ellin6013 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AY234665  
 VERSION AY234665.1 GI:37961822

KEYWORDS bacterium Ellin6013  
 SOURCE Bacterium Ellin6013

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae.

REFERENCE 1 (bases 1 to 403)  
 Joseph, S.J., Hugenholtz, P., Sangwan, P., Osborne, C.A. and Janssen, P.H.

AUTHORS Laboratory Cultivation of Widespread and Previously Uncultured Soil Bacteria

TITLE Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)

JOURNAL 14660368

REFERENCE 2 (bases 1 to 403)

AUTHORS Joseph, S.J., Hugenholtz, P., Rana, P., Osborne, C.A., Sait, M. and Janssen, P.H.

TITLE Direct Submission  
 JOURNAL Submitted (12-FEB-2003) Department of Microbiology and Immunology, University of Melbourne, Parkville, Victoria 3010, Australia

FEATURES Location/Qualifiers

1..403  
 /organism="bacterium Ellin6013"  
 /mol\_type="genomic DNA"  
 /isolate="Ellin6013"  
 /db\_xref="taxon:234120"  
 <1..>403  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 403;  
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22  
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 Db 34 GTCGAACGGAAGGCTTTTCGG 55

RESULT 39

AY792017/c  
 LOCUS Mycobacterium sp. 5BR6 407 bp DNA linear BCT 20-NOV-2004  
 DEFINITION Mycobacterium sp. 5BR6 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AY792017  
 VERSION AY792017.1 GI:55740316  
 KEYWORDS

SOURCE Mycobacterium sp. 5BR6

ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE 1 (bases 1 to 407)

AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.

TITLE Bioremediation of radioactive water with metallic materials

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 407)

AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.

TITLE Direct Submission  
 JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain

FEATURES Location/Qualifiers

source 1..407  
 /organism="Mycobacterium sp. 5BR6"  
 /mol\_type="genomic DNA"  
 /isolate="5BR6"  
 /isolation\_source="radioactive water"  
 /db\_xref="taxon:300866"  
 <1..>407  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 92.7%; Score 20.4; DB 15; Length 407;  
 Best Local Similarity 95.5%; Pred. No. 1.9e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22

|||||  
 Db 362 GTCGAACGGAAGGCTTTTCGG 341

RESULT 40  
 BSSMKN12

LOCUS Bacterium sp. (SMKN12) DNA. 410 bp DNA linear ENV 22-FEB-1995  
 DEFINITION Bacterium sp. (SMKN12) DNA.  
 ACCESSION X78654

VERSION X78654.1 GI:509723

KEYWORDS 16S ribosomal RNA.

SOURCE unidentified bacterium

ORGANISM unidentified bacterium  
 Bacteria; environmental samples.

REFERENCE 1

Schuppler, M., Mertens, F., Schon, G. and Gobel, U.B.

AUTHORS Molecular characterization of nocardiform actinomycetes in activated sludge by 16S rRNA analysis

TITLE Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)

JOURNAL 7704280

REFERENCE 2 (bases 1 to 410)

AUTHORS Schuppler, M.

TITLE Direct Submission

JOURNAL Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med. Mikrobiologie & Hygiene, Universitaet Freiburg, FRG

11, 79104 Freiburg, FRG

FEATURES Location/Qualifiers

source 1..410  
 /organism="unidentified bacterium"  
 /mol\_type="genomic DNA"  
 /isolate="SMKN12"  
 /db\_xref="taxon:2338"  
 <1..>410  
 /product="16S ribosomal RNA"

rRNA

ORIGIN

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Query Match      92.7%; Score 20.4; DB 1; Length 410;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 6 GTCGAACGGAAGGCCCTTCGG 27

RESULT 41
DQ063154
LOCUS actinobacterium BAL218 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063154
VERSION DQ063154.1 GI:68139192
KEYWORDS .
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source 1..411
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel1/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_dates="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 15 GTCGAACGGAAGGCCCTTCGG 36

RESULT 43
AY792013
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS .
SOURCE Mycobacterium sp. 4BR14
ORGANISM Mycobacterium sp. 4BR14
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
source 1..411
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 55 GTCGAACGGAAGGCCCTTCGG 76

RESULT 44
AM085773
LOCUS actinobacterium BAL263 411 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS .
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

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Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
source 1..411
/organism="actinobacterium BAL263"
/mol_type="genomic DNA"
/strain="BAL263"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel1/R2A media"
/db_xref="taxon:331810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 15 GTCGAACGGAAGGCCCTTCGG 36

RESULT 43
AY792013
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS .
SOURCE Mycobacterium sp. 4BR14
ORGANISM Mycobacterium sp. 4BR14
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
FEATURES
source 1..411
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 411;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTCGG 22
Db 55 GTCGAACGGAAGGCCCTTCGG 76

RESULT 44
AM085773
LOCUS actinobacterium BAL263 411 bp DNA linear ENV 21-SEP-2005
DEFINITION Actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS .
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

```

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DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone T6.
ACCESSION AM085773
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele, M., Vermeir, S., Wattiau, P., Rynjaert, A. and Springael, D.
TITLE Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uytendaele, M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
    source
        1..414
            /organism="uncultured Mycobacterium sp."
            /mol_type="genomic DNA"
            /isolation_source="PAH-contaminated soil"
            /db_xref="taxon:171292"
            /clone="T6"
            /environmental sample
            /country="Belgium"
            <1..>414
            /gene="16S rRNA"
            <1..>414
            /gene="16S rRNA"
            /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 414;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
|||||
Db 4 GTCGAACGGAAGGCGCTTTCGG 25

RESULT 45
DQ223051 414 bp DNA linear ENV 22-OCT-2005
LOCUS Uncultured bacterium clone H070 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION DQ223051
VERSION DQ223051.1 GI:77744948
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 414)
AUTHORS Li, H. and Mu, B.
TITLE Phylogenetic diversity and community structure of bacteria in an
oil-storage cavity as detected by 16S rRNA gene library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Li, H. and Mu, B.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2005) Chemical and Pharmaceutical Institution,
East China University of Science and Technology, Meilong Road,
Shanghai 200237, China
FEATURES
    source
        1..414
            /organism="uncultured bacterium"
            /mol_type="genomic DNA"
            /isolation_source="oil-storage cavity"

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rRNA
/db_xref="taxon:77133"
/clone="H070"
/environmental_sample
<1..>414
/product="16S ribosomal RNA"

ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 414;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
|||||
Db 54 GTCGAACGGAAGGCGCTTTCGG 75

RESULT 46
DQ063108 415 bp DNA linear BCT 27-JUN-2005
LOCUS Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
DEFINITION DQ063108
ACCESSION DQ063108.1 GI:68139141
KEYWORDS actinobacterium BAL168
SOURCE actinobacterium BAL168
ORGANISM actinobacterium BAL168
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 415)
AUTHORS Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source
        1..415
            /organism="actinobacterium BAL168"
            /mol_type="genomic DNA"
            /strain="BAL168"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
            BY31, Zobel/R2A media"
            /db_xref="taxon:331762"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="8 October 2003"
            <1..>415
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 415;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
|||||
Db 4 GTCGAACGGAAGGCGCTTTCGG 25

RESULT 47
AM085786 416 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION AM085786
ACCESSION AM085786
VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental

```

```

samples.
1
REFERENCE
AUTHORS
Uyttbroeck,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
Springael,D.
TITLE
Distribution of the Mycobacterium sp. community and polycyclic
aromatic hydrocarbons (PAHs) among different size fractions of a
weathered PAH-contaminated soil
JOURNAL
Unpublished
REFERENCE
AUTHORS
2. (bases 1 to 416)
Uyttbroeck,M.
TITLE
Direct Submission
JOURNAL
Submitted (13-SEP-2005) Uyttbroeck M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
source
Location/Qualifiers
1. .416
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="K11"
/environmental_sample
/country="Denmark"
<1. .>416
/gene="16S rRNA"
<1. .>416
/gene="16S rRNA"
/product="16S ribosomal RNA"
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Query Match 92.7%; Score 20.4; DB 1; Length 416;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGCCCTTCGG 22
|||||
Db 7 GTCGAACGGAAGCCCTTCGG 28
|||||
RESULT 48
LOCUS
actinobacterium BAL133 417 bp DNA linear BCT 27-JUN-2005
DEFINITION
Actinobacterium BAL133 16S ribosomal RNA gene, partial sequence.
ACCESSION
DQ063073
VERSION
DQ063073.1 GI:68139102
KEYWORDS
actinobacterium BAL133
ORGANISM
Bacteria; Actinobacteria.
REFERENCE
AUTHORS
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL
Unpublished
REFERENCE
AUTHORS
2. (bases 1 to 417)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE
Direct Submission
JOURNAL
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
Location/Qualifiers
1. .417
/organism="actinobacterium BAL133"
/mol_type="genomic DNA"
/strain="BAL133"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331784"
/country="Sweden"
/latlon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"

1. .>417
/product="16S ribosomal RNA"
ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 417;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGCCCTTCGG 22
|||||
Db 1 GTCGAACGGAAGCCCTTCGG 22
|||||
RESULT 49
LOCUS
Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
DEFINITION
AM085788
ACCESSION
AM085788
VERSION
AM085788.1 GI:75754611
KEYWORDS
ENV: 16S ribosomal RNA; 16S rRNA gene.
SOURCE
uncultured Mycobacterium sp.
ORGANISM
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE
AUTHORS
1
Uyttbroeck,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
Springael,D.
TITLE
Distribution of the Mycobacterium sp. community and polycyclic
aromatic hydrocarbons (PAHs) among different size fractions of a
weathered PAH-contaminated soil
JOURNAL
Unpublished
REFERENCE
AUTHORS
2. (bases 1 to 418)
Uyttbroeck,M.
TITLE
Direct Submission
JOURNAL
Submitted (13-SEP-2005) Uyttbroeck M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
source
Location/Qualifiers
1. .418
/organism="uncultured Mycobacterium sp."
/mol_type="genomic DNA"
/isolation_source="PAH-contaminated soil"
/db_xref="taxon:171292"
/clone="K13"
/environmental_sample
/country="Denmark"
<1. .>418
/gene="16S rRNA"
<1. .>418
/gene="16S rRNA"
/product="16S ribosomal RNA"
ORIGIN
Query Match 92.7%; Score 20.4; DB 1; Length 418;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGCCCTTCGG 22
|||||
Db 7 GTCGAACGGAAGCCCTTCGG 28
|||||
RESULT 50
LOCUS
Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
partial sequence.
DEFINITION
AY673261
ACCESSION
AY673261
VERSION
AY673261.1 GI:56683118
KEYWORDS
Mycobacteriaceae bacterium Ellin7095
SOURCE
Mycobacteriaceae bacterium Ellin7095

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ORGANISM  Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 418)
AUTHORS  Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE     Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL   Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED    15691937
REFERENCE 2 (bases 1 to 418)
AUTHORS  Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES  Location/Qualifiers
source    1..418
           /organism="Mycobacteriaceae bacterium Ellin7095"
           /mol_type="genomic DNA"
           /isolate="Ellin7095"
           /isolation_source="soil"
           /db_xref="taxon:305281"
           <1_>418
           /product="16S ribosomal RNA"
rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 418;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 51
AM085770 LOCUS      421 bp DNA linear ENV 21-SEP-2005
DEFINITION  Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION  AM085770
VERSION    AM085770.1 GI:75754591
KEYWORDS  ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1
AUTHORS    Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE      Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 421)
AUTHORS    Uytendaele,M.
TITLE      Direct Submission
JOURNAL    Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES  Location/Qualifiers
source    1..421
           /organism="uncultured bacterium"
           /mol_type="genomic DNA"
           /isolation_source="PAH-contaminated soil"
           /db_xref="taxon:77133"
           /clone="T3"
           /environmental_sample
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gene
rRNA
ORIGIN

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Query Match      92.7%; Score 20.4; DB 1; Length 421;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
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Db 13 GTCGAACGGAAGGCGCTTTCGG 34

RESULT 52
AJ786807 LOCUS      422 bp DNA linear BCT 29-OCT-2004
DEFINITION  Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION  AJ786807
VERSION    AJ786807.1 GI:54887545
KEYWORDS  16S ribosomal RNA; 16S rRNA gene.
SOURCE     Mycobacterium sp. R-22838
ORGANISM   Mycobacterium sp. R-22838
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE  1
AUTHORS    Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
Versaete,W. and De Vos,P.
TITLE      The microbial community composition of a commercial nitrifying
inoculum
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 422)
AUTHORS    Vanparrys,B.
TITLE      Direct Submission
JOURNAL    Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES  Location/Qualifiers
source    1..422
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           /mol_type="genomic DNA"
           /isolate="R-22838"
           /isolation_source="commercial nitrifying inoculum"
           /db_xref="taxon:288999"
           /country="Belgium"
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           /gene="16S rRNA"
           <1_>422
           /gene="16S rRNA"
           /product="16S ribosomal RNA"
gene
rRNA
ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 422;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 53
AY673284 LOCUS      422 bp DNA linear BCT 20-MAY-2005
DEFINITION  Micromonosporaceae bacterium Ellin7118 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673284
VERSION    AY673284.1 GI:56683141
KEYWORDS  Micromonosporineae; Micromonosporaceae.
SOURCE     Micromonosporaceae bacterium Ellin7118
ORGANISM   Micromonosporaceae bacterium Ellin7118
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micromonosporineae; Micromonosporaceae.
REFERENCE  1 (bases 1 to 422)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED    15691937

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REFERENCE 2 (bases 1 to 422)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES             Location/Qualifiers
source              1..422
                    /organism="Micromonosporaceae bacterium Ellin7118"
                    /mol_type="genomic DNA"
                    /isolate="Ellin7118"
                    /isolation_source="soil"
                    /db_xref="taxon:305235"
                    <1..>422
rRNA                /product="16S ribosomal RNA"
ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 422;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 33 GTCGACGGAAAGCCCTTTCGG 54
RESULT 54
AY673205
LOCUS                423 bp DNA linear BCT 20-MAY-2005
DEFINITION           Mycobacteriaceae bacterium Ellin7039 16S ribosomal RNA gene,
partial sequence.
ACCESSION            AY673205.1 GI:56683062
VERSION
KEYWORDS
SOURCE
ORGANISM             Mycobacteriaceae bacterium Ellin7039
                    Mycobacteriaceae bacterium Ellin7039
                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                    Corynebacterineae; Mycobacteriaceae.
REFERENCE            1 (bases 1 to 423)
AUTHORS              Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE                Effects of growth medium, inoculum size, and incubation time on
                    culturability and isolation of soil bacteria
JOURNAL              Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED              15691937
REFERENCE            2 (bases 1 to 423)
AUTHORS              Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE                Direct Submission
JOURNAL              Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                    University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                    Australia
FEATURES             Location/Qualifiers
source              1..423
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                    /mol_type="genomic DNA"
                    /isolate="Ellin7039"
                    /isolation_source="soil"
                    /db_xref="taxon:305258"
                    <1..>423
rRNA                /product="16S ribosomal RNA"
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Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 34 GTCGACGGAAAGCCCTTTCGG 55
RESULT 55
AY673206
LOCUS                423 bp DNA linear BCT 20-MAY-2005
DEFINITION           Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,
partial sequence.
ACCESSION            AY673207.1 GI:56683064
VERSION
KEYWORDS
SOURCE
ORGANISM             Mycobacteriaceae bacterium Ellin7040
                    Mycobacteriaceae bacterium Ellin7041
                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                    Corynebacterineae; Mycobacteriaceae.
REFERENCE            1 (bases 1 to 423)
AUTHORS              Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE                Effects of growth medium, inoculum size, and incubation time on
                    culturability and isolation of soil bacteria
JOURNAL              Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED              15691937
REFERENCE            2 (bases 1 to 423)
AUTHORS              Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE                Direct Submission
JOURNAL              Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                    University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                    Australia
FEATURES             Location/Qualifiers
source              1..423
                    /organism="Mycobacteriaceae bacterium Ellin7041"
                    /mol_type="genomic DNA"
                    /isolate="Ellin7041"
                    /isolation_source="soil"
                    /db_xref="taxon:305260"
                    <1..>423
rRNA                /product="16S ribosomal RNA"
ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 34 GTCGACGGAAAGCCCTTTCGG 55

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DEFINITION           Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,
partial sequence.
ACCESSION            AY673206.1 GI:56683063
VERSION
KEYWORDS
SOURCE
ORGANISM             Mycobacteriaceae bacterium Ellin7040
                    Mycobacteriaceae bacterium Ellin7040
                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                    Corynebacterineae; Mycobacteriaceae.
REFERENCE            1 (bases 1 to 423)
AUTHORS              Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE                Effects of growth medium, inoculum size, and incubation time on
                    culturability and isolation of soil bacteria
JOURNAL              Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED              15691937
REFERENCE            2 (bases 1 to 423)
AUTHORS              Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE                Direct Submission
JOURNAL              Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                    University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                    Australia
FEATURES             Location/Qualifiers
source              1..423
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                    /mol_type="genomic DNA"
                    /isolate="Ellin7040"
                    /isolation_source="soil"
                    /db_xref="taxon:305259"
                    <1..>423
rRNA                /product="16S ribosomal RNA"
ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 34 GTCGACGGAAAGCCCTTTCGG 55
RESULT 56
AY673207
LOCUS                423 bp DNA linear BCT 20-MAY-2005
DEFINITION           Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,
partial sequence.
ACCESSION            AY673207.1 GI:56683064
VERSION
KEYWORDS
SOURCE
ORGANISM             Mycobacteriaceae bacterium Ellin7041
                    Mycobacteriaceae bacterium Ellin7041
                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                    Corynebacterineae; Mycobacteriaceae.
REFERENCE            1 (bases 1 to 423)
AUTHORS              Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE                Effects of growth medium, inoculum size, and incubation time on
                    culturability and isolation of soil bacteria
JOURNAL              Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED              15691937
REFERENCE            2 (bases 1 to 423)
AUTHORS              Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE                Direct Submission
JOURNAL              Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                    University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                    Australia
FEATURES             Location/Qualifiers
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                    /isolation_source="soil"
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rRNA                /product="16S ribosomal RNA"
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Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 34 GTCGACGGAAAGCCCTTTCGG 55
RESULT 56
AY673207
LOCUS                423 bp DNA linear BCT 20-MAY-2005
DEFINITION           Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,
partial sequence.
ACCESSION            AY673207.1 GI:56683064
VERSION
KEYWORDS
SOURCE
ORGANISM             Mycobacteriaceae bacterium Ellin7041
                    Mycobacteriaceae bacterium Ellin7041
                    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                    Corynebacterineae; Mycobacteriaceae.
REFERENCE            1 (bases 1 to 423)
AUTHORS              Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE                Effects of growth medium, inoculum size, and incubation time on
                    culturability and isolation of soil bacteria
JOURNAL              Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED              15691937
REFERENCE            2 (bases 1 to 423)
AUTHORS              Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE                Direct Submission
JOURNAL              Submitted (02-JUL-2004) Department of Microbiology and Immunology,
                    University of Melbourne, Grattan Street, Parkville, Victoria 3010,
                    Australia
FEATURES             Location/Qualifiers
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                    /mol_type="genomic DNA"
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                    /isolation_source="soil"
                    /db_xref="taxon:305260"
                    <1..>423
rRNA                /product="16S ribosomal RNA"
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Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GTCGACGGAAAGCCCTTTCGG 22
Db 34 GTCGACGGAAAGCCCTTTCGG 55

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ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 423;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
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Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 57
LOCUS DQ063156 424 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063156
VERSION DQ063156.1 GI:68139194
KEYWORDS actinobacterium BAL220
SOURCE actinobacterium BAL220
ORGANISM Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 424)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences, University of Kalmar, Bärlastgatan 11, Kalmar 39231, Sweden
FEATURES
source Location/Qualifiers
1..424
/organism="actinobacterium BAL220"
/mol_type="genomic DNA"
/strain="BAL220"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St. BY31, Zobel/R2A media"
/db_xref="taxon:331797"
/country="Sweden"
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/collection_date="17 May 2004"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 18 GTCGAACGGAAGGCGCTTTCGG 39

RESULT 58
LOCUS AY673287 424 bp DNA linear BCT 20-MAY-2005
DEFINITION Streptoporangiaceae bacterium Ellin7121 16S ribosomal RNA gene, partial sequence.
ACCESSION AY673287
VERSION AY673287.1 GI:56683144
KEYWORDS Streptoporangiaceae bacterium Ellin7121
SOURCE Streptoporangiaceae bacterium Ellin7121
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptoporangineae; Streptoporangaceae.
REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on

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culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 424)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
AUTHORS Direct Submission
TITLE Submitted (02-JUL-2004) Department of Microbiology and Immunology, University of Melbourne, Grattan Street, Parkville, Victoria 3010, Australia
JOURNAL
FEATURES
source Location/Qualifiers
1..424
/organism="Streptoporangiaceae bacterium Ellin7121"
/mol_type="genomic DNA"
/isolate="Ellin7121"
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/db_xref="taxon:305348"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 34 GTCGAACGGAAGGCGCTTTCGG 55

RESULT 59
LOCUS AY756031 424 bp DNA linear BCT 08-APR-2005
DEFINITION Unidentified bacterium TMB805 16S ribosomal RNA gene, partial sequence.
ACCESSION AY756031
VERSION AY756031.1 GI:54299184
KEYWORDS Unidentified bacterium TMB805
SOURCE Unidentified bacterium TMB805
ORGANISM Bacteria.
REFERENCE 1 (bases 1 to 424)
AUTHORS Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F., Christen,R., Chevenet,F. and Heulin,T.
TITLE Diversity of Bacteria and Archae in the arid desert of Tataouine Unpublished
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 424)
AUTHORS Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F., Christen,R., Chevenet,F. and Heulin,T.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-2004) LEMIR-DSVM-DSV, CEA, Cadarache, Saint Paul Lez Durance 13108, France
FEATURES
source Location/Qualifiers
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/organism="Unidentified bacterium TMB805"
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/isolation_source="arid soil"
/db_xref="taxon:297191"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 424;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    |||||
Db 4 GTCGAACGGAAGGCGCTTTCGG 25

RESULT 60
LOCUS AY394635

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LOCUS      AY394635                425 bp    DNA        linear    ENV 20-OCT-2003
DEFINITION Uncultured Mycobacterium sp. clone W1-11 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY394635
VERSION     AY394635.1   GI:37677560
KEYWORDS   ENV.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE  1 (bases 1 to 425)
AUTHORS   Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE     Intracellular symbionts and other bacteria associated with deer
ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
Massachusetts
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 425)
AUTHORS   Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE     Direct Submission
JOURNAL   Submitted (19-SEP-2003) Molecular & Cell Biology, University of
Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
USA
FEATURES   Location/Qualifiers
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            1..425
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               /mol_type="genomic DNA"
               /specific_host="Ixodes scapularis"
               /db_xref="taxon:171292"
               /clone="W1-11"
               /environmental sample
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               Wellfleet"
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            rRNA

ORIGIN
Query Match      92.7%;   Score 20.4;   DB 1;   Length 425;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAAGGCCTTTCGG 22
    |||||
Db  34  GTCGAACGGAAAGGCCTTTCGG 55

RESULT 61
AY673136
LOCUS      AY673136                426 bp    DNA        linear    BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673136
VERSION     AY673136.1   GI:56683290
KEYWORDS
SOURCE     Mycobacteriaceae bacterium Ellin5409
ORGANISM   Mycobacteriaceae bacterium Ellin5409
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 426)
AUTHORS   Osborne,C.A. and Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (30-JUN-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES   Location/Qualifiers
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               /isolation_source="soil"
               /db_xref="taxon:305244"
               <1..>426
               /product="16S ribosomal RNA"

            rRNA

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ORIGIN
Query Match      92.7%;   Score 20.4;   DB 15;   Length 426;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAAGGCCTTTCGG 22
    |||||
Db  34  GTCGAACGGAAAGGCCTTTCGG 55

RESULT 62
AB106918
LOCUS      AB106918                428 bp    DNA        linear    BCT 09-SEP-2003
DEFINITION Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
sequence.
ACCESSION  AB106918
VERSION     AB106918.1   GI:29421132
KEYWORDS
SOURCE     Gram-positive bacterium 1-6
ORGANISM   Gram-positive bacterium 1-6
Bacteria.
REFERENCE  1
AUTHORS   Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE     Microbial participation in iodine volatilization from soils
JOURNAL   Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE  2 (bases 1 to 428)
AUTHORS   Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE     Direct Submission
JOURNAL   Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
FEATURES   Location/Qualifiers
            source
            1..428
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               /mol_type="genomic DNA"
               /strain="1-6"
               /db_xref="taxon:226200"
               <1..>428
               /product="16S ribosomal RNA"

            rRNA

ORIGIN
Query Match      92.7%;   Score 20.4;   DB 15;   Length 428;
Best Local Similarity 95.5%;   Pred. No. 1.8e+02;
Matches 21;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1  GTCGAACGGAAAGGCCTTTCGG 22
    |||||
Db  34  GTCGAACGGAAAGGCCTTTCGG 55

RESULT 63
DQ063058
LOCUS      DQ063058                428 bp    DNA        linear    BCT 27-JUN-2005
DEFINITION Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063058
VERSION     DQ063058.1   GI:68139087
KEYWORDS
SOURCE     actinobacterium BAL118
ORGANISM   actinobacterium BAL118
Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 428)
AUTHORS   Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE     Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 428)
AUTHORS   Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.

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TITLE Direct Submission  
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,  
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden

FEATURES  
source  
Location/Qualifiers  
1. 428  
/organism="actinobacterium BAL118"  
/mol\_type="genomic DNA"  
/strain="BAL118"  
/isolation\_source="Baltic Sea, 3m depth, Landsort deep St.  
BY31, Zobel1/R2A media"  
/db\_xref="taxon:331781"  
/country="Sweden"  
/lat\_lon="60.42.726N, 05.05.595E"  
/collection\_date="2 July 2003"  
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/product="16S ribosomal RNA"

rRNA  
ORIGIN  
Query Match 92.7%; Score 20.4; DB 15; Length 428;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22  
|||||  
Db 12 GTCGAACGGAAGGCGCTTCGG 33

RESULT 64  
AJ786822  
LOCUS Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.  
DEFINITION  
ACCESSION AJ786822  
VERSION  
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
SOURCE  
ORGANISM Mycobacterium sp. R-23262  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE  
AUTHORS Vanparrys B., Heylen, K., Lebbe, L., Boon, N., Wittebolle, L.,  
Verstraete, W. and De Vos, P.  
TITLE The microbial community composition of a commercial nitrifying  
inoculum  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 430)  
AUTHORS Vanparrys B.  
TITLE Direct Submission  
JOURNAL Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,  
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM

FEATURES  
source  
Location/Qualifiers  
1. 430  
/organism="Mycobacterium sp. R-23262"  
/mol\_type="genomic DNA"  
/isolate="R-23262"  
/isolation\_source="commercial nitrifying inoculum"  
/db\_xref="taxon:289008"  
/country="Belgium"  
1. 430  
/gene="16S rRNA"  
/rRNA /gene="16S rRNA"  
/product="16S ribosomal RNA"

ORIGIN  
Query Match 92.7%; Score 20.4; DB 15; Length 430;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22  
|||||  
Db 34 GTCGAACGGAAGGCGCTTCGG 55

RESULT 65  
AY673202  
LOCUS Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,  
DEFINITION partial sequence.  
ACCESSION AY673202  
VERSION  
KEYWORDS AY673202.1 GI:56683059  
SOURCE  
ORGANISM Mycobacteriaceae bacterium Ellin7036  
Mycobacteriaceae bacterium Ellin7036  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae.  
REFERENCE  
AUTHORS Davis, K.E., Joseph, S.J. and Janssen, P.H.  
TITLE Effects of growth medium, inoculum size, and incubation time on  
JOURNAL culturability and isolation of soil bacteria  
PUBMED Appl. Environ. Microbiol. 71 (2), 826-834 (2005)  
15691937  
2 (bases 1 to 430)  
REFERENCE Davis, K.E.R., Joseph, S.J. and Janssen, P.H.  
AUTHORS Direct Submission  
TITLE Submitted (02-JUL-2004) Department of Microbiology and Immunology,  
JOURNAL University of Melbourne, Grattan Street, Parkville, Victoria 3010,  
Australia

FEATURES  
source  
Location/Qualifiers  
1. 430  
/organism="Mycobacteriaceae bacterium Ellin7036"  
/mol\_type="genomic DNA"  
/isolate="Ellin7036"  
/isolation\_source="soil"  
/db\_xref="taxon:305257"  
<1..>430  
/product="16S ribosomal RNA"

rRNA  
ORIGIN  
Query Match 92.7%; Score 20.4; DB 15; Length 430;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22  
|||||  
Db 34 GTCGAACGGAAGGCGCTTCGG 55

RESULT 66  
AB106919  
LOCUS Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial  
DEFINITION sequence.  
ACCESSION AB106919  
VERSION AB106919.1 GI:29421133  
KEYWORDS  
SOURCE Gram-positive bacterium 2-1  
ORGANISM Gram-positive bacterium 2-1  
Bacteria.  
REFERENCE  
AUTHORS Anachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,  
Fujii, T. and Muramatsu, Y.  
TITLE Microbial participation in iodine volatilization from soils  
JOURNAL Environ. Sci. Technol. 37, 3885-3890 (2003)  
REFERENCE 2 (bases 1 to 431)  
AUTHORS Anachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,  
Fujii, T. and Muramatsu, Y.  
TITLE Direct Submission  
JOURNAL Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of  
Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan  
(E-mail:anachi@faculty.chiba-u.jp, Tel:81-47-308-8868,  
Fax:81-47-308-8866)

FEATURES  
source  
Location/Qualifiers  
1. 431  
/organism="Gram-positive bacterium 2-1"  
/mol\_type="genomic DNA"  
/strain="2-1"

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/db_xref="taxon:226201"
<1_>431
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 431;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 67
AF078232
LOCUS      AF078232          432 bp DNA linear ENV 10-MAY-2004
DEFINITION Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION  AF078232
VERSION     AF078232.1 GI:4590103
KEYWORDS   ENV.
SOURCE     grassland soil clone saf2_117
ORGANISM   Grassland soil clone saf2_117
REFERENCE  1 (bases 1 to 432)
AUTHORS    McCaig,A.E., Glover,L.A. and Prosser,J.I.
TITLE      Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
JOURNAL    Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED     10103273
REFERENCE  2 (bases 1 to 432)
AUTHORS    McCaig,A.E., Prosser,J.I. and Glover,L.A.
TITLE      Direct Submission
JOURNAL    Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

FEATURES   Location/Qualifiers
source     1..432
            /organism="grassland soil clone saf2_117"
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            /db_xref="taxon:80202"
            /clone_lib="unimproved grassland soil SAF2"
            /environmental_sample
            <1_>432
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 432;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 12 GTCGAACGGAAGCCCTTCGG 33

RESULT 68
AY673198
LOCUS      AY673198          433 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673198
VERSION     AY673198.1 GI:56683055
KEYWORDS   Mycobacteriaceae bacterium Ellin7032
SOURCE     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 433)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937

FEATURES   Location/Qualifiers
source     1..433
            /organism="Mycobacteriaceae bacterium Ellin7032"
            /mol_type="genomic DNA"
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            /isolation_source="soil"
            /db_xref="taxon:305283"
            <1_>433
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 70

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JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 433)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES   Location/Qualifiers
source     1..433
            /organism="Mycobacteriaceae bacterium Ellin7032"
            /mol_type="genomic DNA"
            /isolate="Ellin7032"
            /isolation_source="soil"
            /db_xref="Taxon:305255"
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            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 69
AY673266
LOCUS      AY673266          433 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673266
VERSION     AY673266.1 GI:56683123
KEYWORDS   Mycobacteriaceae bacterium Ellin7100
SOURCE     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 433)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937

FEATURES   Location/Qualifiers
source     1..433
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            /mol_type="genomic DNA"
            /isolate="Ellin7100"
            /isolation_source="soil"
            /db_xref="taxon:305283"
            <1_>433
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 433;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 70

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DQ063195
LOCUS      DQ063195          435 bp      DNA          linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063195
VERSION    DQ063195.1  GI:68139233
KEYWORDS
SOURCE     actinobacterium BAL259
ORGANISM   actinobacterium BAL259
            Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 435)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="actinobacterium BAL259"
                        /mol_type="genomic DNA"
                        /strain="BAL259"
                        /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                        BY31, Zobel1/R2A media"
                        /db_xref="taxon:331808"
                        /country="Sweden"
                        /lat_lon="60.42.726N, 05.05.595E"
                        /collection_date="17 May 2004"
                        <1..>435
                        /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCCTTCGG 22
      |||||
Db   19 GTCGAACGGAAGGCCCTTCGG 40

RESULT 71
AY234692
LOCUS      Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
DEFINITION  Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234692
VERSION    AY234692.1  GI:37961849
KEYWORDS   bacterium Ellin6040
SOURCE     bacterium Ellin6040
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE      Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL    Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED     14560368
REFERENCE  2 (bases 1 to 435)
AUTHORS    Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="bacterium Ellin6040"
                        /mol_type="genomic DNA"

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/isolate="Ellin6040"
/db_xref="taxon:234122"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCCTTCGG 22
      |||||
Db   34 GTCGAACGGAAGGCCCTTCGG 55

RESULT 72
AY673233
LOCUS      Mycobacteriaceae bacterium Ellin7067 16S ribosomal RNA gene,
            partial sequence.
DEFINITION  Mycobacteriaceae bacterium Ellin7067
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE  1 (bases 1 to 435)
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED     15691937
REFERENCE  2 (bases 1 to 435)
AUTHORS    Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE      Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES   Location/Qualifiers
            source          1..435
                        /organism="Mycobacteriaceae bacterium Ellin7067"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7067"
                        /isolation_source="soil"
                        /db_xref="taxon:305274"
                        <1..>435
                        /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 435;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCCCTTCGG 22
      |||||
Db   34 GTCGAACGGAAGGCCCTTCGG 55

RESULT 73
DQ063046
LOCUS      Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
DEFINITION  Actinobacterium BAL106
            actinobacterium BAL106
            Bacteria; Actinobacteria.
REFERENCE  1 (bases 1 to 436)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed

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by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 436)
Riemann, U., Letet, C., Pommier, T., Simu, K., Holmfeldt, K. and
Hagstrom, A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
FEATURES
    source
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            /strain="BAL106"
            /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
            BY31, Zobell/R2A media"
            /db_xref="taxon:331778"
            /country="Sweden"
            /lat_lon="60.42.726N, 05.05.595E"
            /collection_date="2 July 2003"
            <1..>436
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 436;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 23 GTCGAACGGAAGCCCTTCGG 44

RESULT 74
AY673199 436 bp DNA linear BCT 20-MAY-2005
LOCUS
DEFINITION
Mycobacteriaceae bacterium Ellin7033 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673199.1 GI:56683056
KEYWORDS
ORGANISM
Mycobacteriaceae bacterium Ellin7033
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 436)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937

REFERENCE
2 (bases 1 to 436)
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
Location/Qualifiers
FEATURES
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        1..436
            /organism="Mycobacteriaceae bacterium Ellin7033"
            /mol_type="genomic DNA"
            /isolate="Ellin7033"
            /isolation_source="soil"
            /db_xref="taxon:305288"
            <1..>436
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 436;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 75
AY673304 436 bp DNA linear BCT 20-MAY-2005
LOCUS
DEFINITION
Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673304.1 GI:56683161
KEYWORDS
ORGANISM
Mycobacteriaceae bacterium Ellin7138
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 436)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937

REFERENCE
2 (bases 1 to 436)
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
Location/Qualifiers
FEATURES
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            /organism="Mycobacteriaceae bacterium Ellin7138"
            /mol_type="genomic DNA"
            /isolate="Ellin7138"
            /isolation_source="soil"
            /db_xref="taxon:305288"
            <1..>436
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 436;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 34 GTCGAACGGAAGCCCTTCGG 55

RESULT 76
AF078419 437 bp DNA linear ENV 10-MAY-2004
LOCUS
DEFINITION
Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
sequence.
ACCESSION
AF078419.1 GI:4590290
VERSION
AF078419.1
KEYWORDS
ENV.
SOURCE
grassland soil clone sl3_612
Bacteria; environmental samples.
1 (bases 1 to 437)
McCaig, A.E., Glover, L.A. and Prosser, J.I.
Molecular analysis of bacterial community structure and diversity
in unimproved and improved upland grass pastures
Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
10103273

REFERENCE
2 (bases 1 to 437)
McCaig, A.E., Prosser, J.I. and Glover, L.A.
Direct Submission
Submitted (16-JUL-1998) Institute of Medical Sciences, Department
of Molecular and Cell Biology, University of Aberdeen,
Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
Location/Qualifiers
FEATURES
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        1..437
            /organism="grassland soil clone sl3_612"

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/mol_type="genomic DNA"
/db_xref="taxon:80115"
/clone_lib="improved grassland soil SL3"
/environmental_sample
<1..>437
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 437;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 12 GTCGAGCGGAAGGCGCTTTCGG 33

RESULT 77
AB232370          441 bp      DNA      linear      BCT 25-JAN-2006
LOCUS             Mycobacterium kansasii gene for 16S rRNA, partial sequence,
DEFINITION        strain:SA-10.
ACCESSION         AB232370
VERSION           AB232370.1 GI:73589607
KEYWORDS           .
SOURCE            Mycobacterium kansasii
ORGANISM           Mycobacterium kansasii
                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS           Iwamoto, T. and Saito, H.
TITLE             Comparative study of two typing methods, hsp65 PRA and ITS
                   sequencing, revealed a possible evolutionary link between
                   Mycobacterium kansasii type I and II isolates
JOURNAL           FEMS Microbiol. Lett. 254, 129-133 (2006)
AUTHORS           Iwamoto, T.
TITLE             (bases 1 to 441)
JOURNAL           Direct Submission
AUTHORS           Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
TITLE             Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
JOURNAL           Hyogo 6500046, Japan (E-mail: kx2t-iwmt@asahi-net.or.jp,
                   URL: http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
                   top, Tel: 81-78-302-6251, Fax: 81-78-302-0894)
FEATURES
source
   1..441
   /organism="Mycobacterium kansasii"
   /mol_type="genomic DNA"
   /strain="SA-10"
   /db_xref="taxon:1768"
   /note="type II"
   <1..>441
   /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 441;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 8 GTCGAACGGAAGGCGCTTTCGG 29

RESULT 78
AY306201          442 bp      DNA      linear      BCT 25-JUN-2003
LOCUS             Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
DEFINITION        AY306201
ACCESSION         AY306201.1 GI:32250950
KEYWORDS           .
SOURCE            Mycobacterium sp. 1351
ORGANISM           Mycobacterium sp. 1351
                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
1 (bases 1 to 442)
Pauls, R.J., Turenne, C.Y., Wolfe, J.N. and Kabani, A.
A High Proportion of Novel Mycobacteria Species Identified by 16S
rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
Clinical Setting
Unpublished
REFERENCE
2 (bases 1 to 442)
Turenne, C.Y.
Direct Submission
Submitted (26-MAY-2003) National Reference Centre for
Mycobacteriology, National Microbiology Laboratory, Health Canada,
1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES
source
   1..442
   /organism="Mycobacterium sp. 1351"
   /mol_type="genomic DNA"
   /strain="1351"
   /isolation_source="mouth ulcer"
   /specific_host="Homo sapiens"
   /db_xref="taxon:235254"
   <1..>442
   /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 442;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCGG 22
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Db 8 GTCGAACGGAAGGCGCTTTCGG 29

RESULT 79
AY306205          444 bp      DNA      linear      BCT 25-JUN-2003
LOCUS             Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
DEFINITION        AY306205
ACCESSION         AY306205.1 GI:32250954
KEYWORDS           .
SOURCE            Mycobacterium sp. HSC507
ORGANISM           Mycobacterium sp. HSC507
                   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                   Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS           Pauls, R.J., Turenne, C.Y., Wolfe, J.N. and Kabani, A.
TITLE             A High Proportion of Novel Mycobacteria Species Identified by 16S
                   rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
                   Clinical Setting
Unpublished
REFERENCE
2 (bases 1 to 444)
Turenne, C.Y.
Direct Submission
Submitted (26-MAY-2003) National Reference Centre for
Mycobacteriology, National Microbiology Laboratory, Health Canada,
1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
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   /specific_host="Homo sapiens"
   /db_xref="taxon:235258"
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   /product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GTCGAACGGAAGGCCCTTTCGG 22  
|||||  
Db 8 GTCGAACGGAAGGCCCTTTCGG 29

RESULT 80  
AB106917 445 bp DNA linear BCT 09-SEP-2003  
LOCUS Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial  
DEFINITION sequence.  
ACCESSION AB106917  
VERSION AB106917.1 GI:29421131  
KEYWORDS Gram-positive bacterium 1-3  
SOURCE Gram-positive bacterium 1-3  
ORGANISM Bacteria.  
REFERENCE 1  
AUTHORS Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,  
Fujii,T. and Muramatsu,Y.  
TITLE Microbial participation in iodine volatilization from soils  
JOURNAL Environ. Sci. Technol. 37, 3885-3890 (2003)  
REFERENCE 2  
AUTHORS Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,  
Fujii,T. and Muramatsu,Y.  
TITLE Direct Submission  
JOURNAL Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of  
Bioresources Chem.: 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan  
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,  
Fax:81-47-308-8866)  
FEATURES  
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1. .445  
/organism="Gram-positive bacterium 1-3"  
/mol\_type="genomic DNA"  
/strain="1-3"  
/db\_xref="taxon:226199"  
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/product="16S ribosomal RNA"

rRNA

ORIGIN  
Query Match 92.7%; Score 20.4; DB 15; Length 445;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCGG 22  
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Db 34 GTCGAACGGAAGGCCCTTTCGG 55

RESULT 81  
DQ067466 445 bp DNA linear BCT 18-JUL-2005  
LOCUS Mycobacterium sp. F105167 16S ribosomal RNA gene, partial sequence.  
DEFINITION DQ067466  
ACCESSION DQ067466  
VERSION DQ067466.1 GI:67528039  
KEYWORDS Unusual mycobacteria isolated from clinical samples  
SOURCE Mycobacterium sp. F105167  
ORGANISM Mycobacterium sp. F105167  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Unpublished  
JOURNAL Unusual mycobacteria isolated from clinical samples  
REFERENCE 2  
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,  
Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le  
Morgagni 85, Firenze, FI 50134, Italy  
FEATURES  
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/organism="Mycobacterium sp. F105167"  
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rRNA

ORIGIN  
Query Match 92.7%; Score 20.4; DB 15; Length 445;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCGG 22  
|||||  
Db 12 GTCGAACGGAAGGCCCTTTCGG 33

RESULT 82  
AY957708 447 bp DNA linear ENV 16-SEP-2005  
LOCUS Uncultured bacterium clone P3DKE08 16S small subunit ribosomal RNA  
DEFINITION gene, partial sequence.  
ACCESSION AY957708  
VERSION AY957708.1 GI:62005486  
KEYWORDS ENV.  
SOURCE uncultured bacterium  
ORGANISM uncultured bacterium  
Bacteria; environmental samples.  
REFERENCE 1  
AUTHORS McManus,C.J. and Kelley,S.T.  
TITLE Molecular survey of aeroplane bacterial contamination  
JOURNAL J. Appl. Microbiol. 99 (3), 502-508 (2005)  
REFERENCE 2  
AUTHORS McManus,C.J. and Kelley,S.T.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2005) Biology, San Diego State University, 5500  
Campanile Dr., San Diego, CA 92182, USA  
FEATURES  
source Location/Qualifiers  
1. .447  
/organism="uncultured bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="airplane"  
/db\_xref="taxon:77133"  
/clone="P3DKE08"  
/environmental\_sample  
<1..>447  
/product="16S small subunit ribosomal RNA"

rRNA

ORIGIN  
Query Match 92.7%; Score 20.4; DB 1; Length 447;  
Best Local Similarity 95.5%; Pred. No. 1.8e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTCGG 22  
|||||  
Db 2 GTCGAACGGAAGGCCCTTTCGG 23

RESULT 83  
MS91016SR 450 bp DNA linear BCT 01-AUG-1997  
LOCUS Mycobacterium sp.16S rRNA gene, isolate BN910, partial.  
DEFINITION Y08205  
ACCESSION Y08205.1 GI:2292948  
KEYWORDS 16S ribosomal RNA; 16S rRNA.  
SOURCE Mycobacterium sp.  
ORGANISM Mycobacterium sp.  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1  
AUTHORS Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and  
Schulze-Roebecke,R.  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 450)

```

AUTHORS      Hagenau,C.
TITLE        Direct Submission
JOURNAL      Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University
              of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT      Related sequence M95469
FEATURES     Location/Qualifiers
              source
                1..450
                /organism="Mycobacterium sp."
                /mol_type="genomic DNA"
                /isolate="BN910"
                /db_xref="taxon:1785"
                /map="E.coli position 38-503"
              gene
                1..450
                /gene="16S rRNA"
              rRNA
                <1..>450
                /gene="16S rRNA"
                /product="16S ribosomal RNA"

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 450;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
    |||||
Db 24 GTCGAACGGAAGGCGCTTCGG 45

RESULT 84
MSPI6SR          MSP16SR          450 bp      DNA      linear      BCT 01-AUG-1997
LOCUS            Mycobacterium sp. 16S rRNA gene.
DEFINITION       Y07954
ACCESSION        Y07954
VERSION          Y07954.1 GI:2292951
KEYWORDS         16S ribosomal RNA; 16S rRNA gene.
SOURCE           Mycobacterium sp.
ORGANISM         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE        1 Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and
                  Schulze-Roebecke,R.
JOURNAL          Unpublished
REFERENCE        2 (bases 1 to 450)
AUTHORS          Hagenau,C.
TITLE            Direct Submission
JOURNAL          Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University
                  of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG
COMMENT          Related sequence: M95469.
FEATURES         Location/Qualifiers
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                    /map="E.coli 38-503"
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                    1..450
                    /gene="16S rRNA"
                  rRNA
                    <1..>450
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                    /product="16S ribosomal RNA"

ORIGIN
Query Match      92.7%; Score 20.4; DB 15; Length 450;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
    |||||
Db 24 GTCGAACGGAAGGCGCTTCGG 45

RESULT 85
MSPI6SR          MSP16SR          450 bp      DNA      linear      BCT 19-AUG-2005
LOCUS            Actinobacterium irIII7 16S ribosomal RNA gene, partial sequence.
DEFINITION       AV358002
ACCESSION        AV358002
VERSION          AV358002.1 GI:34500643
KEYWORDS         actinobacterium irIII7
SOURCE           actinobacterium irIII7
ORGANISM         Bacteria; Actinobacteria.
REFERENCE        1 (bases 1 to 450)
AUTHORS          Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
                  Sessitsch,A.
TITLE            Bacterial Communities Associated with Flowering Plants of the Ni
                  Hyperaccumulator Thlaspi goesingense
JOURNAL          Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED          15128517
REFERENCE        2 (bases 1 to 450)
AUTHORS          Idris,R. and Sessitsch,A.
TITLE            Direct Submission
JOURNAL          Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
                  Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES         Location/Qualifiers
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                    1..450
                    /organism="actinobacterium irIII7"
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                    /strain="irIII7"
                    /db_xref="taxon:244182"
                    <1..>450
                    /product="16S ribosomal RNA"
                  rRNA
                    <1..>450
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Query Match      92.7%; Score 20.4; DB 15; Length 450;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTCGG 22
    |||||
Db 56 GTCGAACGGAAGGCGCTTCGG 77

RESULT 86
AJ746062          MYCOBACTERIUM SP. MG5 PARTIAL 16S rRNA gene, isolate MGS.
LOCUS            Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MGS.
DEFINITION       AJ746062
ACCESSION        AJ746062
VERSION          AJ746062.1 GI:61097518
KEYWORDS         16S ribosomal RNA; 16S rRNA gene.
SOURCE           Mycobacterium sp. MG5
ORGANISM         Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                  Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE        1 Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
                  and Lalucat,J.
TITLE            Identification of culturable bacteria present in haemodialysis
                  water and fluid
JOURNAL          FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
REFERENCE        2 (bases 1 to 454)
AUTHORS          Gomila,M.
TITLE            Direct Submission
JOURNAL          Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia,
                  Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
                  Palma de Mallorca, SPAIN
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                    /country="Spain:Mallorca"
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/gene="16S rRNA"
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ORIGIN
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
    |||||
Db 27 GTCGAACGGAAAGCCCTTCGG 48

RESULT 87
LOCUS AY358001 456 bp DNA linear BCT 19-AUG-2005
DEFINITION Actinobacterium iriII6 16S ribosomal RNA gene, partial sequence.
ACCESSION AY358001
VERSION AY358001.1 GI:34500642
SOURCE actinobacterium iriII6
ORGANISM actinobacterium iriII6
REFERENCE 1 (bases 1 to 456)
AUTHORS Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and Sessitsch,A.
TITLE Bacterial Communities Associated with Flowering Plants of the Ni
JOURNAL Hyperaccumulator Thlaspi goesingense
PUBMED Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
REFERENCE 2 (bases 1 to 456)
AUTHORS Idris,R. and Sessitsch,A.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES
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/organism="actinobacterium iriII6"
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rRNA
<1..>456
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ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 456;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
    |||||
Db 56 GTCGAACGGAAAGCCCTTCGG 77

RESULT 88
LOCUS AJ609008 459 bp DNA linear ENV 20-JAN-2004
DEFINITION Uncultured bacterium partial 16S rRNA gene, clone 24-9.
ACCESSION AJ609008
VERSION AJ609008.1 GI:41033549
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
REFERENCE 1
AUTHORS Schneider,B.A., Huettli,R.F. and Schneider,B.U.
TITLE Evidence for a diverse bacterial consortium specialized to the
degradation of aliphatic and aromatic hydrocarbons in lignite
matter of a forest reclamation site
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)

AUTHORS Schneider,B.A.
Direct Submission
Submitted (20-NOV-2003) Schneider B.A., Soil Protection and
Recultivation, Brandenburg Technical University,
Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY
FEATURES
source 1..459
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolation_source="lignite matter from the subsurface soil
of a 20 year old Black pine forest"
/db_xref="taxon:77133"
/clone="24-9"
/environmental_sample
/country="Germany:North-eastern Germany, Lusatian lignite
mining area"
1..459
/gene="16S rRNA"
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/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 1; Length 459;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
    |||||
Db 12 GTCGAACGGTAAGCCCTTCGG 33

RESULT 89
LOCUS AY754884 459 bp DNA linear BCT 17-OCT-2004
DEFINITION Mycobacterium vaccae strain FI04098 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY754884
VERSION AY754884.1 GI:54065968
KEYWORDS Mycobacterium vaccae
SOURCE Mycobacterium vaccae
ORGANISM Mycobacterium vaccae
REFERENCE 1 (bases 1 to 459)
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 459)
AUTHORS Tortoli,E.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
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/organism="Mycobacterium vaccae"
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rRNA
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/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 459;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22
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Db 28 GTCGAACGGAAAGCCCTTCGG 49

RESULT 90

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AY754885
LOCUS AY754885 459 bp DNA linear BCT 17-OCT-2004
DEFINITION Mycobacterium sp. FI02139 16S ribosomal RNA gene, partial sequence.
ACCESSION AY754885
VERSION AY754885.1 GI:54065976
KEYWORDS
SOURCE Mycobacterium sp. FI02139
ORGANISM Mycobacterium sp. FI02139
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 459)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
AUTHORS Tortoli,E.
TITLE Direct Submission
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
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Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 27 GTCGAACGGAAGGCGCTTCGG 48
|||||

RESULT 91
AB118817
LOCUS AB118817 464 bp DNA linear BCT 01-JUN-2005
DEFINITION Denitrifying bacterium W67a gene for 16S ribosomal RNA, partial
sequence.
ACCESSION AB118817
VERSION AB118817.1 GI:66841148
KEYWORDS denitrifying bacterium W67a
SOURCE denitrifying bacterium W67a
ORGANISM Bacteria; Actinobacteria.
REFERENCE
1 Hashimoto,T., Whang,K.S. and Nagaoka,K.
A Quantitative Evaluation and Phylogenetic Characterization of
Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland
Soil Using Improved Culturability
JOURNAL Biol. Fertil. Soils (2005) In press
REFERENCE
2 (bases 1 to 464)
Hashimoto,T. and Whang,K.
Direct Submission
JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural
Research Center for Kyushu Okinawa Region, Department of
Agro-Environmental Research; Nishigoushi-cho Suya 2421,
Kikuchi-gun, Kumamoto, 861-1192, Japan
(E-mail:hashimoto@affrc.go.jp, Tel:0962427765, Fax:0962491002)
FEATURES
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1..464
/organism="denitrifying bacterium W67a"
/mol_type="genomic DNA"
/isolate="W67a"
/db_xref="taxon:245681"
/country="Japan"
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/product="16S ribosomal RNA"
rRNA
1..464
ORIGIN

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Query Match 92.7%; Score 20.4; DB 15; Length 464;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 50 GTCGAACGGAAGGCGCTTCGG 71
|||||

RESULT 92
DQ142669
LOCUS DQ142669 464 bp DNA linear BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI03023 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ142669
VERSION DQ142669.1 GI:71912648
KEYWORDS
SOURCE Mycobacterium sp. FI03023
ORGANISM Mycobacterium sp. FI03023
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 464)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-2005) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1..464
/organism="Mycobacterium sp. FI03023"
/mol_type="genomic DNA"
/strain="FI03023"
/db_xref="taxon:339672"
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/product="16S ribosomal RNA"
rRNA
1..464
ORIGIN
Query Match 92.7%; Score 20.4; DB 15; Length 464;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCGCTTCGG 22
|||||
Db 27 GTCGAACGGAAGGCGCTTCGG 48
|||||

RESULT 93
DQ142672
LOCUS DQ142672 464 bp DNA linear BCT 13-AUG-2005
DEFINITION Mycobacterium sp. FI05244 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ142672
VERSION DQ142672.1 GI:71912651
KEYWORDS
SOURCE Mycobacterium sp. FI05244
ORGANISM Mycobacterium sp. FI05244
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
1 (bases 1 to 464)
Tortoli,E., Mariottini,A. and Mazzarelli,G.
Unusual mycobacteria isolated from clinical specimens
JOURNAL Unpublished
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2005) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
FEATURES
source
1..464
/organism="Mycobacterium sp. FI05244"
/mol_type="genomic DNA"

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/strain="FI05244"
/db_xref="taxon:339674"
<1_>464
/product="16S ribosomal RNA"

ORIGIN
Query Match          92.7%; Score 20.4; DB 15; Length 464;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1  GTCGAACGGAAGCCCTTCGG 22
    |||||
Db 27 GTCGAACGGAAGCCCTTCGG 48

RESULT 94
LOCUS DQ067465 466 bp DNA linear BCT 05-JAN-2006
DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ067465
VERSION DQ067465.1 GI:67528030
KEYWORDS
SOURCE Mycobacterium sp. FI05038
ORGANISM Mycobacterium sp. FI05038
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Tortoli,E., Mantella,A., Mariottini,A., Mazzarelli,G., Pecile,P.,
Rogaii,P.G., Sterrantino,G., Fantoni,E. and Leoncini,F.
TITLE Successfully treated spindylodiscitis due to a previously
unreported mycobacterium
JOURNAL J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
PUBMED 1638040
REFERENCE
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Direct Submission
JOURNAL Submitted (18-MAY-2005) Reg. Reference Center for Mycobacterias,
Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
Morgagni 85, Firenze, FI 50134, Italy

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DEFINITION Mycobacterium sp. FI02027 16S ribosomal RNA gene, partial sequence.
ACCESSION AY524839
VERSION AY524839.1 GI:41387175
KEYWORDS
SOURCE Mycobacterium sp. FI02027
ORGANISM Mycobacterium sp. FI02027
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE
AUTHORS Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE Unusual mycobacteria isolated from clinical samples
JOURNAL Unpublished
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2 (bases 1 to 466)
Tortoli,E.
Direct Submission
Submitted (08-JAN-2004) Microbiology, Careggi Hospital, viale
Morgagni 85, Firenze, FI 50134, Italy
JOURNAL Location/Qualifiers
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RESULT 96
LOCUS DQ154332 468 bp DNA linear BCT 27-AUG-2005
DEFINITION Soil bacterium RFS-II28 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ154332
VERSION DQ154332.1 GI:73672122
KEYWORDS
SOURCE soil bacterium RFS-II28
ORGANISM soil bacterium RFS-II28
Bacteria.
REFERENCE
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Low nutrient fluxes result in high cultivation efficiencies of soil
bacteria
JOURNAL Unpublished
REFERENCE
AUTHORS Becker,J.M., Nakatsu,C.H., Turco,R.F. and Konopka,A.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2005) Biological Sciences, Purdue University, 915
West State Street, West Lafayette, IN 47907-2054, USA

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Db 23 GTCGAACGGAAGCCCTTCGG 44

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LOCUS AY043719 473 bp DNA linear ENV 05-MAY-2004
DEFINITION Uncultured actinobacterium clone NOW2.35WL 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY043719
VERSION AY043719.1 GI:22267092
KEYWORDS ENV.
SOURCE uncultured actinobacterium
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ORGANISM uncultured actinobacterium
REFERENCE Bacteria; Actinobacteria; environmental samples.
AUTHORS Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and Davies, J.
TITLE Molecular characterization of bacterial diversity from British Columbia forest soils subjected to disturbance
JOURNAL Can. J. Microbiol. 48 (7), 655-674 (2002)
PUBMED 12224564
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall, Vancouver, BC V6S 2L2, Canada
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DEFINITION Uncultured bacterium clone SC27 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ136108
VERSION DQ136108.1 GI:71905197
KEYWORDS ENV, uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
AUTHORS Microbiological remediation studies on diesel-contaminated soil of Baekun Mountain
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 474)
AUTHORS Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Sillimdong Kwanakgu 151-921, Korea
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KEYWORDS ENV, uncultured bacterium
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
AUTHORS Microbiological remediation studies on diesel-contaminated soil of Baekun Mountain
TITLE Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 474)
AUTHORS Ka, J.-O., Kim, M.-S. and Ahn, J.-H.
TITLE Direct Submission
JOURNAL Submitted (19-JUL-2005) School of Applied Biology and Chemistry, Seoul National University, San 56-1 Sillimdong Kwanakgu 151-921, Korea
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Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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LOCUS AY559492 476 bp DNA linear BCT 22-MAR-2004
DEFINITION Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial sequence.
ACCESSION AY559492
VERSION AY559492.1 GI:45511545
KEYWORDS Mycobacterium porcinum
SOURCE Mycobacterium porcinum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 476)
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Characterization of various plant growth-promoting bacteria
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 476)
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada
FEATURES
    Location/Qualifiers

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Query Match 92.7%; Score 20.4; DB 1; Length 474;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Mycobacterium sp. 6BR15 16S ribosomal RNA gene, partial sequence.
ACCESSION AY792024
VERSION AY792024.1 GI:55740323
KEYWORDS Mycobacterium sp. 6BR15
SOURCE Mycobacterium sp. 6BR15
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 474)
AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 474)
AUTHORS Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales, Escuela Tecnica Superior de Ingenieros Industriales, Universidad Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid 28006, Spain
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DEFINITION Mycobacterium porcinum strain M552 16S ribosomal RNA gene, partial sequence.
ACCESSION AY559492
VERSION AY559492.1 GI:45511545
KEYWORDS Mycobacterium porcinum
SOURCE Mycobacterium porcinum
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 476)
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Characterization of various plant growth-promoting bacteria
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 476)
AUTHORS Hontzeas, N., Belimov, A., Safronova, V. and Glick, B.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Biology, University of Waterloo, 200 University Ave. West, Waterloo, ON N2L 3G1, Canada
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

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9: gb\_un.\*  
10: gb\_vi.\*  
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13: gb\_in.\*  
14: gb\_om.\*  
15: gb\_ba.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	20.4	92.7	1456	15	MGAD16S
9	20.4	92.7	1459	15	MC016S
10	20.4	92.7	1467	15	AB006161
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14	19.4	88.2	177016	6	AC015658
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24	18.8	85.5	424	15	AY756031	Unidentif
25	18.8	85.5	661	1	AY095406	Unculture
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105	18.8	85.5	1445	15	AF163123	AF163123 Spirillos	178	17.4	79.1	985	1	DQ200423
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107	18.8	85.5	1448	15	AYU293714	AY293714 Actinomadr	180	17.4	79.1	12945	15	AE009898
108	18.8	85.5	1450	15	AF163114	AF163114 Actinomadr	c 181	17.4	79.1	60361	15	AE015928_62
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115	18.8	85.5	1466	15	ABO06167	ABO06167 Virgospo	188	17.4	79.1	173518	6	AL772358
116	18.8	85.5	1466	15	AF163116	AF163116 Actinomadr	189	17.4	79.1	181132	13	AC008206
117	18.8	85.5	1470	15	D85479	D85479 Couchioplan	190	17.4	79.1	227219	13	AE003750
118	18.8	85.5	1474	15	MFL276274	AY276274 Mycobacte	191	17.2	78.2	425	15	AY673249
119	18.8	85.5	1510	15	ALO293707	AY293707 Actinomadr	192	17.2	78.2	569	2	QO99662
120	18.8	85.5	1513	15	AFO293703	AY293703 Actinomadr	193	17.2	78.2	569	2	CQ138647
121	18.8	85.5	1516	15	AHI293705	AY293705 Actinomadr	194	17.2	78.2	569	2	CQ175449
122	18.8	85.5	1521	15	AOL293709	AY293709 Actinomadr	195	17.2	78.2	569	2	CQ222062
123	18.8	85.5	14453	15	AE013036	AE013036 Methanopy	196	17.2	78.2	569	2	CQ260007
124	18.8	85.5	110000	4	CR382130_25	Continuation (26 o	197	17.2	78.2	569	2	CQ297766
125	18.8	85.5	110000	4	CR382130_26	Continuation (27 o	198	17.2	78.2	569	2	CQ334130
126	18.4	83.6	181705	5	AC144400	AC144400 Lemur cat	199	17.2	78.2	836	15	AF131299
127	18	81.8	3024	2	BD180343	BD180343 Highly th	200	17.2	78.2	836	15	AF131332
128	18	81.8	110000	15	AE017221_05	Continuation (6 of	201	17.2	78.2	1154	4	AK119939
129	18	81.8	110000	15	AP008226_08	Continuation (9 of	202	17.2	78.2	1355	15	MSGRR16SA
130	17.8	80.9	277	15	AF504932	AF504932 Mycobacte	203	17.2	78.2	1409	15	AAU49000
131	17.8	80.9	352	13	DME303156	AJ303156 Drosophil	204	17.2	78.2	1484	15	GA16SRR
132	17.8	80.9	431	1	UEU232874	AJ232874 Unidentif	205	17.2	78.2	1504	15	PAAJ3055
133	17.8	80.9	467	1	AY186868	AY186868 Unculture	206	17.2	78.2	2268	6	MUSZFPB3
134	17.8	80.9	467	15	AM113987	AM113987 Mycobacte	207	17.2	78.2	2342	6	MMZFP35
135	17.8	80.9	487	5	AB076381	AB076381 Homo sapi	208	17.2	78.2	2807	6	BC089850
136	17.8	80.9	487	5	HSPBR2	L21952 Human perip	209	17.2	78.2	5091	6	BC027782
137	17.8	80.9	495	15	MSF458957	AY358957 Mycobacte	210	17.2	78.2	9693	6	AF092536
138	17.8	80.9	501	1	AY037720	AY037720 Unculture	c 211	17.2	78.2	35641	12	AC014835
139	17.8	80.9	502	15	AY215241	AY215241 Mycobacte	212	17.2	78.2	58822	2	AX695431
140	17.8	80.9	502	15	AY215362	AY215362 Mycobacte	c 213	17.2	78.2	59726	5	AL133354
141	17.8	80.9	503	15	AY215329	AY215329 Mycobacte	c 214	17.2	78.2	107066	12	AC138264
142	17.8	80.9	504	15	AY215347	AY215347 Mycobacte	c 215	17.2	78.2	110000	4	AP007157_00
143	17.8	80.9	513	2	AR503310	AR503310 Sequence	216	17.2	78.2	110000	4	AP007169_01
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145	17.8	80.9	515	15	AY215363	AY215363 Mycobacte	c 218	17.2	78.2	110000	15	AY596297_02
146	17.8	80.9	516	15	AY215282	AY215282 Mycobacte	c 219	17.2	78.2	124230	12	AC005259
147	17.8	80.9	516	15	AY215357	AY215357 Mycobacte	c 220	17.2	78.2	152209	16	AL591023
148	17.8	80.9	517	15	AY215358	AY215358 Mycobacte	c 221	17.2	78.2	162877	5	AC018509
149	17.8	80.9	542	15	AY438070	AY438070 Mycobacte	c 222	17.2	78.2	164194	12	CT025629
150	17.8	80.9	682	13	AY095073	AY095073 Drosophil	c 223	17.2	78.2	165439	13	AC008215
151	17.8	80.9	775	1	AY197796	AY197796 Unculture	c 224	17.2	78.2	170403	13	AC008214
152	17.8	80.9	1022	1	DQ165139	DQ165139 Unculture	225	17.2	78.2	176395	13	AC007928
153	17.8	80.9	1373	1	AY922013	AY922013 Unculture	c 226	17.2	78.2	182126	12	AC128821
154	17.8	80.9	1376	1	AY921952	AY921952 Unculture	c 227	17.2	78.2	183330	5	AC011372
155	17.8	80.9	1408	6	BC029736	BC029736 Mus muscu	c 228	17.2	78.2	190349	5	AC009475
156	17.8	80.9	1443	6	BC069938	BC069938 Mus muscu	c 229	17.2	78.2	191834	13	AE003757
157	17.8	80.9	1449	15	MCR02416S	X93031 Mycobacteri	c 230	17.2	78.2	193456	12	AC112410
158	17.8	80.9	1470	15	AF260434	AF260434 Corynebac	231	17.2	78.2	201092	6	AC099614
159	17.8	80.9	1490	15	MSU65104	U65104 Mycobacteri	c 232	17.2	78.2	201732	12	AC125483
160	17.8	80.9	1511	15	AF262996	AF262996 Corynebac	233	17.2	78.2	204317	12	AC119659
161	17.8	80.9	1519	15	AF162028	AF162028 Mycobacte	234	17.2	78.2	205812	12	AC141146
162	17.8	80.9	1526	15	MHO310467	AJ310467 Mycobacte	235	17.2	78.2	208030	6	AL672276
163	17.8	80.9	13942	5	AY383615	AY383615 Homo sapi	c 236	17.2	78.2	210568	6	AC154426
164	17.8	80.9	14660	12	AC014636	AC014636 Drosophil	c 237	17.2	78.2	216124	6	AC124139

CP000182 Drosophil	
AC163823 Bos tauru	
AC151463 Xenopus t	
Continuation (5 of	
282214 Human DNA s	
DQ200500 Unculture	
DQ200437 Unculture	
DQ200486 Unculture	
DQ200536 Unculture	
DQ200475 Unculture	
DQ200545 Unculture	
DQ200537 Unculture	
DQ200469 Unculture	
DQ200423 Unculture	
AR227358 Sequence	
AE009898 Pyrobacul	
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AC139694 Homo sapi	
AL591509 Human DNA	
AE015924 Porphyrom	
AC013932 Drosophil	
AC007853 Drosophil	
AC023475 Homo sapi	
AL772358 Mouse DNA	
AC008206 Drosophil	
AE003750 Drosophil	
AY673249 Mycobacte	
QO99662 Sequence	
CQ138647 Sequence	
CQ175449 Sequence	
CQ222062 Sequence	
CQ260007 Sequence	
CQ297766 Sequence	
CQ334130 Sequence	
AF131299 Actinomadr	
AF131332 Actinomadr	
AK119939 Oryza sat	
M29554 Mycobacteri	
AY9000 Actinomadr	
X86635 Gordonia am	
AJ003055 Propionib	
M36146 Mouse zinc	
X17617 Mouse zfp-3	
BC089850 Rattus no	
BC027782 Mus muscu	
AF092536 Mus muscu	
AC014835 Drosophil	
AX695431 Sequence	
AL133354 Human DNA	
AP007157 Aspergill	
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Continuation (3 of	
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AL591023 Homo sapi	
AC018509 Homo sapi	
CT025629 Mus muscu	
AC008215 Drosophil	
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AC007928 Drosophil	
AC128821 Rattus no	
AC011372 Homo sapi	
AC009475 Homo sapi	
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AC112410 Rattus no	
AC099614 Mus muscu	
AC125483 Mus muscu	
AC119659 Rattus no	
AC141146 Rattus no	
AL672276 Mouse DNA	
AC154426 Mus muscu	
AC124139 Mus muscu	

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c 241	17.2	78.2	222189	12	AC125697	AC125697 Rattus no
c 242	17.2	78.2	224786	12	AC118501	AC118501 Rattus no
c 243	17.2	78.2	227119	12	AC017740	AC017740 Drosophila
c 244	17.2	78.2	237705	12	AC171299	AC171299 Bos taurus
c 245	17.2	78.2	238286	12	AC109400	AC109400 Rattus no
c 246	17.2	78.2	242303	12	AC164888	AC164888 Bos taurus
c 247	17.2	78.2	244566	6	AC126807	AC126807 Mus muscu
c 248	17.2	78.2	250597	12	AC097118	AC097118 Rattus no
c 249	17.2	78.2	254111	12	AC111645	AC111645 Rattus no
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c 252	17.2	78.2	286957	12	AC131144	AC131144 Rattus no
c 253	17.2	78.2	298575	12	HSBA2284	AC080244 Homo sapi
c 254	17.2	78.2	318505	12	AC123174	AC123174 Rattus no
c 255	17.2	78.2	341469	12	AC111349	AC111349 Rattus no
c 256	17	77.3	80640	12	AM050693	AM050693 Triticum
c 257	17	77.3	254496	12	AC109857	AC109857 Rattus no
c 258	16.8	76.4	613	7	BV064643	BV064643 S212P6046
c 259	16.8	76.4	613	7	BV413737	BV413737 S229P6267
c 260	16.8	76.4	679	4	AY375496	AY375496 Protium t
c 261	16.8	76.4	679	4	AY375519	AY375519 Protium s
c 262	16.8	76.4	850	7	BV029782	BV029782 S212P6015
c 263	16.8	76.4	874	4	AF382374	AF382374 Seimatosp
c 264	16.8	76.4	2220	4	DQ008835	DQ008835 Pinus sp.
c 265	16.8	76.4	2666	15	PT173BHYD	X63379 P.testoster
c 266	16.8	76.4	5444	4	AY354948	AY354948 Marattia
c 267	16.8	76.4	5509	4	AY354947	AY354947 Angiopter
c 268	16.8	76.4	7446	4	AY354940	AY354940 Equisetum
c 269	16.8	76.4	107166	12	AC080120	AC080120 Homo sapi
c 270	16.8	76.4	110000	15	AE017345	Continuation (11 o
c 271	16.8	76.4	110000	15	AE016958	Continuation (36 o
c 272	16.8	76.4	141299	12	AC132080	AC132080 Felis cat
c 273	16.8	76.4	145620	12	AC107324	AC107324 Felis cat
c 274	16.8	76.4	147401	12	AC067778	AC067778 Homo sapi
c 275	16.8	76.4	148345	5	AL592151	AL592151 Human DNA
c 276	16.8	76.4	152161	12	AC139975	AC139975 Rattus no
c 277	16.8	76.4	154691	12	AC142054	AC142054 Rattus no
c 278	16.8	76.4	161198	5	AC069120	AC069120 Homo sapi
c 279	16.8	76.4	164741	12	AC027278	AC027278 Mus muscu
c 280	16.8	76.4	166011	12	AC019307	AC019307 Homo sapi
c 281	16.8	76.4	171378	12	AC151303	AC151303 Xenopus t
c 282	16.8	76.4	192812	12	AC179561	AC179561 Strongylo
c 283	16.8	76.4	193286	12	AC110119	AC110119 Rattus no
c 284	16.8	76.4	199704	6	AC020968	AC020968 Mus muscu
c 285	16.8	76.4	202441	6	AL683879	AL683879 Mouse DNA
c 286	16.8	76.4	204237	12	AC145179	AC145179 Gallus ga
c 287	16.8	76.4	204287	6	AC126442	AC126442 Mus muscu
c 288	16.8	76.4	214960	12	AC142361	AC142361 Rattus no
c 289	16.8	76.4	218905	6	AC087772	AC087772 Genomic S
c 290	16.8	76.4	220893	12	AC106234	AC106234 Rattus no
c 291	16.8	76.4	231736	12	AC117323	AC117323 Rattus no
c 292	16.8	76.4	231896	6	AC115116	AC115116 Mus muscu
c 293	16.8	76.4	233440	12	AC094560	AC094560 Rattus no
c 294	16.8	76.4	233905	12	AC131518	AC131518 Rattus no
c 295	16.8	76.4	240987	12	AC104055	AC104055 Rattus no
c 296	16.8	76.4	242531	6	AC108805	AC108805 Mus muscu
c 297	16.8	76.4	249571	6	AC152418	AC152418 Mus muscu
c 298	16.8	76.4	258207	12	AC115279	AC115279 Rattus no
c 299	16.8	76.4	261093	6	AC027740	AC027740 Mus muscu
c 300	16.8	76.4	285739	12	AC164385	AC164385 Bos taurus

ALIGNMENTS

RESULT 1						
AR438657	AR438657	Sequence 25 from patent US 6664081.	22 bp	DNA	linear	PAT 20-FEB-2004
LOCUS	AR438657					
DEFINITION	Sequence 25 from patent US 6664081.					
ACCESSION	AR438657					

VERSION	AR438657.1	GI:42663581				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 22)					
AUTHORS	Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodrigue, M.					
TITLE	Nucleic acid amplification and detection of mycobacterium species					
JOURNAL	Patent, US 6664081-A 25 16-DEC-2003;					
FEATURES	Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA					
source	Location/Qualifiers					
ORIGIN	1..22					
Query Match	100.0%;	Score 22;	DB 2;	Length 22;		
Best Local Similarity	100.0%;	Pred. No. 42;				
Matches	22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	GAAGGCGCTTTCGGGGTGCTC	22			
Db	1	GAAGGCGCTTTCGGGGTGCTC	22			
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AX166859	AX166859	22 bp	DNA	linear		PAT 04-JUL-2001
LOCUS	Sequence 25 from Patent WO0144510.					
DEFINITION	AX166859					
ACCESSION	AX166859					
VERSION	AX166859.1	GI:14596462				
KEYWORDS	synthetic construct					
SOURCE	other sequences; artificial sequences.					
ORGANISM	other sequences; artificial sequences.					
REFERENCE	1					
AUTHORS	Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodrigue, M.					
TITLE	Nucleic acid amplification and detection of mycobacterium species					
JOURNAL	Patent: WO 0144510-A 25 21-JUN-2001;					
FEATURES	Gen-Probe Incorporated (US); Biomerieux S.A. (FR)					
source	Location/Qualifiers					
ORIGIN	1..22					
Query Match	100.0%;	Score 22;	DB 2;	Length 22;		
Best Local Similarity	100.0%;	Pred. No. 42;				
Matches	22;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1	GAAGGCGCTTTCGGGGTGCTC	22			
Db	1	GAAGGCGCTTTCGGGGTGCTC	22			
RESULT 3						
AR438658	AR438658	Sequence 26 from patent US 6664081.	25 bp	DNA	linear	PAT 20-FEB-2004
LOCUS	Sequence 26 from patent US 6664081.					
DEFINITION	AR438658					
ACCESSION	AR438658					
VERSION	AR438658.1	GI:42663582				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 25)					
AUTHORS	Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and Rodrigue, M.					
TITLE	Nucleic acid amplification and detection of mycobacterium species					

JOURNAL Patent: US 6664081-A 26 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
source Location/Qualifiers  
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/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22  
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Db 1 GAAAGGCTTTTCGGGGGTGCTC 22

RESULT 4  
AX166860  
LOCUS AX166860 25 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 26 from Patent WO0144510.  
ACCESSION AX166860  
VERSION AX166860.1 GI:14596463  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 26 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 22; DB 2; Length 25;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGGCTTTTCGGGGGTGCTC 22

RESULT 5  
MSGRGDSA  
LOCUS MSGRGDSA 1460 bp DNA linear BCT 21-SEP-1993  
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.  
ACCESSION L08169  
VERSION L08169.1 GI:293249  
KEYWORDS 16S ribosomal RNA.  
SOURCE Mycobacterium celatum  
ORGANISM Mycobacterium celatum  
REFERENCE  
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W., Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O., Vadney,F.S. and Gross,W.M.  
TITLE Mycobacterium celatum sp. nov  
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)  
PUBMED 8102246  
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51131)  
DNA.  
FEATURES  
source Location/Qualifiers  
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rRNA

ORIGIN

Query Match 95.5%; Score 21; DB 15; Length 1460;  
Best Local Similarity 95.5%; Pred. No. 68;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 20 GAAAGGCTTTTCGGGGGTGCTC 41

RESULT 6  
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LOCUS MSGRGDSB 1479 bp DNA linear BCT 21-SEP-1993  
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.  
ACCESSION L08170  
VERSION L08170.1 GI:293250  
KEYWORDS 16S ribosomal RNA.  
SOURCE Mycobacterium celatum  
ORGANISM Mycobacterium celatum  
REFERENCE  
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W., Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O., Vadney,F.S. and Gross,W.M.  
TITLE Mycobacterium celatum sp. nov  
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)  
PUBMED 8102246  
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51130)  
DNA.  
FEATURES  
source Location/Qualifiers  
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/product="16S ribosomal RNA"  
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rRNA

ORIGIN

Query Match 95.5%; Score 21; DB 15; Length 1479;  
Best Local Similarity 95.5%; Pred. No. 68;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTTCGGGGGTGCTC 22  
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Db 41 GAAAGGCTTTTCGGGGGTGCTC 62

RESULT 7  
AF547926  
LOCUS AF547926 541 bp DNA linear BCT 24-JAN-2006  
DEFINITION Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene, partial sequence.  
ACCESSION AF547926  
VERSION AF547926.1 GI:27733750  
KEYWORDS  
SOURCE Mycobacterium gadium  
ORGANISM Mycobacterium gadium  
REFERENCE  
AUTHORS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
TITLE 1 (bases 1 to 541)  
Devluder,G., de Montclos,M.P. and Flandrois,J.P.  
A multigene approach to phylogenetic analysis using the genus Mycobacterium as a model



JOURNAL Int. J. Syst. Evol. Microbiol. 55 (Pt 1), 293-302 (2005)  
 PUBLISHED 15653890  
 REFERENCE 2 (bases 1 to 541)  
 AUTHORS Devulder G., Pichat, C. and Flandrois, J.P.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,  
 Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,  
 Faculte de Medecine de Lyon Sud, BP 12, Oullins 69622, France  
 FEATURES Location/Qualifiers  
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 /note="type strain of Mycobacterium gadium"  
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 rRNA  
 ORIGIN  
 Query Match 92.7%; Score 20.4; DB 15; Length 541;  
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
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 Db 26 GAAAGGCTTTCGGGGGTACTC 47  
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 RESULT 8  
 MGAD16S  
 LOCUS MGAD16S 1456 bp DNA linear BCT 06-JUN-2003  
 DEFINITION M.gadium 16S ribosomal RNA, part.  
 ACCESSION X55594  
 VERSION X55594.1 GI:44291  
 KEYWORDS 16S ribosomal RNA.  
 SOURCE Mycobacterium gadium  
 ORGANISM Mycobacterium gadium  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE 1 (bases 1 to 1456)  
 AUTHORS Pitulle, C., Dorach, M., Kazda, J., Wolters, J. and Stackebrandt, E.  
 TITLE Phylogeny of rapidly growing members of the genus Mycobacterium  
 JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)  
 PUBLISHED 1380284  
 REFERENCE 2 (bases 1 to 1456)  
 AUTHORS Wolters, J.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine  
 Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen  
 Garten 1-9, 2300 Kiel 1  
 FEATURES Location/Qualifiers  
 source  
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 /organism="Mycobacterium gadium"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:1794"  
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 /product="16S ribosomal RNA"  
 rRNA  
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 Query Match 92.7%; Score 20.4; DB 15; Length 1456;  
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 70 GAAAGGCTTTCGGGGGTACTC 91  
 |||||  
 RESULT 9  
 MCO16S  
 LOCUS MCO16S 1459 bp DNA linear BCT 11-JUN-2003  
 DEFINITION Mycobacterium cookii partial 16S rRNA.

X53896  
 X53896.1 GI:44201  
 16S ribosomal RNA; ribosomal RNA.  
 SOURCE Mycobacterium cookii  
 ORGANISM Mycobacterium cookii  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE 1 (bases 1 to 1225)  
 AUTHORS Kazda, J., Stackebrandt, E., Smida, J., Minnikin, D.E., Daffe, M.,  
 Parlett, J.H. and Pitulle, C.  
 TITLE Mycobacterium cookii sp. nov  
 JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)  
 PUBLISHED 1697763  
 REFERENCE 2 (bases 1 to 1459)  
 AUTHORS Stackebrandt, E.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-AUG-1990) Stackebrandt E  
 FEATURES Location/Qualifiers  
 source  
 1. .1459  
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 /mol\_type="genomic DNA"  
 /strain="ATCC 49103 (T) = N22."  
 /db\_xref="taxon:1775"  
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 /product="16S ribosomal RNA"  
 rRNA  
 ORIGIN  
 Query Match 92.7%; Score 20.4; DB 15; Length 1459;  
 Best Local Similarity 95.5%; Pred. No. 1.3e+02;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 70 GAAAGGCTTTCGGGGGTACTC 91  
 |||||  
 RESULT 10  
 AB006161  
 LOCUS AB006161 1467 bp DNA linear BCT 30-OCT-2001  
 DEFINITION Virgosporangium ochraceum gene for 16S rRNA, partial sequence,  
 strain:YU794-41.  
 ACCESSION AB006161  
 VERSION AB006161.1 GI:16519342  
 KEYWORDS  
 SOURCE Virgosporangium ochraceum  
 ORGANISM Virgosporangium ochraceum  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Micromonosporineae; Micromonosporaceae; Virgisporangium.  
 REFERENCE 1  
 AUTHORS Tamura, T., Hayakawa, M. and Hatano, K.  
 TITLE A new genus of the order Actinomycetales, Virgosporangium gen.  
 nov., with descriptions of Virgosporangium ochraceum sp. nov. and  
 Virgosporangium aurantiacum sp. nov.  
 JOURNAL Int. J. Syst. Evol. Microbiol. 51 (Pt 5), 1809-1816 (2001)  
 PUBLISHED 11594613  
 REFERENCE 2 (bases 1 to 1467)  
 AUTHORS Tamura, T.  
 TITLE Direct Submission  
 JOURNAL Submitted (31-JUL-1997) Tomohiko Tamura, Institute for  
 Fermentation, Osaka, Actinomycetes Group; 17-85, Juso-honmachi  
 2-chome, Yodogawa-ku, Osaka, Osaka 532-8686, Japan  
 (E-mail: tamura-tomohiko@ifo.or.jp, Tel: 81-6-6300-6555,  
 Fax: 81-6-6300-6814)  
 COMMENT Sequence updated (24-Jun-1998).  
 FEATURES Location/Qualifiers  
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 /product="16S ribosomal RNA"  
 rRNA  
 ORIGIN



----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
----- Summary Statistics  
Center project name: M BB0361P07

**NOTICE:** This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality  $\geq 30$ ); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**  
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

**SOURCE INFORMATION:**  
The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:  
This sequence is the entire insert of the clone.

## FEATURES

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		/chromosome="1"	34220. .34365	repeat_region
		/map="1"	/rpt_family="L1"	repeat_region
		/clone="RP24-361P7"	34364. .34582	repeat_region
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repeat_region	9728. .10130	/rpt_family="L1"	/rpt_family="Alu"	repeat_region
repeat_region	10150. .10579	/rpt_family="MaLR"	42175. .42390	repeat_region
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Query Match 88.2%; Score 19.4; DB 6; Length 121141;  
 Best Local Similarity 95.2%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GAAAGGCTTTCGGGGTGCT 21
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Db 108302 GAAAGGCTTTCGGTGCT 108282

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RESULT 14
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LOCUS Mus musculus chromosome 1, clone RP23-130F18, complete sequence.
DEFINITION AC015658
ACCESSION AC015658.11 GI:21306800
VERSION AC015658.11
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE 1 (bases 1 to 177016)
AUTHORS Birren,B., Nusbaum,C. and Lander,E.
TITLE Mus musculus chromosome 1, clone RP23-130F18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177016)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelilano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Diaz,J.S., Dodge,S.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczyk,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

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TITLE Direct Submission
JOURNAL Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 177016)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
Chazaro,B., Choepel,J., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeArelilano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
Johnson,R., Jones,C., Kanat,A., Karatas,A., Kells,C., LaRocque,K.,
Lamazares,R., Landers,T., Lehoczyk,J., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,

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O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 4 (bases 1 to 177016)
AUTHORS Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,M., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cooke,P., Corum,B., DeArelilano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,X., Mabbitt,R., Maclean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-SEP-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Jun 1, 2002 this sequence version replaced gi:13958481.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L1249
Center clone name: 130_F_18
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/clone_lib="RPCI-23 Female Mouse BAC"
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repeat_region 682..816
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repeat_region 2429..2810
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repeat_region 4645..4739
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repeat_region 6504..6551
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repeat_region 6647..6667
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25716..25904
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Query Match 88.2%; Score 19.4; DB 6; Length 177016;
Best Local Similarity 95.2%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 53844 GAAAGGCTTTTCGGGGTGCT 53824

RESULT 15
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LOCUS Mus musculus BAC clone RP23-174122 from 1, complete sequence.
DEFINITION AC148982
ACCESSION AC148982
VERSION AC148982.4 GI:53382933
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 195580)
Deng,S. and Cotton,M.
The sequence of Mus musculus BAC clone RP23-174122
2 (bases 1 to 195580)
Unpublished (2001)
REFERENCE 1
AUTHORS Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (30-APR-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 195580)
Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (27-JUL-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 195580)
Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
5 (bases 1 to 195580)
Wilson,R.K.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 1, 2004 this sequence version replaced gi:50582872.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
----- Summary Statistics
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Center project name: M_BA0174122
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NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

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MAPPING INFORMATION:  
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Oseawa and Minako Tatenio in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

## FEATURES

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unsure

## ORIGIN

Query Match 88.2%; Score 19.4; DB 6; Length 195580;  
Best Local Similarity 95.3%; Pred. No. 1.9e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAAAGCCTTCGGGGTGCT 21  
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Db 28433 GAAAGCCTTCGGGGTGCT 28453

## RESULT 16

AF051395  
LOCUS  
DEFINITION  
Actinomadura viridis strain ATCC27103 16S ribosomal RNA gene, partial sequence.  
ACCESSION  
AF051385  
VERSION  
AF051385.1 GI:6652697  
KEYWORDS  
SOURCE  
Actinomadura viridis  
Actinomadura viridis  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
1 (bases 1 to 105)  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Molecular Identification of Actinomycetes  
JOURNAL  
Unpublished  
AUTHORS  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco, Madrid 28049, Spain

## FEATURES

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## rRNA

## ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 105;

Best Local Similarity 90.9%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAAAGCCTTCGGGGTGCTC 22  
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Db 40 GAAAGCCTTCGGGGTGCTC 61

## RESULT 17

AF051382  
LOCUS  
DEFINITION  
Actinomadura livida strain ATCC33578 16S ribosomal RNA gene, partial sequence.  
ACCESSION  
AF051382  
VERSION  
AF051382.1 GI:6652694  
KEYWORDS  
SOURCE  
Actinomadura livida  
Actinomadura livida  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
1 (bases 1 to 108)  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Molecular Identification of Actinomycetes  
JOURNAL  
Unpublished  
AUTHORS  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco, Madrid 28049, Spain

## FEATURES

source  
1. 108  
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## ORIGIN

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Best Local Similarity 90.9%; Pred. No. 1.1e+03;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAAAGCCTTCGGGGTGCTC 22  
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## RESULT 18

AF051377  
LOCUS  
DEFINITION  
Actinomadura citrea strain ATCC27887 16S ribosomal RNA gene, partial sequence.  
ACCESSION  
AF051377  
VERSION  
AF051377.1 GI:6652689  
KEYWORDS  
SOURCE  
Actinomadura citrea  
Actinomadura citrea  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
1 (bases 1 to 117)  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Molecular Identification of Actinomycetes  
JOURNAL  
Unpublished  
AUTHORS  
Rodriguez, V., Parro, V. and Mellado, R.P.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco, Madrid 28049, Spain

## FEATURES

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ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
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Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 19
AF051378
LOCUS
DEFINITION
Actinomadura coerulea strain ATCC33576 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AF051378
VERSION
AF051378.1 GI:6652690
KEYWORDS
Actinomadura coerulea
SOURCE
Actinomadura coerulea
ORGANISM
Actinomadura coerulea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Molecular Identification of Actinomycetes
JOURNAL
Unpublished
REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Direct Submission
JOURNAL
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
Location/Qualifiers
1. .117
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rRNA

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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 20
AF051379
LOCUS
DEFINITION
Actinomadura cremea subsp. cremea strain ATCC33577 16S ribosomal
RNA gene, partial sequence.
ACCESSION
AF051379
VERSION
AF051379.1 GI:6652691
KEYWORDS
Actinomadura cremea subsp. cremea
SOURCE
Actinomadura cremea subsp. cremea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

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rRNA

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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 20
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LOCUS
DEFINITION
Actinomadura cremea subsp. cremea strain ATCC33577 16S ribosomal
RNA gene, partial sequence.
ACCESSION
AF051379
VERSION
AF051379.1 GI:6652691
KEYWORDS
Actinomadura cremea subsp. cremea
SOURCE
Actinomadura cremea subsp. cremea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Molecular Identification of Actinomycetes
JOURNAL
Unpublished
REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Direct Submission
JOURNAL
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
Location/Qualifiers
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<1..>117
/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 43 GAAAGGCCCTTCGGGGGTACTC 64

RESULT 20
AF051379
LOCUS
DEFINITION
Actinomadura cremea subsp. cremea strain ATCC33577 16S ribosomal
RNA gene, partial sequence.
ACCESSION
AF051379
VERSION
AF051379.1 GI:6652691
KEYWORDS
Actinomadura cremea subsp. cremea
SOURCE
Actinomadura cremea subsp. cremea
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Molecular Identification of Actinomycetes
JOURNAL
Unpublished
REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Direct Submission
JOURNAL
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
Location/Qualifiers
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/organism="Actinomadura spadix"
/mol_type="genomic DNA"
/strain="ATCC27298"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 118;
Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 44 GAAAGGCCCTTCGGGGGTACTC 65

RESULT 22
AF051380
LOCUS
DEFINITION
Actinomadura spadix strain ATCC27298 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AF051380
VERSION
AF051380.1 GI:6652692
KEYWORDS
Actinomadura spadix
SOURCE
Actinomadura spadix
Bacteria; Actinobacteriia; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.

REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Molecular Identification of Actinomycetes
JOURNAL
Unpublished
REFERENCE
AUTHORS
Rodriguez,V., Parro,V. and Mellado,R.P.
TITLE
Direct Submission
JOURNAL
Submitted (27-FEB-1998) Biotechnology Microbiana, Centro Nacional
de Biotecnologia, Campus de la Universidad Autonoma, Cantoblanco,
Madrid 28049, Spain
Location/Qualifiers
1. .118
/organism="Actinomadura spadix"
/mol_type="genomic DNA"
/strain="ATCC27298"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 118;
Best Local Similarity 90.9%; Pred. No. 1.1e+03;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCGCTTTCGGGGGTGCTC 22
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Db 44 GAAAGGCCCTTCGGGGGTACTC 65

RESULT 22
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AY2344506
LOCUS      Bacterium Ellin5089 401 bp DNA linear BCT 08-DEC-2003
DEFINITION Bacterium Ellin5089 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234506
VERSION     AY234506.1 GI:37961663
KEYWORDS   .
SOURCE     bacterium Ellin5089
ORGANISM   Bacterium Ellin5089
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Nocardiopsaceae.
REFERENCE  1 (bases 1 to 401)
AUTHORS   Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE     Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL   Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED    14660368
AUTHORS   Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES   Location/Qualifiers
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                /product="16S ribosomal RNA"
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ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 401;
Best Local Similarity 90.9%; Pred. No. 9.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTTCGGGGTGCTC 22
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Db  18 GAAAGGCCCTTCGGGGTGACTC 39

RESULT 23
AY234445
LOCUS      Bacterium Ellin5028 422 bp DNA linear BCT 08-DEC-2003
DEFINITION Bacterium Ellin5028 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234445
VERSION     AY234445.1 GI:37961602
KEYWORDS   .
SOURCE     bacterium Ellin5028
ORGANISM   Bacterium Ellin5028
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Nocardiopsaceae.
REFERENCE  1 (bases 1 to 422)
AUTHORS   Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
            Janssen,P.H.
TITLE     Laboratory Cultivation of Widespread and Previously Uncultured Soil
            Bacteria
JOURNAL   Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED    14660368
AUTHORS   Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
            Janssen,P.H.
TITLE     Direct Submission
JOURNAL   Submitted (12-FEB-2003) Department of Microbiology and Immunology,
            University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES   Location/Qualifiers
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ORIGIN
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Best Local Similarity 90.9%; Pred. No. 9.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| ||||| |||||
Db  31 GAAAGGCCCTTCGGGGTGACTC 52

RESULT 24
AY756031
LOCUS      Unidentified bacterium TMB805 424 bp DNA linear BCT 08-APR-2005
DEFINITION Unidentified bacterium TMB805 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  AY756031
VERSION     AY756031.1 GI:54299184
KEYWORDS   .
SOURCE     Unidentified bacterium TMB805
ORGANISM   Unidentified bacterium TMB805
            Bacteria.
REFERENCE  1 (bases 1 to 424)
AUTHORS   Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
            Christen,R., Chevenet,F. and Heulin,T.
TITLE     Diversity of Bacteria and Archae in the arid desert of Tataouine
            Unpublished
REFERENCE  2 (bases 1 to 424)
AUTHORS   Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
            Christen,R., Chevenet,F. and Heulin,T.
TITLE     Direct Submission
JOURNAL   Submitted (21-SEP-2004) LEMIR-DEVIM-DSV, CEA, Cadarache, Saint Paul
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FEATURES   Location/Qualifiers
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Query Match      85.5%; Score 18.8; DB 15; Length 424;
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QY  1 GAAAGGCCTTTCGGGGTGCTC 22
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Db  12 GAAAGGCCCTTCGGGGTGACTC 33

RESULT 25
AY095406
LOCUS      Uncultured yard-trimming-compost bacterium clone S-35 661 bp DNA linear ENV 05-MAY-2004
DEFINITION RNA gene, partial sequence.
ACCESSION  AY095406
VERSION     AY095406.1 GI:21320122
KEYWORDS   ENV.
SOURCE     uncultured yard-trimming-compost bacterium
ORGANISM   Bacteria; environmental samples.
REFERENCE  1 (bases 1 to 661)
AUTHORS   Ding,Y., Whitman,W.B., Das,K. and Kastner,J.R.
TITLE     Changes in the microbial community of a biofilter-treating hydrogen
            sulfide and methanol
            Unpublished
            2 (bases 1 to 661)
REFERENCE  Ding,Y., Whitman,W.B., Das,K. and Kastner,J.R.
            Direct Submission

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JOURNAL Submitted (09-APR-2002) Department of Biological and Agricultural Engineering, Department of Microbiology, University of Georgia, Athens, GA 30602, USA

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ORIGIN

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Qy 1 GAAAGGCCTTTCGGGGTGCTC 22  
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Db 33 GAAAGCCCTTTCGGGGGTACTC 54

RESULT 26

AF131473

LOCUS AF131473 829 bp DNA linear BCT 01-MAR-2000

DEFINITION Nonomuraea sp. IM-7031 16S ribosomal RNA gene, partial sequence.

ACCESSION AF131473

VERSION AF131473.1 GI:7109907

KEYWORDS

SOURCE Nonomuraea sp. IM-7031

ORGANISM Nonomuraea sp. IM-7031

REFERENCE 1 (bases 1 to 829)  
Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.

TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 829)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore

FEATURES  
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rRNA

ORIGIN

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Qy 1 GAAAGGCCTTTCGGGGTGCTC 22  
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Db 32 GAAAGCCCTTTCGGGGGTACTC 53

RESULT 27

AF131452

LOCUS AF131452 830 bp DNA linear BCT 01-MAR-2000

DEFINITION Nonomuraea sp. IM-0194 16S ribosomal RNA gene, partial sequence.

ACCESSION AF131452

VERSION AF131452.1 GI:7109886

KEYWORDS

SOURCE Nonomuraea sp. IM-0194

ORGANISM Nonomuraea sp. IM-0194

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

REFERENCE 1 (bases 1 to 830)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 830)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore

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Qy 1 GAAAGGCCTTTCGGGGTGCTC 22  
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Db 32 GAAAGCCCTTTCGGGGGTACTC 53

RESULT 28

AF131455

LOCUS AF131455 830 bp DNA linear BCT 01-MAR-2000

DEFINITION Nonomuraea sp. IM-1409 16S ribosomal RNA gene, partial sequence.

ACCESSION AF131455

VERSION AF131455.1 GI:7109889

KEYWORDS

SOURCE Nonomuraea sp. IM-1409

ORGANISM Nonomuraea sp. IM-1409

REFERENCE 1 (bases 1 to 830)  
Bacteria; Actinobacteridae; Actinobacteriaceae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.

TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore

JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 830)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore

FEATURES  
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rRNA

ORIGIN

Query Match 85.5%; Score 18.8; DB 15; Length 830;  
Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22  
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Db 32 GAAAGCCCTTTCGGGGGTACTC 53

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RESULT 29
LOCUS      AF131469
DEFINITION Nonomuraea sp. IM-6942 830 bp DNA linear BCT 01-MAR-2000
ACCESSION AF131469
VERSION    AF131469.1 GI:7109903
KEYWORDS
SOURCE
ORGANISM   Nonomuraea sp. IM-6942
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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rRNA

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GAAAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db   32 GAAAGGCCTTTCGGGGTGACTC 53

RESULT 30
LOCUS      AF131474
DEFINITION Nonomuraea sp. IM-7062 830 bp DNA linear BCT 01-MAR-2000
ACCESSION AF131474
VERSION    AF131474.1 GI:7109908
KEYWORDS
SOURCE
ORGANISM   Nonomuraea sp. IM-7062
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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LOCUS      AF131453
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ACCESSION AF131453
VERSION    AF131453.1 GI:7109887
KEYWORDS
SOURCE
ORGANISM   Nonomuraea sp. IM-0975
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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rRNA

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
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Db   32 GAAAGGCCTTTCGGGGTGACTC 53

RESULT 32
LOCUS      AF131461
DEFINITION Nonomuraea sp. IM-2224 831 bp DNA linear BCT 01-MAR-2000
ACCESSION AF131461
VERSION    AF131461.1 GI:7109895
KEYWORDS
SOURCE
ORGANISM   Nonomuraea sp. IM-2224
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE
AUTHORS    Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
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rRNA

ORIGIN

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rRNA

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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
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Qy 1 GAAAGGCCTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 33
AF131463
LOCUS      831 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-3235 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131463
VERSION     AF131463.1 GI:7109897
KEYWORDS
SOURCE      Nonomuraea sp. IM-3235
            Nonomuraea sp. IM-3235
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE   1 (bases 1 to 831)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 831)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
FEATURES    Location/Qualifiers
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rRNA

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Query Match      85.5%; Score 18.8; DB 15; Length 831;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 34
AF131298
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Actinocorallia sp. IM-5291 16S ribosomal RNA gene, partial
            sequence.
ACCESSION  AF131298
VERSION     AF131298.1 GI:7109732
KEYWORDS
SOURCE      Actinocorallia sp. IM-5291
            Actinocorallia sp. IM-5291
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Thermomonosporaceae; Actinocorallia.
REFERENCE   1 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
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TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
FEATURES    Location/Qualifiers
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            /product="16S ribosomal RNA"

rRNA

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Query Match      85.5%; Score 18.8; DB 15; Length 832;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 35
AF131456
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-1682 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131456
VERSION     AF131456.1 GI:7109890
KEYWORDS
SOURCE      Nonomuraea sp. IM-1682
            Nonomuraea sp. IM-1682
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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REFERENCE   1 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL    J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 832)
AUTHORS    Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL    Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
FEATURES    Location/Qualifiers
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rRNA

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Query Match      85.5%; Score 18.8; DB 15; Length 832;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 36
AF131465
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomuraea sp. IM-6230 16S ribosomal RNA gene, partial sequence.
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ACCESSION AF131465.1 GI:7109899  
VERSION AF131465.1  
SOURCE Nonomuraea sp. IM-6230  
ORGANISM Nonomuraea sp. IM-6230  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
FEATURES  
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Db 32 GAAAGCCTTCGGGGTACTC 53  
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DEFINITION Nonomuraea sp. IM-6588 832 bp DNA linear BCT 01-MAR-2000  
ACCESSION AF131466  
VERSION AF131466.1 GI:7109900  
KEYWORDS Nonomuraea sp. IM-6588  
SOURCE Nonomuraea sp. IM-6588  
ORGANISM Nonomuraea sp. IM-6588  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
FEATURES  
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Db 32 GAAAGCCTTCGGGGTACTC 53

ACCESSION AF131465.1 GI:7109899  
VERSION AF131465.1  
SOURCE Nonomuraea sp. IM-6230  
ORGANISM Nonomuraea sp. IM-6230  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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ACCESSION AF131466.1 GI:7109900  
VERSION AF131466.1  
SOURCE Nonomuraea sp. IM-6911  
ORGANISM Nonomuraea sp. IM-6911  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
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Db 32 GAAAGCCTTCGGGGTACTC 53

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Db 32 GAAAGCCTTCGGGGTACTC 53  
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AF131467  
LOCUS Nonomuraea sp. IM-6794  
DEFINITION Nonomuraea sp. IM-6794 832 bp DNA linear BCT 01-MAR-2000  
ACCESSION AF131467  
VERSION AF131467.1 GI:7109901  
KEYWORDS Nonomuraea sp. IM-6794  
SOURCE Nonomuraea sp. IM-6794  
ORGANISM Nonomuraea sp. IM-6794  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
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Db 32 GAAAGCCTTCGGGGTACTC 53  
RESULT 39  
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DEFINITION Nonomuraea sp. IM-6911 832 bp DNA linear BCT 01-MAR-2000  
ACCESSION AF131468  
VERSION AF131468.1 GI:7109902  
KEYWORDS Nonomuraea sp. IM-6911  
SOURCE Nonomuraea sp. IM-6911  
ORGANISM Nonomuraea sp. IM-6911  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE 1 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
REFERENCE 2 (bases 1 to 832)  
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
FEATURES  
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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ORIGIN
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAAAGGCCCTTCGGGGGTGCTC 22
      ||||| ||||| ||||| ||||| |||||
Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 40
AF131470
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomurea sp. IM-6943 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131470
VERSION     AF131470.1 GI:7109904
KEYWORDS
SOURCE      Nonomurea sp. IM-6943
ORGANISM    Nonomurea sp. IM-6943
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomurea.
REFERENCE   1 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE       Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL     J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE       Direct Submission
JOURNAL     Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore

FEATURES
source      1..832
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ORIGIN
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 41
AF131471
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomurea sp. IM-6949 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131471
VERSION     AF131471.1 GI:7109905
KEYWORDS
SOURCE      Nonomurea sp. IM-6949
ORGANISM    Nonomurea sp. IM-6949
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomurea.
REFERENCE   1 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE       Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL     J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
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Direct Submission
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
Location/Qualifiers
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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      ||||| ||||| ||||| ||||| |||||
Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 42
AF131472
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomurea sp. IM-6966 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131472
VERSION     AF131472.1 GI:7109906
KEYWORDS
SOURCE      Nonomurea sp. IM-6966
ORGANISM    Nonomurea sp. IM-6966
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomurea.
REFERENCE   1 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE       Investigation of actinomycete diversity in the tropical rainforests
            of Singapore
JOURNAL     J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE   2 (bases 1 to 832)
AUTHORS     Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE       Direct Submission
JOURNAL     Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
            National University of Singapore, 30 Medical Drive, Singapore
            117609, Republic of Singapore
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1..832
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ORIGIN
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GAAAGGCCCTTCGGGGGTGCTC 22
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Db  32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 43
AF131475
LOCUS      832 bp      DNA      linear      BCT 01-MAR-2000
DEFINITION Nonomurea sp. IM-7078 16S ribosomal RNA gene, partial sequence.
ACCESSION  AF131475
VERSION     AF131475.1 GI:7109909
KEYWORDS
SOURCE      Nonomurea sp. IM-7078
ORGANISM    Nonomurea sp. IM-7078
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Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomurea.  
1 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests  
of Singapore  
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
2 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore  
Location/Qualifiers  
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QY 1 GAAAGGCCTTCGGGGTGCTC 22  
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Db 32 GAAAGGCCTTCGGGGTGACTC 53  
RESULT 44  
AF131476  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomurea.  
1 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests  
of Singapore  
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
2 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore  
Location/Qualifiers  
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/organism="Nonomurea sp. IM-7116"  
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QY 1 GAAAGGCCTTCGGGGTGCTC 22  
||||| ||||||| |||||  
Db 32 GAAAGGCCTTCGGGGTGACTC 53  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomurea.  
1 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests  
of Singapore  
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
2 (bases 1 to 832)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore  
Location/Qualifiers  
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QY 1 GAAAGGCCTTCGGGGTGCTC 22  
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Db 32 GAAAGGCCTTCGGGGTGACTC 53

RESULT 45  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Microbispora sp. IM-7566  
Microbispora sp. IM-7566  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Microbispora.  
1 (bases 1 to 833)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests  
of Singapore  
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
2 (bases 1 to 833)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore  
Location/Qualifiers  
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Db 32 GAAAGGCCTTCGGGGTGACTC 53  
Microtetraspora sp. IM-3183  
Microtetraspora sp. IM-3183  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Microtetraspora.  
1 (bases 1 to 833)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Investigation of actinomycete diversity in the tropical rainforests  
of Singapore  
J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
2 (bases 1 to 833)  
Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
Direct Submission  
Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
National University of Singapore, 30 Medical Drive, Singapore  
117609, Republic of Singapore  
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Db 32 GAAAGGCCTTCGGGGTGACTC 53

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 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22  
 |||||  
 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 47  
 AF131434  
 LOCUS AF131434 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Microtetraspora sp. IM-6228 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131434  
 VERSION AF131434.1 GI:7109868  
 KEYWORDS Microtetraspora sp. IM-6228  
 SOURCE Microtetraspora sp. IM-6228  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Microtetraspora.  
 REFERENCE 1 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

FEATURES  
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QY 1 GAAAGGCTTTCGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 48  
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 LOCUS AF131435 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Microtetraspora sp. IM-7010 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131435  
 VERSION AF131435.1 GI:7109869  
 KEYWORDS Microtetraspora sp. IM-7010  
 SOURCE Microtetraspora sp. IM-7010  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Microtetraspora.  
 REFERENCE 1 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,

National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

FEATURES  
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ORIGIN  
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QY 1 GAAAGGCTTTCGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 49  
 AF131436  
 LOCUS AF131436 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Microtetraspora sp. IM-7249 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131436  
 VERSION AF131436.1 GI:7109870  
 KEYWORDS Microtetraspora sp. IM-7249  
 SOURCE Microtetraspora sp. IM-7249  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Microtetraspora.  
 REFERENCE 1 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 833)  
 AUTHORS Wang, Y., Zhang, Z. S., Ruan, J. S., Wang, Y. M. and Ali, S. M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore

FEATURES  
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QY 1 GAAAGGCTTTCGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 50  
 AF131454  
 LOCUS AF131454 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Nonomurea sp. IM-0984 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131454  
 VERSION AF131454.1 GI:7109889  
 KEYWORDS Nonomurea sp. IM-0984  
 SOURCE Nonomurea sp. IM-0984  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;





Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCCCTTCGGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 54  
 AF131460  
 LOCUS AF131460 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Nonomuraea sp. IM-2156 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AF131460  
 VERSION AF131460.1 GI:7109894  
 KEYWORDS  
 SOURCE Nonomuraea sp. IM-2156  
 ORGANISM Nonomuraea sp. IM-2156

REFERENCE 1 (bases 1 to 833)  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 833)  
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
 LOCATION/Qualifiers

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 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
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QY 1 GAAAGGCCCTTCGGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 55  
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 LOCUS AF131462 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Nonomuraea sp. IM-2637 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AF131462  
 VERSION AF131462.1 GI:7109896  
 KEYWORDS  
 SOURCE Nonomuraea sp. IM-2637  
 ORGANISM Nonomuraea sp. IM-2637

REFERENCE 1 (bases 1 to 833)  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 833)  
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
 LOCATION/Qualifiers

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 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 56  
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 LOCUS AF131464 833 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Nonomuraea sp. IM-3385 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AF131464  
 VERSION AF131464.1 GI:7109898  
 KEYWORDS  
 SOURCE Nonomuraea sp. IM-3385  
 ORGANISM Nonomuraea sp. IM-3385

REFERENCE 1 (bases 1 to 833)  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Nonomuraea.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)

REFERENCE 2 (bases 1 to 833)  
 Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology, National University of Singapore, 30 Medical Drive, Singapore 117609, Republic of Singapore  
 LOCATION/Qualifiers

FEATURES  
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 1. .833  
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QY 1 GAAAGGCCCTTCGGGGGTGCTC 22  
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 Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 57  
 AF131384  
 LOCUS AF131384 834 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Microbispora sp. IM-7541 16S ribosomal RNA gene, partial sequence.  
 ACCESSION AF131384  
 VERSION AF131384.1 GI:7109818  
 KEYWORDS  
 SOURCE Microbispora sp. IM-7541  
 ORGANISM Microbispora sp. IM-7541

REFERENCE 1 (bases 1 to 834)  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Microbispora.

AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests of Singapore

J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 834)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
 National University of Singapore, 30 Medical Drive, Singapore  
 117609, Republic of Singapore  
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53  
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 LOCUS AF131641 835 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Thermomonosporaceae str. IM-6903 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131641  
 VERSION AF131641.1 GI:7110075  
 KEYWORDS Thermomonosporaceae str. IM-6903  
 SOURCE Thermomonosporaceae str. IM-6903  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Thermomonosporaceae.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests  
 of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
 National University of Singapore, 30 Medical Drive, Singapore  
 117609, Republic of Singapore  
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 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53  
 RESULT 59  
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 DEFINITION Thermomonosporaceae str. IM-6932 16S ribosomal RNA gene, partial  
 sequence.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests  
 of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
 National University of Singapore, 30 Medical Drive, Singapore  
 117609, Republic of Singapore  
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53

AF131643  
 AF131643.1 GI:7110077  
 Thermomonosporaceae str. IM-6932  
 Thermomonosporaceae str. IM-6932  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Thermomonosporaceae.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests  
 of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
 National University of Singapore, 30 Medical Drive, Singapore  
 117609, Republic of Singapore  
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 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAAAGCCCTTCGGGGTGCTC 22  
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 Db 32 GAAAGCCCTTCGGGGGTACTC 53  
 RESULT 60  
 AF131644  
 LOCUS AF131644 835 bp DNA linear BCT 01-MAR-2000  
 DEFINITION Thermomonosporaceae str. IM-7042 16S ribosomal RNA gene, partial  
 sequence.  
 ACCESSION AF131644  
 VERSION AF131644.1 GI:7110078  
 KEYWORDS Thermomonosporaceae str. IM-7042  
 SOURCE Thermomonosporaceae str. IM-7042  
 ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Thermomonosporaceae.  
 REFERENCE 1 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Investigation of actinomycete diversity in the tropical rainforests  
 of Singapore  
 JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)  
 REFERENCE 2 (bases 1 to 835)  
 AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,  
 National University of Singapore, 30 Medical Drive, Singapore  
 117609, Republic of Singapore  
 FEATURES Location/Qualifiers  
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 /organism="Thermomonosporaceae str. IM-7042"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:116546"  
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 /product="16S ribosomal RNA"  
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 Query Match 85.5%; Score 18.8; DB 15; Length 835;  
 Best Local Similarity 90.9%; Pred. No. 8.3e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 61
AF131646 835 bp DNA linear BCT 01-MAR-2000
LOCUS Thermomonosporaceae str. IM-7209 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF131646
VERSION AF131646.1 GI:7110080
SOURCE Thermomonosporaceae str. IM-7209
ORGANISM Thermomonosporaceae str. IM-7209
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES source
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/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 62
AF131647 835 bp DNA linear BCT 01-MAR-2000
LOCUS Thermomonosporaceae str. IM-7387 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF131647
VERSION AF131647.1 GI:7110081
SOURCE Thermomonosporaceae str. IM-7387
ORGANISM Thermomonosporaceae str. IM-7387
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 835)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES source
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 63
AF131302 836 bp DNA linear BCT 01-MAR-2000
LOCUS Actinomadura sp. IM-3046 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AF131302
VERSION AF131302.1 GI:7109736
SOURCE Actinomadura sp. IM-3046
ORGANISM Actinomadura sp. IM-3046
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES source
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/mol_type="genomic DNA"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAAAGGCCTTTCGGGGTGCTC 22
    ||||| ||||| ||||| |||||
Db 32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 64
AF131308 836 bp DNA linear BCT 01-MAR-2000
LOCUS Actinomadura sp. IM-6226 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AF131308
VERSION AF131308.1 GI:7109742
SOURCE Actinomadura sp. IM-6226
ORGANISM Actinomadura sp. IM-6226
Bacteria: Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
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JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source
1. .836
/organism="Actinomadura sp. IM-6226"
/mol_type="genomic DNA"
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rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGTGACTC 53

RESULT 65
AF131309
LOCUS Actinomadura sp. IM-6793 836 bp DNA linear BCT 01-MAR-2000
DEFINITION Actinomadura sp. IM-6793 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131309
VERSION AF131309.1 GI:7109743
KEYWORDS
SOURCE Actinomadura sp. IM-6793
ORGANISM Actinomadura sp. IM-6793
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source
1. .836
/organism="Actinomadura sp. IM-6793"
/mol_type="genomic DNA"
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/db_xref="taxon:116209"
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rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
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Db 32 GAAAGGCCCTTCGGGGTGACTC 53

RESULT 66
AF131330
LOCUS Actinomadura sp. IM-7397 836 bp DNA linear BCT 01-MAR-2000
DEFINITION Actinomadura sp. IM-7397 16S ribosomal RNA gene, partial sequence.
ACCESSION AF131330
VERSION AF131330.1 GI:7109764
KEYWORDS
SOURCE Actinomadura sp. IM-7397
ORGANISM Actinomadura sp. IM-7397
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source
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/organism="Actinomadura sp. IM-7397"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
|||||
Db 32 GAAAGGCCCTTCGGGGTGACTC 53

RESULT 67
AF131645
LOCUS Thermomonosporaceae str. IM-7058 836 bp DNA linear BCT 01-MAR-2000
DEFINITION Thermomonosporaceae str. IM-7058 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF131645
VERSION AF131645.1 GI:7110079
KEYWORDS
SOURCE Thermomonosporaceae str. IM-7058
ORGANISM Thermomonosporaceae str. IM-7058
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
source
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/product="16S ribosomal RNA"

rRNA

ORIGIN
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Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22

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KEYWORDS
SOURCE Actinomadura sp. IM-7397
ORGANISM Actinomadura sp. IM-7397
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
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rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22
|||||
Db 32 GAAAGGCCCTTCGGGGTGACTC 53

RESULT 67
AF131645
LOCUS Thermomonosporaceae str. IM-7058 836 bp DNA linear BCT 01-MAR-2000
DEFINITION Thermomonosporaceae str. IM-7058 16S ribosomal RNA gene, partial
sequence.
ACCESSION AF131645
VERSION AF131645.1 GI:7110079
KEYWORDS
SOURCE Thermomonosporaceae str. IM-7058
ORGANISM Thermomonosporaceae str. IM-7058
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae.
REFERENCE 1 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Investigation of actinomycete diversity in the tropical rainforests
of Singapore
JOURNAL J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
REFERENCE 2 (bases 1 to 836)
AUTHORS Wang,Y., Zhang,Z.S., Ruan,J.S., Wang,Y.M. and Ali,S.M.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES
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/db_xref="taxon:116547"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 85.5%; Score 18.8; DB 15; Length 836;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAAAGGCTTTCGGGGTGCTC 22

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Db      32 GAAAGGCCCTTCGGGGGTACTC 53
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RESULT 68
AF131642      837 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Thermomonosporaceae str. IM-6923 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF131642
VERSION      AF131642.1 GI:7110076
KEYWORDS      Thermomonosporaceae str. IM-6923
SOURCE      Thermomonosporaceae str. IM-6923
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Streptosporangineae; Thermomonosporaceae.
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
JOURNAL      of Singapore
REFERENCE      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..837
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/mol_type="genomic DNA"
/strain="IM 6923"
/db_xref="taxon:116544"
<1..>837
/product="16S ribosomal RNA"

rRNA
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 837;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCCCTTCGGGGGTGCTC 22
||||||| ||||||| |||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 69
AF131326      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7213 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF131326
VERSION      AF131326.1 GI:7109760
KEYWORDS      Actinomadura sp. IM-7213
SOURCE      Actinomadura sp. IM-7213
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Streptosporangineae; Thermomonosporaceae; Actinomadura.
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
JOURNAL      of Singapore
REFERENCE      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..838
/mol_type="Actinomadura sp. IM-7213"
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/product="16S ribosomal RNA"

rRNA
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCCCTTCGGGGGTGCTC 22
||||||| ||||||| |||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 70
AF131327      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7214 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF131327
VERSION      AF131327.1 GI:7109761
KEYWORDS      Actinomadura sp. IM-7214
SOURCE      Actinomadura sp. IM-7214
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Streptosporangineae; Thermomonosporaceae; Actinomadura.
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
JOURNAL      of Singapore
REFERENCE      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..838
/mol_type="Actinomadura sp. IM-7214"
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/product="16S ribosomal RNA"

rRNA
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCCCTTCGGGGGTGCTC 22
||||||| ||||||| |||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 71
AF163338      1013 bp      DNA      linear      BCT 14-DEC-2002
LOCUS      Mycobacterium sp. IP20010664 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF163338
VERSION      AF163338.1 GI:26892049
KEYWORDS      Mycobacterium sp. IP20010664
SOURCE      Mycobacterium sp. IP20010664
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS      Le Dantec, C., Jackson, M., Duguet, J.-P., Montiel, A., Dumoutier, N.,
Dubrou, S. and Vincent, V.
TITLE      Isolation of unusual Mycobacterium species from water supplies
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1013)

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/db_xref="taxon:116226"
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/product="16S ribosomal RNA"

ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCCCTTCGGGGGTGCTC 22
||||||| ||||||| |||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 70
AF131327      838 bp      DNA      linear      BCT 01-MAR-2000
LOCUS      Actinomadura sp. IM-7214 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF131327
VERSION      AF131327.1 GI:7109761
KEYWORDS      Actinomadura sp. IM-7214
SOURCE      Actinomadura sp. IM-7214
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Streptosporangineae; Thermomonosporaceae; Actinomadura.
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Investigation of actinomycete diversity in the tropical rainforests
JOURNAL      of Singapore
REFERENCE      J. Ind. Microbiol. Biotechnol. 23, 178-187 (1999)
AUTHORS      Wang, Y., Zhang, Z.S., Ruan, J.S., Wang, Y.M. and Ali, S.M.
TITLE      Direct Submission
JOURNAL      Submitted (26-FEB-1999) Institute of Molecular and Cell Biology,
National University of Singapore, 30 Medical Drive, Singapore
117609, Republic of Singapore
FEATURES      Location/Qualifiers
source      1..838
/mol_type="Actinomadura sp. IM-7214"
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rRNA
ORIGIN

Query Match      85.5%; Score 18.8; DB 15; Length 838;
Best Local Similarity 90.9%; Pred. No. 8.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAAAGGCCCTTCGGGGGTGCTC 22
||||||| ||||||| |||
Db      32 GAAAGGCCCTTCGGGGGTACTC 53

RESULT 71
AF163338      1013 bp      DNA      linear      BCT 14-DEC-2002
LOCUS      Mycobacterium sp. IP20010664 16S ribosomal RNA gene, partial
DEFINITION      sequence.
ACCESSION      AF163338
VERSION      AF163338.1 GI:26892049
KEYWORDS      Mycobacterium sp. IP20010664
SOURCE      Mycobacterium sp. IP20010664
ORGANISM      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
REFERENCE      Corynebacterineae; Mycobacteriaceae; Mycobacterium.
AUTHORS      Le Dantec, C., Jackson, M., Duguet, J.-P., Montiel, A., Dumoutier, N.,
Dubrou, S. and Vincent, V.
TITLE      Isolation of unusual Mycobacterium species from water supplies
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1013)

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AUTHORS TITLE JOURNAL FEATURES source  rRNA  ORIGIN	Le Dantec,C., Jackson,M., Duguet,J.-P., Montiel,A., Dumoutier,N., Dubrou,S. and Vincent,V. Direct Submission Submitted (15-OCT-2002) Mycobacterie, Institut Pasteur, 25 rue du Docteur Roux, Paris 75015, France Location/Qualifiers 1. .1013 /organism="Mycobacterium sp. IP20010664" /mol_type="genomic DNA" /strain="IP20010664" /db_xref="taxon:215916" <1. .>1013 /product="16S ribosomal RNA"									
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RESULT 72 AEU49004 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Actinomadura echinospira Actinomadura echinospira Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1401) Wang,Y. Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1401 /organism="Actinomadura echinospira" /mol_type="genomic DNA" /strain="IFO 14042" /db_xref="taxon:1992" 1. .1401 /product="16S ribosomal RNA"									
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	Db	63	GAAGGCCCTTCGGGGTACTC 84							
REFERENCE AUTHORS TITLE JOURNAL FEATURES source  rRNA  ORIGIN	Actinomadura echinospira Actinomadura echinospira Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1401) Wang,Y. Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1401 /organism="Actinomadura echinospira" /mol_type="genomic DNA" /strain="IFO 14042" /db_xref="taxon:1992" 1. .1401 /product="16S ribosomal RNA"									
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	Best Local Similarity	90.9%;	Pred. No. 7.7e+02;							
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	Db	13	GAAGGCCCTTCGGGGTACTC 34							
RESULT 73 ALU49007 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Actinocorallia libanotica Actinocorallia libanotica Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinocorallia. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1404) Wang,Y. Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1404 /organism="Actinocorallia libanotica" /mol_type="genomic DNA" /strain="IFO 14095" /db_xref="taxon:46162" 1. .1404 /product="16S ribosomal RNA"									
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	Db	13	GAAGGCCCTTCGGGGTACTC 34							
REFERENCE AUTHORS TITLE JOURNAL FEATURES source  rRNA  ORIGIN	Actinomadura rugatobispora Actinomadura rugatobispora Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Thermomonosporaceae; Actinomadura. Wang,Y. Phylogenetic analysis of Actinomadura species Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore 2 (bases 1 to 1406) Wang,Y. Direct Submission Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore Location/Qualifiers 1. .1406 /organism="Actinomadura rugatobispora" /mol_type="genomic DNA" /strain="IFO 14382" /db_xref="taxon:1994" 1. .1406 /product="16S ribosomal RNA"									
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	Db	13	GAAGGCCCTTCGGGGTACTC 34							

RESULT 75  
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LOCUS ACU49002 1409 bp DNA linear BCT 08-MAY-1996  
DEFINITION Actinomadura coerulea 16S rRNA gene.  
ACCESSION U49002  
VERSION U49002.1 GI:1305434  
KEYWORDS  
SOURCE Actinomadura coerulea  
ORGANISM Actinomadura coerulea  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Phylogenetic analysis of Actinomadura species  
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
2 (bases 1 to 1409)  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
FEATURES  
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rRNA

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Best Local Similarity 90.9%; Pred. No. 7.7e+02;  
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|||||  
Db 13 GAAAGCCCTTCGGGGGTACTC 34

RESULT 76  
MSU48983  
LOCUS MSU48983 1409 bp DNA linear BCT 09-JUL-1997  
DEFINITION Microtetraspora spiralis 16S rRNA gene.  
ACCESSION U48983  
VERSION U48983.1 GI:2251228  
KEYWORDS  
SOURCE Nonomuraea spiralis  
ORGANISM Nonomuraea spiralis  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Phylogenetic analysis of Microtetraspora species  
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
2 (bases 1 to 1409)  
REFERENCE  
AUTHORS Wang, Y., Zhang, Z., and Ruan, J.  
TITLE Phylogenetic analysis reveals new relationships among members of the genera Microtetraspora and Microbispora  
JOURNAL Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)  
PUBMED 8782672  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
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/db\_xref="taxon:46182"  
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rRNA

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Best Local Similarity 90.9%; Pred. No. 7.7e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GAAAGCCCTTCGGGGGTGCTC 22  
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Db 13 GAAAGCCCTTCGGGGGTACTC 34

RESULT 77  
AKU49006  
LOCUS AKU49006 1409 bp DNA linear BCT 08-MAY-1996  
DEFINITION Actinomadura kijaniata 16S rRNA gene.  
ACCESSION U49006  
VERSION U49006.1 GI:1305438  
KEYWORDS  
SOURCE Actinomadura kijaniata  
ORGANISM Actinomadura kijaniata  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Phylogenetic analysis of Actinomadura species  
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
2 (bases 1 to 1409)  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
FEATURES  
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rRNA

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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GAAAGCCCTTCGGGGGTGCTC 22  
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Db 13 GAAAGCCCTTCGGGGGTACTC 34

RESULT 78  
ALU49008  
LOCUS ALU49008 1409 bp DNA linear BCT 08-MAY-1996  
DEFINITION Actinomadura luteofluorescens 16S rRNA gene.  
ACCESSION U49008  
VERSION U49008.1 GI:1305440  
KEYWORDS  
SOURCE Actinomadura luteofluorescens  
ORGANISM Actinomadura luteofluorescens  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptosporangineae; Thermomonosporaceae; Actinomadura.  
REFERENCE  
AUTHORS Wang, Y.  
TITLE Phylogenetic analysis of Actinomadura species  
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore

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REFERENCE 2 (bases 1 to 1409)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 13 GAAAGCCCTTCGGGGGTACTC 34
RESULT 79
ACU49001
LOCUS Actinomadura citrea 1410 bp DNA linear BCT 08-MAY-1996
DEFINITION Actinomadura citrea 16S rRNA gene.
ACCESSION U49001
VERSION U49001.1 GI:1305433
KEYWORDS
SOURCE
ORGANISM
Actinomadura citrea
Actinomadura citrea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Phylogenetic analysis of Actinomadura species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 13 GAAAGCCCTTCGGGGGTACTC 34
RESULT 80
ACU49003
LOCUS Actinomadura citrea 1410 bp DNA linear BCT 08-MAY-1996
DEFINITION Actinomadura citrea rifamycin 16S rRNA gene.
ACCESSION U49003
VERSION U49003.1 GI:1305435
KEYWORDS
SOURCE
ORGANISM
Actinomadura citrea
Actinomadura citrea
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE 1 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Phylogenetic analysis of Actinomadura species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1410)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
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Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GAAAGGCCTTTCGGGGTGCTC 22
|||||
Db 13 GAAAGCCCTTCGGGGGTACTC 34
RESULT 81
MAU48843
LOCUS Microtetraspora angiospora 1411 bp DNA linear BCT 08-MAY-1996
DEFINITION Microtetraspora angiospora 16S rRNA gene.
ACCESSION U48843
VERSION U48843.1 GI:1305420
KEYWORDS
SOURCE
ORGANISM
Nonomuraea angiospora
Nonomuraea angiospora
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1411)
AUTHORS Wang, Y.
TITLE Phylogenetic analysis of Microtetraspora species
JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National
University of Singapore
REFERENCE 2 (bases 1 to 1411)
AUTHORS Wang, Y.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
Biology, National University of Singapore, 10 Kent Ridge Crescent,
Singapore 0511, Singapore
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QY 1 GAAAGGCCTTTCGGGGTGCTC 22
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Db 13 GAAAGCCCTTCGGGGGTACTC 34
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Db      13 GAAAGGCCCTTCGGGGGTACTC 34
RESULT 82
MHU48975
LOCUS      1411 bp      DNA      linear      BCT 09-JUL-1997
DEFINITION Microtetraspora helvata 16S rRNA gene.
ACCESSION  U48975
VERSION     U48975.1 GI:2251221
KEYWORDS
SOURCE
ORGANISM    Nonomuraea helvata
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE   1 (bases 1 to 1411)
AUTHORS     Wang, Y.
TITLE       Phylogenetic analysis of Microtetraspora species
JOURNAL     Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE   2 (bases 1 to 1411)
AUTHORS     Wang, Y., Zhang, Z. and Ruan, J.
TITLE       Phylogenetic analysis reveals new relationships among members of
            the genera Microtetraspora and Microbispora
JOURNAL     Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED      8782672
REFERENCE   3 (bases 1 to 1411)
AUTHORS     Wang, Y.
TITLE       Direct Submission
JOURNAL     Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
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Db      13 GAAAGGCCCTTCGGGGGTACTC 34
RESULT 83
AVU49011
LOCUS      1411 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Actinomadura verrucospora 16S rRNA gene.
ACCESSION  U49011
VERSION     U49011.1 GI:1305443
KEYWORDS
SOURCE
ORGANISM    Actinomadura verrucospora
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Thermomonosporaceae; Actinomadura.
REFERENCE   1 (bases 1 to 1411)
AUTHORS     Wang, Y.
TITLE       Phylogenetic analysis of Actinomadura species
JOURNAL     Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE   2 (bases 1 to 1411)
AUTHORS     Wang, Y.
TITLE       Direct Submission
JOURNAL     Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
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    /db_xref="taxon:46165"
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ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1412;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
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Db      13 GAAAGGCCCTTCGGGGGTACTC 34
RESULT 84
MFU48844
LOCUS      1412 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Microtetraspora fastidiosa 16S rRNA gene.
ACCESSION  U48844
VERSION     U48844.1 GI:1305421
KEYWORDS
SOURCE
ORGANISM    Nonomuraea fastidiosa
            Nonomuraea fastidiosa
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE   1 (bases 1 to 1412)
AUTHORS     Wang, Y.
TITLE       Phylogenetic analysis of Microtetraspora species
JOURNAL     Thesis (1996) Institute of Molecular and Cell Biology, National
            University of Singapore
REFERENCE   2 (bases 1 to 1412)
AUTHORS     Wang, Y.
TITLE       Direct Submission
JOURNAL     Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
            Biology, National University of Singapore, 10 Kent Ridge Crescent,
            Singapore 0511, Singapore
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ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1412;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy      1 GAAAGGCCCTTCGGGGGTGCTC 22
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Db      13 GAAAGGCCCTTCGGGGGTACTC 34
RESULT 85
MAU48842
LOCUS      1413 bp      DNA      linear      BCT 08-MAY-1996
DEFINITION Microtetraspora africana 16S rRNA gene.
ACCESSION  U48842
VERSION     U48842.1 GI:1305419
KEYWORDS
SOURCE
ORGANISM    Nonomuraea africana
            Nonomuraea africana
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE   1 (bases 1 to 1413)
AUTHORS     Wang, Y.
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TITLE      Phylogenetic analysis of Microtetraspota species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
REFERENCE  Biology, National University of Singapore, 10 Kent Ridge Crescent,
AUTHORS    Singapore 0511, Singapore
JOURNAL    Location/Qualifiers
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ORIGIN
Query Match      85.5%; Score 18.8; DB 15; Length 1413;
Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GAAAGGCCCTTCGGGGTGCTC 22
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Db   13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 86
MDU48990
LOCUS      Microbispora diastatica 1413 bp DNA linear BCT 08-MAY-1996
DEFINITION Microbispora diastatica 16S rRNA gene.
ACCESSION U48990
VERSION   U48990.1 GI:1305428
KEYWORDS
SOURCE    Microbispora rosea subsp. rosea
           Microbispora rosea subsp. rosea
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Streptosporangineae; Streptosporangiaceae; Microbispora.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Phylogenetic analysis of Microbispora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
REFERENCE  Biology, National University of Singapore, 10 Kent Ridge Crescent,
AUTHORS    Singapore 0511, Singapore
JOURNAL    Location/Qualifiers
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ORIGIN
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Best Local Similarity 90.9%; Pred. No. 7.7e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 GAAAGGCCCTTCGGGGTGCTC 22
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Db   13 GAAAGGCCCTTCGGGGGTACTC 34

RESULT 87
MPU48977
LOCUS      Microtetraspora polychroma 1413 bp DNA linear BCT 09-JUL-1997
DEFINITION Microtetraspora polychroma 16S rRNA gene.
ACCESSION U48977
VERSION   U48977.1 GI:2251225
KEYWORDS
SOURCE    Nonomuraea recticatena
           Nonomuraea recticatena
           Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
           Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang,Y., Zhang,Z. and Ruan,J.
TITLE      Phylogenetic analysis reveals new relationships among members of
           the genera Microtetraspora and Microbispora
JOURNAL    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
AUTHORS    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
JOURNAL    Wang,Y.
REFERENCE  3 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
REFERENCE  Biology, National University of Singapore, 10 Kent Ridge Crescent,
AUTHORS    Singapore 0511, Singapore
JOURNAL    Location/Qualifiers
FEATURES   source
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ACCESSION U48977
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KEYWORDS
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REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang,Y., Zhang,Z. and Ruan,J.
TITLE      Phylogenetic analysis reveals new relationships among members of
           the genera Microtetraspora and Microbispora
JOURNAL    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
AUTHORS    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
JOURNAL    Wang,Y.
REFERENCE  3 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
REFERENCE  Biology, National University of Singapore, 10 Kent Ridge Crescent,
AUTHORS    Singapore 0511, Singapore
JOURNAL    Location/Qualifiers
FEATURES   source
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VERSION   U48979.1 GI:2251225
KEYWORDS
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           Streptosporangineae; Streptosporangiaceae; Nonomuraea.
REFERENCE 1 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Phylogenetic analysis of Microtetraspora species
JOURNAL    Thesis (1996) Institute of Molecular and Cell Biology, National
REFERENCE  2 (bases 1 to 1413)
AUTHORS    Wang,Y., Zhang,Z. and Ruan,J.
TITLE      Phylogenetic analysis reveals new relationships among members of
           the genera Microtetraspora and Microbispora
JOURNAL    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
AUTHORS    Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)
PUBMED    8782672
JOURNAL    Wang,Y.
REFERENCE  3 (bases 1 to 1413)
AUTHORS    Wang,Y.
TITLE      Direct Submission
JOURNAL    Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell
REFERENCE  Biology, National University of Singapore, 10 Kent Ridge Crescent,
AUTHORS    Singapore 0511, Singapore
JOURNAL    Location/Qualifiers
FEATURES   source
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DEFINITION	Microbispora parva 16S rRNA gene.				
ACCESSION	U48985				
VERSION	U48985.1	GI:1305429			
KEYWORDS	Microbispora rosea subsp. rosea				
SOURCE	Microbispora rosea subsp. rosea				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Streptosporangiaceae; Microbispora.				
REFERENCE	Wang, Y.				
AUTHORS	Phylogenetic analysis of Microbispora species				
TITLE	Thesis (1996) Institute of Molecular and Cell Biology, National				
JOURNAL	University of Singapore				
REFERENCE	Wang, Y.				
AUTHORS	Direct Submission				
TITLE	Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell				
JOURNAL	Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore				
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DEFINITION	Microtetraspora roseola 16S rRNA gene.				
ACCESSION	U48980				
VERSION	U48980.1	GI:2251226			
KEYWORDS	Nonomuraea roseola				
SOURCE	Nonomuraea roseola				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Streptosporangiaceae; Nonomuraea.				
REFERENCE	Wang, Y.				
AUTHORS	Phylogenetic analysis of Microtetraspora species				
TITLE	Thesis (1996) Institute of Molecular and Cell Biology, National				
JOURNAL	University of Singapore				
REFERENCE	Wang, Y., Zhang, Z. and Ruan, J.				
AUTHORS	Phylogenetic analysis reveals new relationships among members of				
TITLE	the genera Microtetraspora and Microbispora				
JOURNAL	Int. J. Syst. Bacteriol. 46 (3), 658-663 (1996)				
PUBMED	8782672				
REFERENCE	Wang, Y.				
AUTHORS	Direct Submission				
TITLE	Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell				
JOURNAL	Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore				
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DEFINITION	Microbispora thermosea 16S rRNA gene.				
ACCESSION	U48987				
VERSION	U48987.1	GI:1305431			
KEYWORDS	Microbispora rosea subsp. aerata				
SOURCE	Microbispora rosea subsp. aerata				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Streptosporangiaceae; Microbispora.				
REFERENCE	Wang, Y.				
AUTHORS	Phylogenetic analysis of Microbispora species				
TITLE	Thesis (1996) Institute of Molecular and Cell Biology, National				
JOURNAL	University of Singapore				
REFERENCE	Wang, Y.				
AUTHORS	Direct Submission				
TITLE	Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell				
JOURNAL	Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore				
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VERSION	U48984.1	GI:1305425			
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SOURCE	Microbispora rosea subsp. aerata				
ORGANISM	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Streptosporangiaceae; Microbispora.				

REFERENCE 1 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Phylogenetic analysis of Microbispora species  
 JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
 REFERENCE 2 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
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 Streptosporangineae; Streptosporangiaceae; Nonomuraea.  
 REFERENCE 1 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Phylogenetic analysis of Microtetraspora species  
 JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
 REFERENCE 2 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
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 DEFINITION Actinomadura fulvescens 16S rRNA gene.  
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 SOURCE Actinomadura fulvescens  
 ORGANISM Actinomadura fulvescens  
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 REFERENCE 1 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Phylogenetic analysis of Actinomadura species  
 JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
 REFERENCE 2 (bases 1 to 1415)  
 AUTHORS Wang,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
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 VERSION U48974.1 GI:2251220  
 KEYWORDS  
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 ORGANISM Microtetraspora glauca  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 Streptosporangineae; Streptosporangiaceae; Microtetraspora.  
 REFERENCE 1 (bases 1 to 1416)  
 AUTHORS Wang,Y.  
 TITLE Phylogenetic analysis of Microtetraspora species  
 JOURNAL Thesis (1996) Institute of Molecular and Cell Biology, National University of Singapore  
 REFERENCE 2 (bases 1 to 1416)  
 AUTHORS Wang,Y., Zhang,Z. and Ruan,J.  
 TITLE Phylogenetic analysis reveals new relationships among members of the genera Microtetraspora and Microbispora  
 JOURNAL Int. J. Syst. Bacteriol. 46 (3), 659-663 (1996)  
 PUBMED 8782672  
 REFERENCE 3 (bases 1 to 1416)  
 AUTHORS Wang,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-FEB-1996) Yue Wang, Institute of Molecular and Cell Biology, National University of Singapore, 10 Kent Ridge Crescent, Singapore 0511, Singapore  
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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
1829.273 Million cell updates/sec

Title: US-10-665-708-24

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database :

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1: gb\_env:\*

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9: gb\_un:\*

10: gb\_vi:\*

11: gb\_ov:\*

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13: gb\_in:\*

14: gb\_cm:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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11	18	94.7	25	2	AX166855 Sequence
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13	18	94.7	1479	15	MSGRGDSB L08170 Mycobacteri
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133	17.4	91.6	500	15	AY215256	AY215256 Mycobacte	206	17.4	91.6	540	15	AY438071	AY438071 Mycobacte
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138	17.4	91.6	500	15	AY215289	AY215289 Mycobacte	211	17.4	91.6	542	15	AF547917	AF547917 Mycobacte
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143	17.4	91.6	500	15	AY215304	AY215304 Mycobacte	216	17.4	91.6	552	15	AY438073	AY438073 Mycobacte
144	17.4	91.6	500	15	AY215316	AY215316 Mycobacte	217	17.4	91.6	552	15	AY438074	AY438074 Mycobacte
145	17.4	91.6	500	15	AY215320	AY215320 Mycobacte	218	17.4	91.6	568	15	AY039481	AY039481 Soil bact
146	17.4	91.6	500	15	AY215323	AY215323 Mycobacte	219	17.4	91.6	576	15	AY367021	AY367021 Mycobacte
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149	17.4	91.6	500	15	AY215348	AY215348 Mycobacte	222	17.4	91.6	616	1	AY242618	AY242618 Unculture
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239 17.4 91.6 773 15 AJ746072 Mycobacte  
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248 17.4 91.6 828 15 AJ746061 Mycobacte  
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251 17.4 91.6 863 15 AJ699171 Mycobacte  
252 17.4 91.6 878 15 AY429701 Mycobacte  
253 17.4 91.6 893 15 AY494645 Unculture  
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257 17.4 91.6 1013 15 AY163338 Mycobacte  
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262 17.4 91.6 1025 15 AJ863315 Unculture  
263 17.4 91.6 1036 15 AJ863365 Unculture  
264 17.4 91.6 1049 15 MSP441306 Mycobacte  
265 17.4 91.6 1274 15 AJ871634 Mycobacte  
266 17.4 91.6 1276 15 MFOA16915 Mycobacte  
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274 17.4 91.6 1362 15 AY897829 Unculture  
275 17.4 91.6 1362 15 AY897828 Mycobacte  
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277 17.4 91.6 1372 15 AJ833917 Mycobacte  
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279 17.4 91.6 1374 15 AY897830 Unculture  
280 17.4 91.6 1374 15 AY921741 Unculture  
281 17.4 91.6 1374 15 AY162040 Actinobac  
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283 17.4 91.6 1382 15 MFOA16910 Mycobacte  
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287 17.4 91.6 1393 15 DQ145802 Mycobacte  
288 17.4 91.6 1394 15 AF387803 Mycobacte  
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290 17.4 91.6 1397 15 AY173352 Mycobacte  
291 17.4 91.6 1399 15 AF408990 Mycobacte  
292 17.4 91.6 1399 15 AJ849466 Mycobacte  
293 17.4 91.6 1400 15 AM056051 Mycobacte  
294 17.4 91.6 1413 15 AF408993 Mycobacte  
295 17.4 91.6 1418 15 DQ370011 Mycobacte  
296 17.4 91.6 1418 15 AF284430 Mycobacte  
297 17.4 91.6 1420 15 AF409022 Mycobacte  
298 17.4 91.6 1422 15 DQ370010 Mycobacte  
299 17.4 91.6 1422 15 MFU441307 Mycobacte  
300 17.4 91.6 1422 15 AY234735 Bacterium

## ALIGNMENTS

RESULT 1  
AR438656 AR438656 19 bp DNA linear PAT 20-FEB-2004  
LOCUS Sequence 24 from patent US 6664081.  
DEFINITION  
ACCESSION AR438656

VERSION AR438656.1 GI:42663580  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and  
Rodrigue, M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 24 16-DEC-2003;  
FEATURES Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGGCCTTCGG 19  
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Db 1 GAACGGAAAGGCCTTCGG 19  
RESULT 2  
LOCUS AX166858 19 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 24 from Patent WO0144510.  
ACCESSION AX166858  
VERSION AX166858.1 GI:14596461  
KEYWORDS synthetic construct  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and  
Rodrigue, M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 24 21-JUN-2001;  
FEATURES Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
source Location/Qualifiers  
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/db\_xref="taxon:32630"  
/note="primer oligonucleotide"  
ORIGIN  
Query Match 100.0%; Score 19; DB 2; Length 19;  
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGGCCTTCGG 19  
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Db 1 GAACGGAAAGGCCTTCGG 19  
RESULT 3  
LOCUS AR438655 22 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 23 from patent US 6664081.  
ACCESSION AR438655  
VERSION AR438655.1 GI:42663579  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Brentano, S.T., Jucker, M.T., Delgado, F.D., Cleuziat, P. and  
Rodrigue, M.  
TITLE Nucleic acid amplification and detection of mycobacterium species

JOURNAL Patent: US 6664081-A 23 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA

FEATURES  
source  
Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 2; Length 22;  
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
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Db 4 GAACGGAAGGCTTTTCGG 22  
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RESULT 4  
LOCUS AX166857 22 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 23 from Patent WO0144510.  
ACCESSION AX166857  
VERSION AX166857.1 GI:14596460  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and  
Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 23 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)

FEATURES  
source  
Location/Qualifiers  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 GAACGGAAGGCTTTTCGG 22  
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RESULT 5  
AF547926 541 bp DNA linear BCT 24-JAN-2006  
LOCUS Mycobacterium gadium strain CIP 105388 16S ribosomal RNA gene,  
partial sequence.  
DEFINITION  
ACCESSION AF547926  
VERSION AF547926.1 GI:27733750  
KEYWORDS  
SOURCE Mycobacterium gadium  
ORGANISM Mycobacterium gadium

REFERENCE 1  
AUTHORS Devulder,G., de Montclos,M.P. and Flandrois,J.P.  
TITLE A multigene approach to phylogenetic analysis using the genus  
JOURNAL Mycobacterium as a model  
PUBMED Int. J. Syst. Evol. Microbiol. 55 (PT 1), 293-302 (2005)  
15653890

REFERENCE 2  
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,  
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

FEATURES  
source  
Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 15; Length 541;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
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Db 21 GAACGGAAGGCTTTTCGG 39  
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RESULT 6  
MGAD16S 1456 bp DNA linear BCT 06-JUN-2003  
LOCUS M.gadium 16S ribosomal RNA, part.  
DEFINITION  
ACCESSION X55594  
VERSION X55594.1 GI:44291  
KEYWORDS 16S ribosomal RNA.  
SOURCE Mycobacterium gadium  
ORGANISM Mycobacterium gadium

REFERENCE 1  
AUTHORS Pitulle,C., Dorsch,M., Kazda,J., Wolters,J. and Stackebrandt,E.  
TITLE Phylogeny of rapidly growing members of the genus Mycobacterium  
JOURNAL Int. J. Syst. Bacteriol. 42 (3), 337-343 (1992)  
PUBMED 1380284

REFERENCE 2  
AUTHORS Wolters,J.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-1990) Wolters J., Institut fuer Allgemeine  
Mikrobiologie der Universitaet, Biologiezentrum, Am Botanischen  
Garten 1-9, 2300 Kiel 1

FEATURES  
source  
Location/Qualifiers  
1. 1456  
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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
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Db 65 GAACGGAAGGCTTTTCGG 83  
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## ORIGIN

RESULT 7  
MC016S 1459 bp DNA linear BCT 11-JUN-2003  
LOCUS Mycobacterium cookii partial 16S rRNA.  
DEFINITION  
ACCESSION X53896  
VERSION X53896.1 GI:44201  
KEYWORDS 16S ribosomal RNA; ribosomal RNA.  
SOURCE Mycobacterium cookii  
ORGANISM Mycobacterium cookii

REFERENCE 1  
AUTHORS Devulder,G., Pichat,C. and Flandrois,J.P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2002) Dynamique des populations bacteriennes,  
Universite Claude Bernard Lyon1 UMR CNRS 5558 & C.H.U. Lyon Sud,

REFERENCE 1 (bases 1 to 1225)  
AUTHORS Kazda,J., Stackebrandt,E., Smida,J., Minnikin,D.E., Daffe,M., Parlett,J.H. and Pitullie,C.  
TITLE Mycobacterium cookii sp. nov  
JOURNAL Int. J. Syst. Bacteriol. 40 (3), 217-223 (1990)  
PUBMED 1697763  
REFERENCE 2 (bases 1 to 1459)  
AUTHORS Stackebrandt,E.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-1990) Stackebrandt E  
FEATURES  
source Location/Qualifiers  
1..1459  
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1..>1459  
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTCG 19  
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Db 65 GAACGGAAGGCCTTTCG 83

RESULT 8  
LOCUS AR438654 24 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 22 from patent US 6664081.  
ACCESSION AR438654  
VERSION AR438654.1 GI:42663578  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 22 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 94.7%; Score 18; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTCG 18  
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Db 7 GAACGGAAGGCCTTTCG 24

RESULT 9  
LOCUS AX166856 24 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 22 from Patent W00144510.  
ACCESSION AX166856  
VERSION AX166856.1 GI:14596459  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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/db\_xref="taxon:32630"  
/note="primer oligonucleotide"

TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 22 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
FEATURES  
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Query Match 94.7%; Score 18; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTCG 18  
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Db 7 GAACGGAAGGCCTTTCG 24

RESULT 10  
LOCUS AR438653 25 bp DNA linear PAT 20-FEB-2004  
DEFINITION Sequence 21 from patent US 6664081.  
ACCESSION AR438653  
VERSION AR438653.1 GI:42663577  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: US 6664081-A 21 16-DEC-2003;  
Gen-Probe Incorporated and Bio Merieux S.A.; San Diego, CA  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 4.1e+03;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCTTTCG 18  
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Db 8 GAACGGAAGGCCTTTCG 25

RESULT 11  
LOCUS AX166855 25 bp DNA linear PAT 04-JUL-2001  
DEFINITION Sequence 21 from Patent W00144510.  
ACCESSION AX166855  
VERSION AX166855.1 GI:14596458  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Brentano,S.T., Jucker,M.T., Delgado,F.D., Cleuziat,P. and Rodrigue,M.  
TITLE Nucleic acid amplification and detection of mycobacterium species  
JOURNAL Patent: WO 0144510-A 21 21-JUN-2001;  
Gen-Probe Incorporated (US); Biomerieux S.A. (FR)  
FEATURES  
source Location/Qualifiers  
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 18
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Db 8 GAACGGAAGGCGCTTCG 25

RESULT 12
MSGRDSB
LOCUS MSGRDSB 1460 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08169
VERSION L08169.1 GI:293249
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1460)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.
TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51131)
DNA.
FEATURES
source Location/Qualifiers
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rRNA

ORIGIN
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Best Local Similarity 94.7%; Pred. No. 5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 19
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Db 15 GAACGGAAGGCGCTTCG 33

RESULT 13
MSGRDSB
LOCUS MSGRDSB 1479 bp DNA linear BCT 21-SEP-1993
DEFINITION Mycobacterium celatum 16S ribosomal RNA gene.
ACCESSION L08170
VERSION L08170.1 GI:293250
KEYWORDS 16S ribosomal RNA.
SOURCE Mycobacterium celatum
ORGANISM Mycobacterium celatum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Butler,W.R., O'Connor,S.P., Yakrus,M.A., Smithwick,R.W.,
Plikaytis,B.B., Moss,C.W., Floyd,M.M., Woodley,C.L., Kilburn,J.O.,
Vadney,F.S. and Gross,W.M.
TITLE Mycobacterium celatum sp. nov
JOURNAL Int. J. Syst. Bacteriol. 43 (3), 539-548 (1993)
PUBMED 8102246
COMMENT Original source text: Mycobacterium celatum (library: ATCC 51130)
DNA.
FEATURES
source Location/Qualifiers
1..1479
/mol_type="genomic DNA"
/db_xref="taxon:28045"
/tissue_lib="ATCC 51130"
<1..>1479
/product="16S ribosomal RNA"
/note="putative"

rRNA

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Best Local Similarity 94.7%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 19
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Db 36 GAACGGAAGGCGCTTCG 54

RESULT 14
AX245066
LOCUS AX245066 25 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 31 from Patent WO0166797.
ACCESSION AX245066
VERSION AX245066.1 GI:15859740
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fischer,S.H., Rampal,J.B., Fahle,G.A. and Conville,P.S.
TITLE Multiplex hybridization system for identification of pathogenic
Mycobacterium and method of use
JOURNAL Patent: WO 0166797-A 31 13-SEP-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; Beckman Coulter,
Inc. (US)
FEATURES
source Location/Qualifiers
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/note="Mycobacterium-specific oligonucleotide"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 2; Length 25;
Best Local Similarity 94.7%; Pred. No. 8.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCG 19
    |||||
Db 1 GAACGGAAGGCGCTTCG 19

RESULT 15
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LOCUS AX245068 25 bp DNA linear PAT 28-SEP-2001
DEFINITION Sequence 33 from Patent WO0166797.
ACCESSION AX245068
VERSION AX245068.1 GI:15859742
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Fischer,S.H., Rampal,J.B., Fahle,G.A. and Conville,P.S.
TITLE Multiplex hybridization system for identification of pathogenic
Mycobacterium and method of use
JOURNAL Patent: WO 0166797-A 33 13-SEP-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US) ; Beckman Coulter,
Inc. (US)
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source Location/Qualifiers
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Db	1 GAACGGAAGGCCCTTCGG 19 	
RESULT 16	AF059778 171 bp rRNA linear BCT 15-MAY-1998	
LOCUS	Mycobacterium fortuitum isolate 92144 16S ribosomal RNA (rrs) gene, partial sequence.	
ACCESSION	AF059778	
VERSION	1	
KEYWORDS	Mycobacterium fortuitum	
SOURCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.	
ORGANISM	1 (bases 1 to 171)	
REFERENCE	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
AUTHORS	Genome Res. 8 (5), 435-448 (1998)	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
PUBMED	9582189	
REFERENCE	2 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL	PUBMED 9582189	
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REFERENCE	3 (bases 1 to 171)	
AUTHORS	Gingras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J., Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays	
TITLE	Mycobacterium fortuitum	
JOURNAL		



[illegible]





LOCUS AF059841 171 bp rRNA linear BCT 15-MAY-1998  
 DEFINITION Mycobacterium chelonae isolate 95A9151 16S ribosomal RNA (rrs)  
 REFERENCE gene, partial sequence.  
 ACCESSION AF059841  
 VERSION AF059841.1 GI:3132985  
 KEYWORDS  
 SOURCE Mycobacterium chelonae  
 ORGANISM Mycobacterium chelonae  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE 1 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
 JOURNAL Genome Res. 8 (5), 435-448 (1998)  
 PUBMED 9582189  
 REFERENCE 2 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA  
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 1..171  
 /organism="Mycobacterium chelonae"  
 /mol\_type="rRNA"  
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 /db\_xref="taxon:1774"  
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 /product="16S ribosomal RNA"  
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 Query Match 91.6%; Score 17.4; DB 15; Length 171;  
 Best Local Similarity 94.7%; Pred. No. 3e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GAACGGAAGGCGCTTCGG 19  
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 Db 5 GAACGGAAGGCGCTTCGG 23  
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 RESULT 27  
 AF059851  
 LOCUS AF059851 171 bp rRNA linear BCT 15-MAY-1998  
 DEFINITION Mycobacterium fortuitum strain ATCC6841 16S ribosomal RNA (rrs)  
 REFERENCE gene, partial sequence.  
 ACCESSION AF059851  
 VERSION AF059851.1 GI:3132995  
 KEYWORDS  
 SOURCE Mycobacterium fortuitum  
 ORGANISM Mycobacterium fortuitum  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE 1 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
 JOURNAL Genome Res. 8 (5), 435-448 (1998)

PUBMED 9582189  
 REFERENCE 2 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
 JOURNAL Genome Res. 8 (5), 435-448 (1998)  
 PUBMED 9582189  
 REFERENCE 3 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA  
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 /db\_xref="ATCC:6841"  
 /db\_xref="taxon:1766"  
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 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GAACGGAAGGCGCTTCGG 19  
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 Db 5 GAACGGAAGGCGCTTCGG 23  
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 AF059852  
 LOCUS AF059852 171 bp rRNA linear BCT 15-MAY-1998  
 DEFINITION Mycobacterium chelonae strain ATCC35752 16S ribosomal RNA (rrs)  
 REFERENCE gene, partial sequence.  
 ACCESSION AF059852  
 VERSION AF059852.1 GI:3132996  
 KEYWORDS  
 SOURCE Mycobacterium chelonae  
 ORGANISM Mycobacterium chelonae  
 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 REFERENCE 1 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
 JOURNAL Genome Res. 8 (5), 435-448 (1998)  
 PUBMED 9582189  
 REFERENCE 2 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays  
 JOURNAL Genome Res. 8 (5), 435-448 (1998)  
 PUBMED 9582189  
 REFERENCE 3 (bases 1 to 171)  
 AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodny,M. and Drenkow,J.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA  
 FEATURES  
 Location/Qualifiers

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Query Match          91.6%; Score 17.4; DB 1; Length 293;
Best Local Similarity 94.7%; Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
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Db 27 GAACGGAAGCCCTTCGG 45

RESULT 32
MF16SRRN
LOCUS      M.fortuitum 16S rRNA gene, partial.          316 bp      DNA      linear      BCT 14-NOV-1996
ACCESSION Y09325
VERSION    Y09325.1 GI:1669698
KEYWORDS   16S ribosomal RNA; rrr gene.
SOURCE     Mycobacterium fortuitum
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
AUTHORS    De Smet,K., Kampmann,B., Marshall,B., Kroll,S. and Levin,M.
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 316)
AUTHORS    De Smet,K.A.L.
TITLE      Direct Submission
JOURNAL    Submitted (08-NOV-1996) K.A.L. De Smet, Imperial College Medical
            School at St Marys, Medical Microbiology, Norfolk Place, London, W2
            1PG, UK

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source      Location/Qualifiers
1. .316
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/mol_type="genomic DNA"
/isolate="J6718"
/db_xref="taxon:1766"
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<1. .>316
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/product="16S ribosomal RNA"

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Best Local Similarity 94.7%; Pred. No. 2.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
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Db 52 GAACGGAAGCCCTTCGG 70

RESULT 33
DQ063127
LOCUS      Actinobacterium BAL187 16S ribosomal RNA gene, partial sequence. 384 bp      DNA      linear      BCT 27-JUN-2005
ACCESSION DQ063127
VERSION    DQ063127.1 GI:68139160
KEYWORDS   actinobacterium BAL187
SOURCE     actinobacterium BAL187
ORGANISM   Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 384)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.

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TITLE      Bacterial community composition in the central Baltic Sea analyzed
            by cultivation and molecular-based methods
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 384)
AUTHORS    Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
            Hagstrom,A.
TITLE      Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
            University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
            Location/Qualifiers
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source      1. .384
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            /country="Sweden"
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            /collection_date="8 October 2003"
            <1. .>384
            /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 384;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
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Db 4 GAACGGAAGCCCTTCGG 22

RESULT 34
AY395145
LOCUS      Uncultured bacterium clone D29ST 16S ribosomal RNA gene, partial
            sequence.          388 bp      DNA      linear      ENV 07-SEP-2004
DEFINITION
ACCESSION   AY395145
VERSION     AY395145.1 GI:37595660
KEYWORDS    ENV.
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1 (bases 1 to 388)
AUTHORS     Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.
TITLE       Comparison of diversities and compositions of bacterial populations
            inhabiting natural forest soils
JOURNAL     Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
PUBMED      15345382
REFERENCE   2 (bases 1 to 388)
AUTHORS     Hackl,E. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
            Seibersdorf research GmbH, Seibersdorf A-2444, Austria
            Location/Qualifiers
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source      1. .388
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            /clone="D29ST"
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            <1. .>388
            /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 388;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
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Db      57 GAACGGAAGGCCCTTCGG 75
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rRNA
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RESULT 35
LOCUS   BSMKN23
DEFINITION Bacterium sp. (SMKN23) DNA.
ACCESSION X78659
VERSION   X78659.1 GI:509728
KEYWORDS 16S ribosomal RNA.
SOURCE    unidentified bacterium
ORGANISM  Bacteria; environmental samples.
REFERENCE
1 Schuppler, M., Mertens, F., Schon, G. and Gobel, U.B.
  Molecular characterization of nocardioform actinomycetes in
  activated sludge by 16S rRNA analysis
  Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)
7704280
REFERENCE
2 (bases 1 to 393)
Schuppler, M.
Direct Submission
Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Heider-St.
11, 79104 Freiburg, FRG
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/product="16S ribosomal RNA"

rRNA
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Query Match 91.6%; Score 17.4; DB 1; Length 393;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
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Db 14 GAACGGAAGGCCCTTCGG 32

RESULT 36
LOCUS   AY395154
DEFINITION Uncultured actinobacterium clone E02ST 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY395154.1 GI:37595669
VERSION   AY395154
KEYWORDS  uncultured actinobacterium
SOURCE    Bacteria; Actinobacteria; environmental samples.
ORGANISM
REFERENCE
1 (bases 1 to 394)
Hackl, E., Zechmeister-Boltenstern, S., Bodrossy, L. and Sessitsch, A.
Comparison of diversities and compositions of bacterial populations
inhabiting natural forest soils
Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)
15345382
REFERENCE
2 (bases 1 to 394)
Hackl, E. and Sessitsch, A.
Direct Submission
Submitted (19-SEP-2003) Environmental and Life Sciences, ARC
Seibersdorf research GmbH, Seibersdorf A-2444, Austria
FEATURES
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/clone="E02ST"

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Query Match 91.6%; Score 17.4; DB 1; Length 394;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
|||||
Db 57 GAACGGAAGGCCCTTCGG 75

RESULT 37
LOCUS   AY043901
DEFINITION Uncultured actinobacterium clone SMS9.49WL 16S ribosomal RNA gene,
partial sequence.
ACCESSION AY043901
VERSION   AY043901.1 GI:22267274
KEYWORDS  uncultured actinobacterium
SOURCE    uncultured actinobacterium
ORGANISM  Bacteria; Actinobacteria; environmental samples.
REFERENCE
1 (bases 1 to 395)
Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
Davies, J.
Molecular characterization of bacterial diversity from British
Columbia forest soils subjected to disturbance
Can. J. Microbiol. 48 (7), 655-674 (2002)
12224564
REFERENCE
2 (bases 1 to 395)
Axelrood, P.E., Chow, M.L., Radomski, C.C., McDermott, J.M. and
Davies, J.
Direct Submission
Submitted (20-JUN-2001) BC Research Inc., 3650 Westbrook Mall,
Vancouver, BC V6S 2L2, Canada
FEATURES
source
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/organism="uncultured actinobacterium"
/mol_type="genomic DNA"
/db_xref="taxon:152507"
/clone="SMS9.49WL"
/environmental_sample
/note="from forest cut-block mineral soil from the British
Columbia Ministry of Forests Long-term Soil Productivity
(LTSP) installation near Williams Lake, BC, Canada"
<1..>395
/product="16S ribosomal RNA"

rRNA
<1..>394
/product="16S ribosomal RNA"

ORIGIN
Query Match 91.6%; Score 17.4; DB 1; Length 395;
Best Local Similarity 94.7%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
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Db 27 GAACGGAAGGCCCTTCGG 45

RESULT 38
LOCUS   AY395151
DEFINITION Uncultured bacterium clone D36ST 16S ribosomal RNA gene, partial
sequence.
ACCESSION AY395151
VERSION   AY395151.1 GI:37595666
KEYWORDS  uncultured bacterium
SOURCE    uncultured bacterium
ORGANISM  Bacteria; environmental samples.
REFERENCE
1 (bases 1 to 395)

```

AUTHORS Hackl,E., Zechmeister-Boltenstern,S., Bodrossy,L. and Sessitsch,A.  
 TITLE Comparison of diversities and compositions of bacterial populations  
 inhabiting natural forest soils  
 JOURNAL Appl. Environ. Microbiol. 70 (9), 5057-5065 (2004)  
 PUBMED 15345382

REFERENCE 2 (bases 1 to 395)

AUTHORS Hackl,E. and Sessitsch,A.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2003) Environmental and Life Sciences, ARC

Seibersdorf research GmbH, Seibersdorf A-2444, Austria

FEATURES

source

1..395

/organism="uncultured bacterium"

/mol\_type="genomic DNA"

/isolation\_source="forest soil"

/db\_xref="taxon:77133"

/clones="D36ST"

/environmental\_sample

<1..>395

/product="16S ribosomal RNA"

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 395;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19

|||||

Db 57 GAACGGAAGGCCCTTCGG 75

RESULT 39

BSSMKN14

LOCUS

DEFINITION Bacterium sp. (SMKN14) DNA. 396 bp DNA linear ENV 22-FEB-1995

ACCESSION X78655

VERSION X78655.1 GI:509724

KEYWORDS 16S ribosomal RNA.

SOURCE unidentified bacterium

ORGANISM unidentified bacterium

Bacteria; environmental samples.

REFERENCE 1

AUTHORS Schuppler,M., Mertens,F., Schon,G. and Gobel,U.B.

TITLE Molecular characterization of nocardiform actinomycetes in

activated sludge by 16S rRNA analysis

JOURNAL Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)

PUBMED 7704280

REFERENCE 2 (bases 1 to 396)

AUTHORS Schuppler,M.

TITLE Direct Submission

Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.

Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.

11, 79104 Freiburg, FRG

FEATURES

source

1..396

/organism="unidentified bacterium"

/mol\_type="genomic DNA"

/isolate="SMKN14"

/db\_xref="taxon:2338"

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/product="16S ribosomal RNA"

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 396;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19

|||||

Db 14 GAACGGAAGGCCCTTCGG 32

RESULT 40

DQ221681

LOCUS

DEFINITION Uncultured bacterium clone BPH3088 16S ribosomal RNA gene, partial  
 sequence. 400 bp DNA linear ENV 12-NOV-2005

ACCESSION DQ221681

VERSION DQ221681.1 GI:80978382

KEYWORDS ENV.

SOURCE

ORGANISM uncultured bacterium

uncultured bacterium

Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 400)

AUTHORS Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.

TITLE Bacterial diversity on leaf surfaces of the Brazilian Atlantic

JOURNAL Forest

REFERENCE 2 (bases 1 to 400)

AUTHORS Lambais,M.R., Crowley,D.E., Cury,J.C. and Bull,R.C.

TITLE Direct Submission

JOURNAL Submitted (23-SEP-2005) Solos e Nutricao de Plantas, Universidade

de Sao Paulo, Av. Padua Dias,11, Piracicaba, SP 13418-900, Brazil

Location/Qualifiers

source

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/organism="uncultured bacterium"

/mol\_type="genomic DNA"

/isolation\_source="phyllosphere"

/specific\_host="Campomanesia xanthocarpa"

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/clones="BPH3088"

/environmental\_sample

<1..>400

/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 400;

Best Local Similarity 94.7%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTCGG 19

|||||

Db 22 GAACGGAAGGCCCTTCGG 40

RESULT 41

DQ063065

LOCUS

DEFINITION Actinobacterium BAL125 16S ribosomal RNA gene, partial sequence. 401 bp DNA linear BCT 27-JUN-2005

ACCESSION DQ063065

VERSION DQ063065.1 GI:68139094

KEYWORDS

SOURCE

ORGANISM actinobacterium BAL125

actinobacterium BAL125

Bacteria; Actinobacteria.

REFERENCE 1 (bases 1 to 401)

AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

Hagstrom,A.

TITLE Bacterial community composition in the central Baltic Sea analyzed

by cultivation and molecular-based methods

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 401)

AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and

Hagstrom,A.

TITLE Direct Submission

Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,

University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden

Location/Qualifiers

source

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/organism="actinobacterium BAL125"

/mol\_type="genomic DNA"

/strain="BAL125"

/isolation\_source="Baltic Sea, 3m depth, Landsort deep St.

BY31, Zobel/R2A media"

/db\_xref="taxon:331783"

/country="Sweden"

/lat lon="60.42.726N, 05.05.595E"  
/collection\_date="2 July 2003"  
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/product="16S ribosomal RNA"

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 401;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19  
|||||  
Db 7 GAACGGAAGCCCTTCGG 25

RESULT 42  
AY234665  
LOCUS  
DEFINITION  
Bacterium Ellin6013 403 bp DNA linear BCT 08-DEC-2003  
AY234665  
ACCESSION  
AY234665.1 GI:37961822  
VERSION  
KEYWORDS  
SOURCE  
Bacterium Ellin6013  
ORGANISM  
Bacterium Ellin6013  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae.  
1 (bases 1 to 403)  
Joseph, S.J., Hugenholtz, P., Sangwan, P., Osborne, C.A. and  
Janssen, P.H.  
Laboratory Cultivation of Widespread and Previously Uncultured Soil  
Bacteria  
Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)  
14660368  
2 (bases 1 to 403)  
Joseph, S.J., Hugenholtz, P., Rana, P., Osborne, C.A., Sait, M. and  
Janssen, P.H.  
Direct Submission  
Submitted (12-FEB-2003) Department of Microbiology and Immunology,  
University of Melbourne, Parkville, Victoria 3010, Australia  
Location/Qualifiers  
1..403  
/organism="bacterium Ellin6013"  
/mol\_type="genomic DNA"  
/isolate="Ellin6013"  
/db\_xref="taxon:234120"  
<1..>403  
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 403;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19  
|||||  
Db 37 GAACGGAAGCCCTTCGG 55

RESULT 43  
AY792017/c  
LOCUS  
DEFINITION  
Mycobacterium sp. 5BR6 407 bp DNA linear BCT 20-NOV-2004  
AY792017  
ACCESSION  
AY792017.1 GI:55740316  
VERSION  
KEYWORDS  
SOURCE  
Mycobacterium sp. 5BR6  
Mycobacterium sp. 5BR6  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
1 (bases 1 to 407)  
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.  
Blotremediation of radioactive water with metallic materials  
Unpublished

REFERENCE 2 (bases 1 to 407)  
Sarro, M.I., Garcia, A.M., Moreno, D.A. and Montero, F.  
Direct Submission  
Submitted (25-OCT-2004) Dep Ingenieria y Ciencia de los Materiales,  
Escuela Tecnica Superior de Ingenieros Industriales, Universidad  
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid  
28006, Spain  
Location/Qualifiers  
1..407  
/organism="Mycobacterium sp. 5BR6"  
/mol\_type="genomic DNA"  
/isolate="5BR6"  
/isolation\_source="radioactive water"  
/db\_xref="taxon:300866"  
<1..>407  
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 407;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19  
|||||  
Db 359 GAACGGAAGCCCTTCGG 341

RESULT 44  
BSSMKN12  
LOCUS  
DEFINITION  
Bacterium sp. (SMKN12) DNA.  
X78654  
ACCESSION  
X78654.1 GI:509723  
VERSION  
KEYWORDS  
16S ribosomal RNA.  
unidentified bacterium  
unidentified bacterium  
Bacteria; environmental samples.

REFERENCE 1  
Schuppler, M., Mertens, F., Schon, G. and Gobel, U.B.  
Molecular characterization of nocardiform actinomycetes in  
activated sludge by 16S rRNA analysis  
Microbiology (Reading, Engl.) 141 (Pt 2), 513-521 (1995)  
7704280  
2 (bases 1 to 410)  
Schuppler, M.  
Direct Submission  
Submitted (28-MAR-1994) M. Schuppler, Institut fuer Med.  
Mikrobiologie & Hygiene, Universitaet Freiburg, Hermann-Herder-St.  
11, 79104 Freiburg, FRG  
Location/Qualifiers  
1..410  
/organism="unidentified bacterium"  
/mol\_type="genomic DNA"  
/isolate="SMKN12"  
/db\_xref="taxon:2338"  
1..410  
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 410;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19  
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Db 9 GAACGGAAGCCCTTCGG 27

RESULT 45  
DQ063154  
LOCUS  
DEFINITION  
Actinobacterium BAL218 16S ribosomal RNA gene, partial sequence.  
DQ063154

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VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..411
/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>411
/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 46
DQ063199 411 bp DNA linear BCT 27-JUN-2005
LOCUS actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..411
/organism="actinobacterium BAL263"
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BY31, Zobell/R2A media"
/db_xref="taxon:331810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 47
AY792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
ORGANISM Mycobacterium sp. 4BR14
Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES
source
1..411
/organism="Mycobacterium sp. 4BR14"
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
<1..>411
/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 58 GAACGGAAGGCGCTTCGG 76

RESULT 48
AM085773 414 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone 16.
DEFINITION
ACCESSION AM085773
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
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VERSION DQ063154.1 GI:68139192
KEYWORDS
SOURCE actinobacterium BAL218
ORGANISM actinobacterium BAL218
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
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/organism="actinobacterium BAL218"
/mol_type="genomic DNA"
/strain="BAL218"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331796"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
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/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 46
DQ063199 411 bp DNA linear BCT 27-JUN-2005
LOCUS actinobacterium BAL263 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION DQ063199
VERSION DQ063199.1 GI:68139237
KEYWORDS
SOURCE actinobacterium BAL263
ORGANISM actinobacterium BAL263
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1..411
/organism="actinobacterium BAL263"
/mol_type="genomic DNA"
/strain="BAL263"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobell/R2A media"
/db_xref="taxon:331810"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 17 GAACGGAAGGCGCTTCGG 35

RESULT 47
AY792013 411 bp DNA linear BCT 20-NOV-2004
LOCUS Mycobacterium sp. 4BR14 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY792013
VERSION AY792013.1 GI:55740312
KEYWORDS
ORGANISM Mycobacterium sp. 4BR14
Mycobacterium sp. 4BR14
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Biorremediation of radioactive water with metallic materials
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 411)
AUTHORS Sarro,M.I., Garcia,A.M., Moreno,D.A. and Montero,F.
TITLE Direct Submission
JOURNAL Submitted (25-OCT-2004) Dep Ingenieria Y Ciencia de los Materiales,
Escuela Tecnica Superior de Ingenieros Industriales, Universidad
Politecnica de Madrid, Jose Gutierrez Abascal, 2, Madrid, Madrid
28006, Spain
FEATURES
source
1..411
/organism="Mycobacterium sp. 4BR14"
/mol_type="genomic DNA"
/isolate="4BR14"
/isolation_source="radioactive water"
/db_xref="taxon:300864"
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/product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 411;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 58 GAACGGAAGGCGCTTCGG 76

RESULT 48
AM085773 414 bp DNA linear ENV 21-SEP-2005
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone 16.
DEFINITION
ACCESSION AM085773
VERSION AM085773.1 GI:75754596
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
samples.
REFERENCE 1
AUTHORS Uytendaele,M., Vermeir,S., Wattiau,P., Ryngaert,A. and Springael,D.
TITLE Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
```

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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Uyttebroek,M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES
    source      Location/Qualifiers
                1..414
                /organism="uncultured Mycobacterium sp."
                /mol_type="genomic DNA"
                /isolation_source="PAH-contaminated soil"
                /db_xref="taxon:171292"
                /clone="Tc"
                /environmental_sample
                /country="Belgium"
                <1..>414
                /gene="16S rRNA"
                <1..>414
                /gene="16S rRNA"
                /product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%; Score 17.4; DB 1; Length 414;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
DB 7 GAACGGAAGGCGCTTCGG 25

RESULT 49
DQ223051
LOCUS Uncultured bacterium clone HBO70 16S ribosomal RNA gene, Partial
DEFINITION sequence.
ACCESSION DQ223051.1 GI:77744948
VERSION DQ223051
KEYWORDS ENV.
SOURCE uncultured bacterium
ORGANISM Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 414)
AUTHORS Li,H. and Mu,B.
TITLE Phylogenetic diversity and community structure of bacteria in an
oil-storage cavity as detected by 16S rRNA gene library
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 414)
AUTHORS Li,H. and Mu,B.
TITLE Direct Submission
JOURNAL Submitted (26-SEP-2005) Chemical and Pharmaceutical Institution,
East China University of Science and Technology, Meilong Road,
Shanghai 200237, China
FEATURES
    source      Location/Qualifiers
                1..414
                /organism="uncultured bacterium"
                /mol_type="genomic DNA"
                /isolation_source="oil-storage cavity"
                /db_xref="taxon:77133"
                /clone="HBO70"
                /environmental_sample
                <1..>414
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 1; Length 414;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
DB 57 GAACGGAAGGCGCTTCGG 75

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RESULT 50
DQ063108
LOCUS actinobacterium BAL168 415 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL168 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063108
VERSION DQ063108.1 GI:68139141
KEYWORDS
SOURCE actinobacterium BAL168
ORGANISM actinobacterium BAL168
REFERENCE 1 (bases 1 to 415)
AUTHORS Bacteria; Actinobacteria.
                Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 415)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
                Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
    source      Location/Qualifiers
                1..415
                /organism="actinobacterium BAL168"
                /mol_type="genomic DNA"
                /strain="BAL168"
                /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
                BY31, Zobel1/R2A media"
                /db_xref="taxon:331762"
                /country="Sweden"
                /lat_lon="60.42.726N, 05.05.595E"
                /collection_date="8 October 2003"
                <1..>415
                /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 415;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
DB 7 GAACGGAAGGCGCTTCGG 25

RESULT 51
AM085786
LOCUS Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K11.
DEFINITION AM085786
ACCESSION AM085786
VERSION AM085786.1 GI:75754609
KEYWORDS ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE uncultured Mycobacterium sp.
ORGANISM uncultured Mycobacterium sp.
                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
                samples.
REFERENCE 1
AUTHORS Uyttebroek,M., Breugelmans,P., Janssen,M., Wattiau,P., Joffe,B.,
                Karlson,U., Ortega-Calvo,J.J., Bastiaens,L., Ryngaert,A. and
                Springael,D.
TITLE Distribution of the Mycobacterium sp. community and polycyclic
aromatic hydrocarbons (PAHs) among different size fractions of a
weathered PAH-contaminated soil
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 416)
AUTHORS Uyttebroek,M.
TITLE Direct Submission
JOURNAL Submitted (13-SEP-2005) Uyttebroek M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,

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FEATURES
  source
    B-3001 Leuven, BELGIUM
    Location/Qualifiers
      1. .416
      /organism="uncultured Mycobacterium sp."
      /mol_type="genomic DNA"
      /isolation_source="PAH-contaminated soil"
      /db_xref="taxon:171292"
      /clones="K11"
      /environmental_sample
      /country="Denmark"
      <1. .>416
      /gene="16S rRNA"
      <1. .>416
      /gene="16S rRNA"
      /product="16S ribosomal RNA"

  gene
    Query Match          91.6%; Score 17.4; DB 1; Length 416;
    Best Local Similarity 94.7%; Pred. No. 1.9e+03;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  rRNA
    Qy 1 GAACGGAAGGCGCTTTCGG 19
      |||||
    Db 10 GAACGGAAGGCGCTTTCGG 28
      |||||

RESULT 52
DQ063074          416 bp DNA linear BCT 27-JUN-2005
LOCUS
DEFINITION
Actinobacterium BAL134 16S ribosomal RNA gene, partial sequence.
ACCESSION
DQ063074
VERSION
DQ063074.1 GI:68139107
KEYWORDS
SOURCE
actinobacterium BAL134
actinobacterium BAL134
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 416)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 416)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
  1. .416
  /organism="actinobacterium BAL134"
  /mol_type="genomic DNA"
  /strain="BAL134"
  /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
  BY31, Zobel/R2A media"
  /db_xref="taxon:331785"
  /country="Sweden"
  /lat_lon="60.42.726N, 05.05.595E"
  /collection_date="8 October 2003"
  <1. .>416
  /product="16S ribosomal RNA"

  rRNA
    Qy 1 GAACGGAAGGCGCTTTCGG 19
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    Db 3 GAACGGAAGGCGCTTTCGG 21
      |||||

RESULT 53
DQ063074          416 bp DNA linear BCT 27-JUN-2005
LOCUS
DEFINITION
Actinobacterium BAL133 16S ribosomal RNA gene, partial sequence.
ACCESSION
DQ063073
VERSION
DQ063073.1 GI:68139102
KEYWORDS
SOURCE
actinobacterium BAL133
actinobacterium BAL133
Bacteria; Actinobacteria.
REFERENCE
1 (bases 1 to 417)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
2 (bases 1 to 417)
Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
Direct Submission
Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
Location/Qualifiers
  1. .417
  /organism="actinobacterium BAL133"
  /mol_type="genomic DNA"
  /strain="BAL133"
  /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
  BY31, Zobel/R2A media"
  /db_xref="taxon:331784"
  /country="Sweden"
  /lat_lon="60.42.726N, 05.05.595E"
  /collection_date="2 July 2003"
  <1. .>417
  /product="16S ribosomal RNA"

  rRNA
    Qy 1 GAACGGAAGGCGCTTTCGG 19
      |||||
    Db 4 GAACGGAAGGCGCTTTCGG 22
      |||||

RESULT 54
AY673210          417 bp DNA linear BCT 20-MAY-2005
LOCUS
DEFINITION
Mycobacteriaceae bacterium Ellin7044 16S ribosomal RNA gene,
partial sequence.
ACCESSION
AY673210
VERSION
AY673210.1 GI:56683067
KEYWORDS
SOURCE
Mycobacteriaceae bacterium Ellin7044
Mycobacteriaceae bacterium Ellin7044
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE
1 (bases 1 to 417)
Davis,K.E., Joseph,S.J. and Janssen,P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 417)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
Location/Qualifiers
  1. .417
  /organism="Mycobacteriaceae bacterium Ellin7044"
  /mol_type="genomic DNA"

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/isolate="Ellin7044"
/isolation_source="soil"
/db_xref="taxon:305261"
<1..>417
/product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 417;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 2 GAACGGAAGGCGCTTCGG 20
    |||||

RESULT 55
AM085788
LOCUS      418 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION Uncultured Mycobacterium sp. partial 16S rRNA gene, clone K13.
ACCESSION  AM085788
VERSION     AM085788.1 GI:75754611
KEYWORDS   ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE     uncultured Mycobacterium sp.
ORGANISM   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium; environmental
            samples.
REFERENCE  1 Uytendaele, M., Bruggeman, P., Janssen, M., Wattiau, P., Joffe, B.,
            Karlson, U., Ortega-Calvo, J.J., Bastiaens, L., Ryngaert, A. and
            Springael, D.
            Distribution of the Mycobacterium sp. community and polycyclic
            aromatic hydrocarbons (PAHs) among different size fractions of a
            weathered PAH-contaminated soil
            Unpublished
            2 (bases 1 to 418)
            Uytendaele, M.
            Direct Submission
            Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
            Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
            B-3001 Leuven, BELGIUM
FEATURES   Location/Qualifiers
            source          1..418
                        /organism="uncultured Mycobacterium sp."
                        /mol_type="genomic DNA"
                        /isolation_source="PAH-contaminated soil"
                        /db_xref="taxon:171292"
                        /clone="K13"
                        /environmental_sample
                        /country="Denmark"
                        <1..>418
                        /gene="16S rRNA"
                        <1..>418
                        /gene="16S rRNA"
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 418;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 10 GAACGGAAGGCGCTTCGG 28
    |||||

RESULT 56
AY673261
LOCUS      418 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7095 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673261

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VERSION
KEYWORDS
SOURCE
ORGANISM
Myobacteriaceae bacterium Ellin7095
Mycobacteriaceae bacterium Ellin7095
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 418)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
2 (bases 1 to 418)
Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES   Location/Qualifiers
            source          1..418
                        /organism="Mycobacteriaceae bacterium Ellin7095"
                        /mol_type="genomic DNA"
                        /isolate="Ellin7095"
                        /isolation_source="soil"
                        /db_xref="taxon:305281"
                        <1..>418
                        /product="16S ribosomal RNA"

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 418;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCGCTTCGG 55
    |||||

RESULT 57
AM085770
LOCUS      421 bp      DNA      linear      ENV 21-SEP-2005
DEFINITION Uncultured eubacterium partial 16S rRNA gene, clone T3.
ACCESSION  AM085770
VERSION     AM085770.1 GI:75754591
KEYWORDS   ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE     uncultured bacterium
ORGANISM   Bacteria; environmental samples.
1
Uytendaele, M., Vermeir, S., Wattiau, P., Ryngaert, A. and Springael, D.
Enrichment and characterization of a bacterial culture utilizing
pyrene at pH 2 and dominated by a slow-growing Mycobacterium sp.
from acidic polycyclic aromatic hydrocarbon contaminated soil
Unpublished
2 (bases 1 to 421)
Uytendaele, M.
Direct Submission
Submitted (13-SEP-2005) Uytendaele M., Division Soil and Water
Management, Catholic University of Leuven, Kasteelpark Arenberg 20,
B-3001 Leuven, BELGIUM
FEATURES   Location/Qualifiers
            source          1..421
                        /organism="uncultured bacterium"
                        /mol_type="genomic DNA"
                        /isolation_source="PAH-contaminated soil"
                        /db_xref="taxon:77133"
                        /clone="T3"
                        /environmental_sample
                        /country="Belgium"
                        <1..>421
                        /gene="16S rRNA"
                        <1..>421
                        /gene="16S rRNA"

ORIGIN

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ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 421;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 16 GAACGGAAGGCTTCGG 34

/product="16S ribosomal RNA"

RESULT 58
AJ786807
LOCUS      422 bp      DNA      linear      BCT 29-OCT-2004
DEFINITION Mycobacterium sp. R-22838 partial 16S rRNA gene, isolate R-22838.
ACCESSION  AJ786807
VERSION     AJ786807.1 GI:54887545
KEYWORDS   16S ribosomal RNA; 16S rRNA gene.
SOURCE     Mycobacterium sp. R-22838
ORGANISM   Mycobacterium sp. R-22838
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.

REFERENCE
AUTHORS    Vanparys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
            Verstraete,W. and De Vos,P.
TITLE      The microbial community composition of a commercial nitrifying
            inoculum
JOURNAL
REFERENCE  2 (bases 1 to 422)
AUTHORS    Vanparys,B.
TITLE      Direct Submission
JOURNAL    Submitted (30-JUL-2004) Vanparys B., Laboratory of Microbiology,
            University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM

FEATURES
source     1..422
            /organism="Mycobacterium sp. R-22838"
            /mol_type="genomic DNA"
            /isolate="R-22838"
            /isolation_source="commercial nitrifying inoculum"
            /db_xref="taxon:288999"
            /country="Belgium"
            /gene="16S rRNA"
            /product="16S ribosomal RNA"

gene
rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 422;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

RESULT 59
AY673284
LOCUS      422 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Micromonosporaceae bacterium Ellin7118 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673284
VERSION     AY673284.1 GI:56683141
KEYWORDS   Micromonosporaceae bacterium Ellin7118
            Micromonosporaceae bacterium Ellin7118
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Micromonosporineae; Micromonosporaceae.
            1 (bases 1 to 422)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

REFERENCE
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

FEATURES
source     1..423
            /organism="Mycobacteriaceae bacterium Ellin7039"
            /mol_type="genomic DNA"
            /isolate="Ellin7039"
            /isolation_source="soil"
            /db_xref="taxon:305258"
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

2 (bases 1 to 422)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES
source     1..422
            /organism="Micromonosporaceae bacterium Ellin7118"
            /mol_type="genomic DNA"
            /isolate="Ellin7118"
            /isolation_source="soil"
            /db_xref="taxon:305235"
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 422;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 36 GAGCGGAAGGCTTCGG 54

/product="16S ribosomal RNA"

RESULT 60
AY673205
LOCUS      423 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7039 16S ribosomal RNA gene,
            partial sequence.
ACCESSION  AY673205
VERSION     AY673205.1 GI:56683062
KEYWORDS   Mycobacteriaceae bacterium Ellin7039
            Mycobacteriaceae bacterium Ellin7039
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
            1 (bases 1 to 423)
            Davis,K.E., Joseph,S.J. and Janssen,P.H.
            Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
            Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

REFERENCE
AUTHORS    Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE      Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL    Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

FEATURES
source     1..423
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            /mol_type="genomic DNA"
            /isolate="Ellin7039"
            /isolation_source="soil"
            /db_xref="taxon:305258"
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)

2 (bases 1 to 423)
Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
Direct Submission
Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia

FEATURES
source     1..423
            /organism="Mycobacteriaceae bacterium Ellin7039"
            /mol_type="genomic DNA"
            /isolate="Ellin7039"
            /isolation_source="soil"
            /db_xref="taxon:305258"
            /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCTTCGG 55

/product="16S ribosomal RNA"

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RESULT 61
AY673206
LOCUS      423 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7040 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673206
VERSION     GI:56683063
KEYWORDS
SOURCE
ORGANISM    Mycobacteriaceae bacterium Ellin7040
Mycobacteriaceae bacterium Ellin7040
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE   2 (bases 1 to 423)
AUTHORS    Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLES     Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1..423
/organism="Mycobacteriaceae bacterium Ellin7040"
/mol_type="genomic DNA"
/isolate="Ellin7040"
/isolation_source="soil"
/db_xref="taxon:305259"
<1..>423
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 37 GAACGGAAGGCCTTCGG 55

RESULT 62
AY673207
LOCUS      423 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7041 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673207
VERSION     GI:56683064
KEYWORDS
SOURCE
ORGANISM    Mycobacteriaceae bacterium Ellin7041
Mycobacteriaceae bacterium Ellin7041
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
1 (bases 1 to 423)
Davis, K.E., Joseph, S.J. and Janssen, P.H.
Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
15691937
JOURNAL
PUBMED
REFERENCE   2 (bases 1 to 423)
AUTHORS    Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLES     Direct Submission
JOURNAL    Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1..423
/organism="Mycobacteriaceae bacterium Ellin7041"
/mol_type="genomic DNA"
/isolate="Ellin7041"

rRNA

ORIGIN

Query Match      91.6%; Score 17.4; DB 15; Length 423;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 37 GAACGGAAGGCCTTCGG 55

RESULT 63
DQ063156
LOCUS      424 bp      DNA      linear      BCT 27-JUN-2005
DEFINITION Actinobacterium BAL220 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063156
VERSION     GI:68139194
KEYWORDS
SOURCE
ORGANISM    actinobacterium BAL220
actinobacterium BAL220
Bacteria; Actinobacteria.
1 (bases 1 to 424)
Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Ragstrom, A.
Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
Unpublished
REFERENCE   2 (bases 1 to 424)
AUTHORS    Riemann, L., Leitert, C., Pommier, T., Simu, K., Holmfeldt, K. and
Ragstrom, A.
TITLES     Direct Submission
JOURNAL    Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastagan 11, Kalmar 39231, Sweden
FEATURES
source
1..424
/organism="actinobacterium BAL220"
/mol_type="genomic DNA"
/strain="BAL220"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331797"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="17 May 2004"
<1..>424
/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match      91.6%; Score 17.4; DB 15; Length 424;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTCGG 19
Db 21 GAACGGAAGGCCTTCGG 39

RESULT 64
AY673287
LOCUS      424 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION Streptosporangiaceae bacterium Ellin7121 16S ribosomal RNA gene,
partial sequence.
ACCESSION  AY673287
VERSION     GI:56683144
KEYWORDS
SOURCE
ORGANISM    Streptosporangiaceae bacterium Ellin7121
Streptosporangiaceae bacterium Ellin7121
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptosporangiineae; Streptosporangiaceae.

```

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REFERENCE 1 (bases 1 to 424)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 424)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
    source      Location/Qualifiers
                1. .424
                /organism="Streptosporangiaceae bacterium Ellin7121"
                /mol_type="genomic DNA"
                /isolate="Ellin7121"
                /isolation_source="soil"
                /db_xref="taxon:305348"
                <1. .>424
                /product="16S ribosomal RNA"
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        Query Match      91.6%; Score 17.4; DB 15; Length 424;
        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCGCTTTCGG 19
Db      37 GAGCGGAAGGCGCTTTCGG 55

RESULT 65
AV756031
LOCUS      424 bp DNA linear BCT 08-APR-2005
DEFINITION Unidentified bacterium TMB805 16S ribosomal RNA gene, partial
            sequence.
VERSION     AV756031
KEYWORDS    AV756031.1 GI:54299184
SOURCE      Unidentified bacterium TMB805
ORGANISM    Unidentified bacterium TMB805
            Bacteria.
REFERENCE   1 (bases 1 to 424)
AUTHORS     Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
            Christen,R., Chevenet,F. and Heulin,T.
TITLE       Diversity of Bacteria and Archae in the arid desert of Tataouine
JOURNAL     Unpublished
AUTHORS     Chapon,V., Benzerara,K., Barakat,M., Achouak,W., Barras,F.,
            Christen,R., Chevenet,F. and Heulin,T.
TITLE       Direct Submission
JOURNAL     Submitted (21-SEP-2004) LEMIR-DEVN-DSV, CEA, Cadarache, Saint Paul
            Lez Durance 13108, France
FEATURES
    source      Location/Qualifiers
                1. .424
                /organism="Unidentified bacterium TMB805"
                /mol_type="genomic DNA"
                /strain="TMB805"
                /isolation_source="arid soil"
                /db_xref="taxon:297191"
                <1. .>424
                /product="16S ribosomal RNA"
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        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCGCTTTCGG 19
Db      7 GAACGGAAGGCGCTTTCGG 25

REFERENCE 1 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Intracellular symbionts and other bacteria associated with deer
ticks (Ixodes scapularis) from Nantucket and Wellfleet, Cape Cod,
Massachusetts
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 425)
AUTHORS Benson,D.R., Benson,M.J., Gawronski,J.D. and Eveleigh,D.E.
TITLE Direct Submission
JOURNAL Submitted (19-SEP-2003) Molecular & Cell Biology, University of
Connecticut, U-3125, North Eagleville Rd., Storrs, CT 06279-3125,
USA
FEATURES
    source      Location/Qualifiers
                1. .425
                /organism="uncultured Mycobacterium sp."
                /mol_type="genomic DNA"
                /specific_host="Ixodes scapularis"
                /db_xref="taxon:171292"
                /clone="WI-11"
                /environmental sample
                /country="USA: Massachusetts, Cape Cod, Nantucket,
                Wellfleet"
                <1. .>425
                /product="16S ribosomal RNA"
    rRNA
    ORIGIN
        Query Match      91.6%; Score 17.4; DB 1; Length 425;
        Best Local Similarity 94.7%; Pred. No. 1.9e+03;
        Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCGCTTTCGG 19
Db      37 GAACGGAAGGCGCTTTCGG 55

RESULT 67
AV673136
LOCUS      426 bp DNA linear BCT 22-DEC-2004
DEFINITION Mycobacteriaceae bacterium Ellin5409 16S ribosomal RNA gene,
            partial sequence.
VERSION     AV673136
KEYWORDS    AV673136.1 GI:56683290
SOURCE      Mycobacteriaceae bacterium Ellin5409
ORGANISM    Mycobacteriaceae bacterium Ellin5409
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1 (bases 1 to 426)
AUTHORS     Osborne,C.A. and Janssen,P.H.
TITLE       Direct Submission
JOURNAL     Submitted (30-JUN-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
    source      Location/Qualifiers
                1. .426
                /organism="Mycobacteriaceae bacterium Ellin5409"
                /mol_type="genomic DNA"
                /isolate="Ellin5409"
                /isolation_source="soil"

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rRNA      /db_xref="taxon:305244"
<1..>426
/product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 426;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 37 GAACGGAAGGCGCTTTTCGG 55

RESULT 68
AB106918      428 bp      DNA      linear      BCT 09-SEP-2003
LOCUS      Gram-positive bacterium 1-6 for 16S ribosomal RNA, partial
DEFINITION      sequence.
ACCESSION      AB106918
VERSION      AB106918.1 GI:29421132
KEYWORDS      Gram-positive bacterium 1-6
SOURCE      Gram-positive bacterium 1-6
ORGANISM      Bacteria.
REFERENCE      1
AUTHORS      Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE      Microbial participation in iodine volatilization from soils
JOURNAL      Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE      2 (bases 1 to 428)
AUTHORS      Amachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
Fujii,T. and Muramatsu,Y.
TITLE      Direct Submission
JOURNAL      Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
Bioreources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
(E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
Fax:81-47-308-8866)
FEATURES      Location/Qualifiers
source      1..428
/mol_type="Gram-positive bacterium 1-6"
/mol_type="genomic DNA"
/strain="1-6"
/db_xref="taxon:226200"
<1..>428
/product="16S ribosomal RNA"

rRNA
rRNA      /db_xref="taxon:305244"
<1..>426
/product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 428;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 37 GAACGGAAGGCGCTTTTCGG 55

RESULT 69
DQ063058      428 bp      DNA      linear      BCT 27-JUN-2005
LOCUS      Actinobacterium BAL118 16S ribosomal RNA gene, partial sequence.
DEFINITION      sequence.
ACCESSION      DQ063058
VERSION      DQ063058.1 GI:68139087
KEYWORDS      actinobacterium BAL118
SOURCE      actinobacterium BAL118
ORGANISM      actinobacterium BAL118
Bacteria; Actinobacteria.
REFERENCE      1 (bases 1 to 428)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE      Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL      Unpublished

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REFERENCE      2 (bases 1 to 428)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE      Direct Submission
JOURNAL      Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES      Location/Qualifiers
source      1..428
/mol_type="genomic DNA"
/strain="BAL118"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331781"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>428
/product="16S ribosomal RNA"

rRNA
rRNA      /db_xref="taxon:305244"
<1..>426
/product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 428;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 15 GAACGGAAGGCGCTTTTCGG 33

RESULT 70
AJ786822      430 bp      DNA      linear      BCT 29-OCT-2004
LOCUS      Mycobacterium sp. R-23262 partial 16S rRNA gene, isolate R-23262.
DEFINITION      sequence.
ACCESSION      AJ786822
VERSION      AJ786822.1 GI:54887560
KEYWORDS      16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. R-23262
ORGANISM      Mycobacterium sp. R-23262
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE      1
AUTHORS      Vanparrys,B., Heylen,K., Lebbe,L., Boon,N., Wittebolle,L.,
Versaete,W. and De Vos,P.
TITLE      The microbial community composition of a commercial nitrifying
inoculum
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 430)
AUTHORS      Vanparrys,B.
TITLE      Direct Submission
JOURNAL      Submitted (30-JUL-2004) Vanparrys B., Laboratory of Microbiology,
University of Gent, Ledeganckstraat 35, 9000 Gent, BELGIUM
FEATURES      Location/Qualifiers
source      1..430
/mol_type="Mycobacterium sp. R-23262"
/mol_type="genomic DNA"
/isolate="R-23262"
/isolation_source="commercial nitrifying inoculum"
/db_xref="taxon:289008"
/country="Belgium"
1..430
/gene="16S rRNA"
<1..>430
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 430;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
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Db      37 GAACGGAAGGCCCTTCGG 55

RESULT 71
AY673202
LOCUS   430 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION   Mycobacteriaceae bacterium Ellin7036 16S ribosomal RNA gene,
partial sequence.
ACCESSION   AY673202
VERSION     AY673202.1 GI:56683059
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7036
ORGANISM    Mycobacteriaceae bacterium Ellin7036
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1 (bases 1 to 430)
AUTHORS     Davis, K.E., Joseph, S.J. and Janssen, P.H.
TITLE       Effects of growth medium, inoculum size, and incubation time on
            culturability and isolation of soil bacteria
JOURNAL     Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED      15691937
REFERENCE   2 (bases 1 to 430)
AUTHORS     Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUL-2004) Department of Microbiology and Immunology,
            University of Melbourne, Grattan Street, Parkville, Victoria 3010,
            Australia
FEATURES
            Location/Qualifiers
            source
              1..430
              /organism="Mycobacteriaceae bacterium Ellin7036"
              /mol_type="genomic DNA"
              /isolate="Ellin7036"
              /isolation_source="soil"
              /db_xref="taxon:305257"
              <1_>430
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 430;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
|||||
Db      37 GAACGGAAGGCCCTTCGG 55

RESULT 72
AB106919
LOCUS   431 bp      DNA      linear      BCT 09-SEP-2003
DEFINITION   Gram-positive bacterium 2-1 for 16S ribosomal RNA, partial
sequence.
ACCESSION   AB106919
VERSION     AB106919.1 GI:29421133
KEYWORDS
SOURCE      Gram-positive bacterium 2-1
ORGANISM    Gram-positive bacterium 2-1
            Bacteria.
REFERENCE   1
AUTHORS     Anachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,
            Fujii, T. and Muramatsu, Y.
TITLE       Microbial participation in iodine volatilization from soils
JOURNAL     Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE   2 (bases 1 to 431)
AUTHORS     Anachi, S., Kasahara, M., Hanada, S., Kamagata, Y., Shinoyama, H.,
            Fujii, T. and Muramatsu, Y.
TITLE       Direct Submission
JOURNAL     Submitted (27-MAR-2003) Seigo Amachi, Chiba University, Dept. of
            Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail: amachi@faculty.chiba-u.jp, Tel: 81-47-308-8868,
            Fax: 81-47-308-8866)
FEATURES
            Location/Qualifiers
            source
              1..431

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rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 431;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
|||||
Db      37 GAACGGAAGGCCCTTCGG 55

RESULT 73
AF078232
LOCUS   432 bp      DNA      linear      ENV 10-MAY-2004
DEFINITION   Grassland soil clone saf2_117 16S ribosomal RNA gene, partial
sequence.
ACCESSION   AF078232
VERSION     AF078232.1 GI:4590103
KEYWORDS
SOURCE      Grassland soil clone saf2_117
ORGANISM    grassland soil clone saf2_117
            Bacteria; environmental samples.
REFERENCE   1 (bases 1 to 432)
AUTHORS     McCaig, A.E., Glover, L.A. and Prosser, J.I.
TITLE       Molecular analysis of bacterial community structure and diversity
            in unimproved and improved upland grass pastures
JOURNAL     Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
PUBMED      10103273
REFERENCE   2 (bases 1 to 432)
AUTHORS     McCaig, A.E., Prosser, J.I. and Glover, L.A.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-1998) Institute of Medical Sciences, Department
            of Molecular and Cell Biology, University of Aberdeen,
            Foresterhill, Aberdeen AB25 2ZD, Scotland, UK
FEATURES
            Location/Qualifiers
            source
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              /db_xref="taxon:80202"
              /clone_lib="unimproved grassland soil SAF2"
              /environmental_sample
              <1_>432
              /product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match      91.6%; Score 17.4; DB 1; Length 432;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCCTTCGG 19
|||||
Db      15 GAACGGAAGGCCCTTCGG 33

RESULT 74
AY673198
LOCUS   433 bp      DNA      linear      BCT 20-MAY-2005
DEFINITION   Mycobacteriaceae bacterium Ellin7032 16S ribosomal RNA gene,
partial sequence.
ACCESSION   AY673198
VERSION     AY673198.1 GI:56683055
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7032
ORGANISM    Mycobacteriaceae bacterium Ellin7032
            Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae.
REFERENCE   1 (bases 1 to 433)

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AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE        Effects of growth medium, inoculum size, and incubation time on
              culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED       15691937
REFERENCE    2 (bases 1 to 433)
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE        Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
              University of Melbourne, Grattan Street, Parkville, Victoria 3010,
              Australia
FEATURES     Location/Qualifiers
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               1..433
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               /isolate="Ellin7032"
               /isolation_source="soil"
               /db_xref="taxon:305255"
               <1..>433
               /product="16S ribosomal RNA"
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Query Match      91.6%; Score 17.4; DB 15; Length 433;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
    |||||
Db  37 GAACGGAAGCCCTTCGG 55

RESULT 75
AY673266
LOCUS      MYCobacteriaceae bacterium Ellin7100 433 bp DNA linear BCT 20-MAY-2005
DEFINITION Mycobacteriaceae bacterium Ellin7100 16S ribosomal RNA gene,
              partial sequence.
ACCESSION  AY673266
VERSION     AY673266.1 GI:56683123
KEYWORDS
SOURCE      Mycobacteriaceae bacterium Ellin7100
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE    1 (bases 1 to 433)
AUTHORS      Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE        Effects of growth medium, inoculum size, and incubation time on
              culturability and isolation of soil bacteria
JOURNAL      Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED       15691937
REFERENCE    2 (bases 1 to 433)
AUTHORS      Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE        Direct Submission
JOURNAL      Submitted (02-JUL-2004) Department of Microbiology and Immunology,
              University of Melbourne, Grattan Street, Parkville, Victoria 3010,
              Australia
FEATURES     Location/Qualifiers
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               /product="16S ribosomal RNA"
ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 433;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
    |||||
Db  37 GAACGGAAGCCCTTCGG 55

RESULT 76
DQ063195
LOCUS      Actinobacterium BAL259 435 bp DNA linear BCT 27-JUN-2005
DEFINITION Actinobacterium BAL259 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ063195
VERSION     DQ063195.1 GI:68139233
KEYWORDS
SOURCE      actinobacterium BAL259
ORGANISM    Bacteria; Actinobacteria.
REFERENCE    1 (bases 1 to 435)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
              Hagstrom,A.
TITLE        Bacterial community composition in the central Baltic Sea analyzed
              by cultivation and molecular-based methods
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 435)
AUTHORS      Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
              Hagstrom,A.
TITLE        Direct Submission
JOURNAL      Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
              University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES     Location/Qualifiers
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               /strain="BAL259"
               /isolation_source="Baltic Sea, 3m depth, Landsort deep St.
               BY31, Zobel1/R2A media"
               /db_xref="taxon:331808"
               /country="Sweden"
               /lat_lon="60.42.726N, 05.05.595E"
               /collection_date="17 May 2004"
               <1..>435
               /product="16S ribosomal RNA"
ORIGIN
Query Match      91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
    |||||
Db  22 GAACGGAAGCCCTTCGG 40

RESULT 77
AY234692
LOCUS      Bacterium Ellin6040 435 bp DNA linear BCT 08-DEC-2003
DEFINITION Bacterium Ellin6040 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY234692
VERSION     AY234692.1 GI:37961849
KEYWORDS
SOURCE      bacterium Ellin6040
ORGANISM    Bacterium Ellin6040
              Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
              Corynebacterineae; Mycobacteriaceae.
REFERENCE    1 (bases 1 to 435)
AUTHORS      Joseph,S.J., Hugenholtz,P., Sangwan,P., Osborne,C.A. and
              Janssen,P.H.
TITLE        Laboratory Cultivation of Widespread and Previously Uncultured Soil
              Bacteria
JOURNAL      Appl. Environ. Microbiol. 69 (12), 7210-7215 (2003)
PUBMED       14660368
REFERENCE    2 (bases 1 to 435)
AUTHORS      Joseph,S.J., Hugenholtz,P., Rana,P., Osborne,C.A., Sait,M. and
              Janssen,P.H.
TITLE        Direct Submission
JOURNAL      Submitted (12-FEB-2003) Department of Microbiology and Immunology,
              University of Melbourne, Parkville, Victoria 3010, Australia
FEATURES     Location/Qualifiers

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source
1. .435
/organism="bacterium Ellin7067"
/mol_type="genomic DNA"
/isolate="Ellin7067"
/db_xref="taxon:234122"
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/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 78
AY673233
LOCUS
DEFINITION Mycobacteriaceae bacterium Ellin7067 linear BCT 20-MAY-2005
partial sequence.
ACCESSION AY673233
VERSION AY673233.1 GI:56683090
KEYWORDS
SOURCE
ORGANISM Mycobacteriaceae bacterium Ellin7067
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 435)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 435)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .435
/organism="Mycobacteriaceae bacterium Ellin7067"
/mol_type="genomic DNA"
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/isolation_source="soil"
/db_xref="taxon:305274"
<1..>435
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 435;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 79
DQ063046
LOCUS
DEFINITION Actinobacterium BAL106 16S ribosomal RNA gene, partial sequence.
ACCESSION DQ063046
VERSION DQ063046.1 GI:68139075
KEYWORDS
SOURCE
ORGANISM actinobacterium BAL106
actinobacterium BAL106
Bacteria; Actinobacteria.
REFERENCE 1 (bases 1 to 436)

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AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Bacterial community composition in the central Baltic Sea analyzed
by cultivation and molecular-based methods
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 436)
AUTHORS Riemann,L., Leitet,C., Pommier,T., Simu,K., Holmfeldt,K. and
Hagstrom,A.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2005) Dep. of Biology and Environmental Sciences,
University of Kalmar, Barlastgatan 11, Kalmar 39231, Sweden
FEATURES
source
1. .436
/organism="actinobacterium BAL106"
/mol_type="genomic DNA"
/strain="BAL106"
/isolation_source="Baltic Sea, 3m depth, Landsort deep St.
BY31, Zobel/R2A media"
/db_xref="taxon:331778"
/country="Sweden"
/lat_lon="60.42.726N, 05.05.595E"
/collection_date="2 July 2003"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 26 GAACGGAAGGCGCTTCGG 44

RESULT 80
AY673199
LOCUS
DEFINITION Mycobacteriaceae bacterium Ellin7033 linear BCT 20-MAY-2005
partial sequence.
ACCESSION AY673199
VERSION AY673199.1 GI:56683056
KEYWORDS
SOURCE
ORGANISM Mycobacteriaceae bacterium Ellin7033
Mycobacteriaceae bacterium Ellin7033
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 436)
AUTHORS Davis,K.E., Joseph,S.J. and Janssen,P.H.
TITLE Effects of growth medium, inoculum size, and incubation time on
culturability and isolation of soil bacteria
JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
PUBMED 15691937
REFERENCE 2 (bases 1 to 436)
AUTHORS Davis,K.E.R., Joseph,S.J. and Janssen,P.H.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2004) Department of Microbiology and Immunology,
University of Melbourne, Grattan Street, Parkville, Victoria 3010,
Australia
FEATURES
source
1. .436
/organism="Mycobacteriaceae bacterium Ellin7033"
/mol_type="genomic DNA"
/isolate="Ellin7033"
/isolation_source="soil"
/db_xref="taxon:305256"
<1..>436
/product="16S ribosomal RNA"

rRNA

ORIGIN
Query Match 91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 81
AY673304 436 bp DNA linear BCT 20-MAY-2005
LOCUS Mycobacteriaceae bacterium Ellin7138 16S ribosomal RNA gene,
DEFINITION partial sequence.
ACCESSION AY673304
VERSION AY673304.1 GI:56683161
KEYWORDS
SOURCE Mycobacteriaceae bacterium Ellin7138
ORGANISM Mycobacteriaceae bacterium Ellin7138
          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae.
REFERENCE 1 (bases 1 to 436)
          Davis, K.E., Joseph, S.J. and Janssen, P.H.
          Effects of growth medium, inoculum size, and incubation time on
          TITLE culturability and isolation of soil bacteria
          JOURNAL Appl. Environ. Microbiol. 71 (2), 826-834 (2005)
          PUBMED 15691937
          Davis, K.E.R., Joseph, S.J. and Janssen, P.H.
          Direct Submission.
          TITLE Submitted (02-JUL-2004) Department of Microbiology and Immunology,
          JOURNAL University of Melbourne, Grattan Street, Parkville, Victoria 3010,
          Australia
FEATURES             Location/Qualifiers
     source           1..436
                     /organism="Mycobacteriaceae bacterium Ellin7138"
                     /mol_type="genomic DNA"
                     /isolate="Ellin7138"
                     /isolation_source="soil"
                     /db_xref="taxon:305288"
     rRNA             <1..>436
                     /product="16S ribosomal RNA"
ORIGIN
Query Match          91.6%; Score 17.4; DB 15; Length 436;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 82
AF078419 437 bp DNA linear ENV 10-MAY-2004
LOCUS Grassland soil clone sl3_612 16S ribosomal RNA gene, partial
DEFINITION sequence.
ACCESSION AF078419
VERSION AF078419.1 GI:4590290
KEYWORDS
SOURCE grassland soil clone sl3_612
ORGANISM grassland soil clone sl3_612
          Bacteria; environmental samples.
REFERENCE 1 (bases 1 to 437)
          McCaig, A.E., Glover, L.A. and Prosser, J.I.
          TITLE Molecular analysis of bacterial community structure and diversity
          in unimproved and improved upland grass pastures
          JOURNAL Appl. Environ. Microbiol. 65 (4), 1721-1730 (1999)
          PUBMED 10103273
          McCaig, A.E., Prosser, J.I. and Glover, L.A.
          Direct Submission.
          TITLE Submitted (16-JUL-1998) Institute of Medical Sciences, Department
          JOURNAL of Molecular and Cell Biology, University of Aberdeen,
          Foresterhill, Aberdeen AB25 2ZD, Scotland, UK

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FEATURES             Location/Qualifiers
     source           1..437
                     /organism="grassland soil clone sl3_612"
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                     /db_xref="taxon:80115"
                     /clone_lib="improved grassland soil SL3"
                     /environmental_sample
     rRNA             <1..>437
                     /product="16S ribosomal RNA"
ORIGIN
Query Match          91.6%; Score 17.4; DB 1; Length 437;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 15 GAGCGGAAGGCGCTTCGG 33

RESULT 83
AB232370 441 bp DNA linear BCT 25-JAN-2006
LOCUS Mycobacterium kansasii gene for 16S rRNA, partial sequence,
DEFINITION strain:SA-10.
ACCESSION AB232370.1 GI:73589607
VERSION
KEYWORDS
SOURCE Mycobacterium kansasii
ORGANISM Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
          Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE 1
          Iwamoto, T. and Saito, H.
          TITLE Comparative study of two typing methods, hsp65 PRA and ITS
          sequencing, revealed a possible evolutionary link between
          Mycobacterium kansasii type I and II isolates
          JOURNAL FEMS Microbiol. Lett. 254, 129-133 (2006)
          REFERENCE 2 (bases 1 to 441)
          Iwamoto, T.
          TITLE Direct Submission
          JOURNAL Submitted (17-AUG-2005) Tomotada Iwamoto, Kobe Institute of Health,
          Department of Microbiology; Chuo-ku Minatojima-nakamachi 4-6, Kobe,
          Hyogo 6500046, Japan (E-mail: kx2t-iwmt@asahi-net.or.jp,
          URL:http://www.city.kobe.jp/cityoffice/18/menu03/h/kanken/kanken-
          top, Tel:81-78-302-6251, Fax:81-78-302-0894)
FEATURES             Location/Qualifiers
     source           1..441
                     /organism="Mycobacterium kansasii"
                     /mol_type="genomic DNA"
                     /strain="SA-10"
                     /db_xref="taxon:1768"
                     /note="type II"
                     <1..>441
                     /product="16S ribosomal RNA"
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Query Match          91.6%; Score 17.4; DB 15; Length 441;
Best Local Similarity 94.7%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTCGG 19
    |||||
Db 11 GAACGGAAGGCGCTTCGG 29

RESULT 84
AY306201 442 bp DNA linear BCT 25-JUN-2003
LOCUS Mycobacterium sp. 1351 16S ribosomal RNA gene, partial sequence.
DEFINITION
ACCESSION AY306201
VERSION AY306201.1 GI:32250950
KEYWORDS

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SOURCE      Mycobacterium sp. 1351
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 442)
AUTHORS    Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE      A High Proportion of Novel Mycobacteria Species Identified by 16S
            rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
            Clinical Setting
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 442)
AUTHORS    Turenne,C.Y.
TITLE      Direct Submission
JOURNAL    Submitted (26-MAY-2003) National Reference Centre for
            Mycobacteriology, National Microbiology Laboratory, Health Canada,
            1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES   Location/Qualifiers
            source      1..442
                        /organism="Mycobacterium sp. 1351"
                        /mol_type="genomic DNA"
                        /strain="1351"
                        /isolation_source="mouth ulcer"
                        /specific_host="Homo sapiens"
                        /db_xref="taxon:235254"
                        <1..>442
                        /product="16S ribosomal RNA"
            rRNA
            ORIGIN
            Query Match      91.6%; Score 17.4; DB 15; Length 442;
            Best Local Similarity 94.7%; Pred. No. 1.9e+03;
            Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCTTCGG 19
Db      11 GAACGGAAGGCTTCGG 29

RESULT 85
AY306205
LOCUS      Mycobacterium sp. HSC507 444 bp DNA linear BCT 25-JUN-2003
DEFINITION Mycobacterium sp. HSC507 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY306205
VERSION     AY306205.1 GI:32250954
KEYWORDS
SOURCE      Mycobacterium sp. HSC507
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 444)
AUTHORS    Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE      A High Proportion of Novel Mycobacteria Species Identified by 16S
            rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
            Clinical Setting
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 444)
AUTHORS    Turenne,C.Y.
TITLE      Direct Submission
JOURNAL    Submitted (26-MAY-2003) National Reference Centre for
            Mycobacteriology, National Microbiology Laboratory, Health Canada,
            1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES   Location/Qualifiers
            source      1..444
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                        /mol_type="genomic DNA"
                        /strain="HSC507"
                        /isolation_source="sputum"
                        /specific_host="Homo sapiens"
                        /db_xref="taxon:235258"
                        <1..>444
                        /product="16S ribosomal RNA"
            rRNA
            ORIGIN
            Query Match      91.6%; Score 17.4; DB 15; Length 444;

SOURCE      Mycobacterium sp. 1351
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 442)
AUTHORS    Pauls,R.J., Turenne,C.Y., Wolfe,J.N. and Kabani,A.
TITLE      A High Proportion of Novel Mycobacteria Species Identified by 16S
            rDNA Analysis Among Slowly Growing AccuProbe Negative Strains in a
            Clinical Setting
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 442)
AUTHORS    Turenne,C.Y.
TITLE      Direct Submission
JOURNAL    Submitted (26-MAY-2003) National Reference Centre for
            Mycobacteriology, National Microbiology Laboratory, Health Canada,
            1015 Arlington Street, Winnipeg, MB R3E 3R2, Canada
FEATURES   Location/Qualifiers
            source      1..442
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                        /strain="1351"
                        /isolation_source="mouth ulcer"
                        /specific_host="Homo sapiens"
                        /db_xref="taxon:235254"
                        <1..>442
                        /product="16S ribosomal RNA"
            rRNA
            ORIGIN
            Query Match      91.6%; Score 17.4; DB 15; Length 442;
            Best Local Similarity 94.7%; Pred. No. 1.9e+03;
            Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCTTCGG 19
Db      11 GAACGGAAGGCTTCGG 29

RESULT 86
AB106917
LOCUS      Gram-positive bacterium 1-3 for 16S ribosomal RNA, partial
DEFINITION sequence.
ACCESSION  AB106917
VERSION     AB106917.1 GI:29421131
KEYWORDS
SOURCE      Gram-positive bacterium 1-3
ORGANISM    Gram-positive bacterium 1-3
            Bacteria.
REFERENCE   1
AUTHORS    Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
TITLE      Microbial participation in iodine volatilization from soils
JOURNAL    Environ. Sci. Technol. 37, 3885-3890 (2003)
REFERENCE   2 (bases 1 to 445)
AUTHORS    Anachi,S., Kasahara,M., Hanada,S., Kamagata,Y., Shinoyama,H.,
            Fujii,T. and Muramatsu,Y.
TITLE      Direct Submission
JOURNAL    Submitted (27-MAR-2003) Seigo Anachi, Chiba University, Dept. of
            Bioresources Chem.; 648 Matsudo, Matsudo-shi, Chiba 271-8510, Japan
            (E-mail:amachi@faculty.chiba-u.jp, Tel:81-47-308-8868,
            Fax:81-47-308-8866)
FEATURES   Location/Qualifiers
            source      1..445
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                        /mol_type="genomic DNA"
                        /strain="1-3"
                        /db_xref="taxon:226199"
                        <1..>445
                        /product="16S ribosomal RNA"
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            ORIGIN
            Query Match      91.6%; Score 17.4; DB 15; Length 445;
            Best Local Similarity 94.7%; Pred. No. 1.8e+03;
            Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCTTCGG 19
Db      37 GAACGGAAGGCTTCGG 55

RESULT 87
DQ067466
LOCUS      Mycobacterium sp. FI05167 445 bp DNA linear BCT 18-JUL-2005
DEFINITION Mycobacterium sp. FI05167 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067466
VERSION     DQ067466.1 GI:67528039
KEYWORDS
SOURCE      Mycobacterium sp. FI05167
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1 (bases 1 to 445)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Unusual mycobacteria isolated from clinical samples
JOURNAL    Unpublished
REFERENCE   2 (bases 1 to 445)
AUTHORS    Tortoli,E., Mariottini,A. and Mazzarelli,G.
TITLE      Direct Submission
JOURNAL    Submitted (17-MAY-2005) Reg. Reference Center for Mycobacteria,
            Careggi Hospital, Piastra dei Servizi, Ospedale Careggi, v.le
            Morgagni 85, Firenze, FI 50134, Italy
FEATURES   Location/Qualifiers

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source 1. .445  
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/product="16S ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 445;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
|||||  
Db 15 GAACGGAAGGCGCTTTCGG 33

RESULT 88  
AY957708  
LOCUS AY957708 447 bp DNA linear ENV 16-SEP-2005  
DEFINITION Uncultured bacterium clone P3DK208 16S small subunit ribosomal RNA  
gene, partial sequence.  
ACCESSION AY957708  
VERSION AY957708.1 GI:62005486  
KEYWORDS ENV.  
SOURCE uncultured bacterium  
ORGANISM uncultured bacterium  
Bacteria; environmental samples.  
REFERENCE 1 (bases 1 to 447)  
AUTHORS McManus,C.J. and Kelley,S.T.  
TITLE Molecular survey of aeroplane bacterial contamination  
JOURNAL J. Appl. Microbiol. 99 (3), 502-508 (2005)  
PUBMED 16108791  
REFERENCE 2 (bases 1 to 447)  
AUTHORS McManus,C.J. and Kelley,S.T.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2005) Biology, San Diego State University, 5500 Campanile Dr., San Diego, CA 92182, USA

FEATURES  
source 1. .447  
/organism="uncultured bacterium"  
/mol\_type="genomic DNA"  
/isolation\_source="airplane"  
/db\_xref="taxon:77133"  
/clone="P3DK208"  
/environmental\_sample  
<1. .5447  
/product="16S small subunit ribosomal RNA"

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 1; Length 447;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
|||||  
Db 5 GAACGGAAGGCGCTTTCGG 23

RESULT 89  
MS91016SR  
LOCUS MS91016SR 450 bp DNA linear BCT 01-AUG-1997  
DEFINITION Mycobacterium sp.16S rRNA gene, isolate BN910, partial.  
ACCESSION Y08205  
VERSION Y08205.1 GI:2292948  
KEYWORDS 16S ribosomal RNA; 16S rRNA.  
SOURCE Mycobacterium sp.  
ORGANISM Mycobacterium sp.  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
1 Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and

JOURNAL Schulze-Roebecke,R.  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 450)  
Hagenau,C.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-1996) C. Hagenau, Hygiene-Institute, University of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG

COMMENT Related sequence M95469  
FEATURES Location/Qualifiers  
source 1. .450  
/organism="Mycobacterium sp."  
/mol\_type="genomic DNA"  
/isolate="BN910"  
/db\_xref="taxon:1785"  
/map="E.coli position 38-503"  
1. .450  
/gene="16S rRNA"  
<1. .>450  
/gene="16S rRNA"  
/product="16S ribosomal RNA"

gene

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 450;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
|||||  
Db 27 GAACGGAAGGCGCTTTCGG 45

RESULT 90  
MS916SR  
LOCUS MS916SR 450 bp DNA linear BCT 01-AUG-1997  
DEFINITION Mycobacterium sp. 16S rRNA gene.  
ACCESSION Y07954  
VERSION Y07954.1 GI:2292951  
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.  
SOURCE Mycobacterium sp.  
ORGANISM Mycobacterium sp.  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
1 Hagenau,C., Behringer,K., Naumann,L., Kaiser,R. and  
Schulze-Roebecke,R.  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 450)  
Hagenau,C.  
TITLE Direct Submission  
JOURNAL Submitted (12-SEP-1996) C. Hagenau, Hygiene-Institute, University of Bonn, Sigmund-Freud-Strasse 25, D-53105 Bonn, FRG

COMMENT Related sequence: M95469.  
FEATURES Location/Qualifiers  
source 1. .450  
/organism="Mycobacterium sp."  
/mol\_type="genomic DNA"  
/isolate="BN737"  
/db\_xref="taxon:1785"  
/map="E.coli 38-503"  
1. .450  
/gene="16S rRNA"  
<1. .>450  
/gene="16S rRNA"  
/product="16S ribosomal RNA"

gene

rRNA

ORIGIN

Query Match 91.6%; Score 17.4; DB 15; Length 450;  
Best Local Similarity 94.7%; Pred. No. 1.8e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
|||||  
Db 27 GAACGGAAGGCGCTTTCGG 45

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RESULT 91
AY358002
LOCUS      AY358002               450 bp    DNA          linear    BCT 19-AUG-2005
DEFINITION Actinobacterium irIII7 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358002
VERSION     AY358002.1 GI:34500643
KEYWORDS
SOURCE      actinobacterium irIII7
ORGANISM    actinobacterium irIII7
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 450)
AUTHORS     Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE       Bacterial Communities Associated with Flowering Plants of the Ni
            Hyperaccumulator Thlaspi goesingense
JOURNAL     Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED     15128517
REFERENCE   2 (bases 1 to 450)
AUTHORS     Idris,R. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
FEATURES
            Location/Qualifiers
            source
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                /strain="irIII7"
                /db_xref="taxon:244182"
                <1..>450
                /product="16S ribosomal RNA"

rRNA
ORIGIN
Query Match      91.6%;   Score 17.4;   DB 15;   Length 450;
Best Local Similarity 94.7%;   Pred. No. 1.8e+03;
Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1 GAACGGAAGGCGCTTTCGG 19
    |||||
Db   59 GAACGGAAGGCGCTTTCGG 77

RESULT 92
AJ746062
LOCUS      AJ746062               454 bp    DNA          linear    BCT 11-MAR-2005
DEFINITION Mycobacterium sp. MG5 partial 16S rRNA gene, isolate MG5.
ACCESSION  AJ746062
VERSION     AJ746062.1 GI:61097518
KEYWORDS    16S ribosomal RNA; 16S rRNA gene.
SOURCE      Mycobacterium sp. MG5
ORGANISM    Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
            Corynebacterineae; Mycobacteriaceae; Mycobacterium.
REFERENCE   1
AUTHORS     Gomila,M., Gasco,J., Busquets,A., Gil,J., Bernabeu,R., Buades,J.M.
            and Lalucat,J.
TITLE       Identification of culturable bacteria present in haemodialysis
            water and fluid
JOURNAL     FEMS Microbiol. Ecol. 52 (1), 101-114 (2005)
PUBMED
REFERENCE   2 (bases 1 to 454)
AUTHORS     Gomila,M.
TITLE       Direct Submission
JOURNAL     Submitted (07-JUN-2004) Gomila M., Biologia-IMEDEA. Microbiologia,
            Universitat de les Illes Balears, Ctra. Valldemossa, km. 7.5, 07122
            Palma de Mallorca, SPAIN
            Location/Qualifiers
            source
              1..454
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                /mol_type="genomic DNA"
                /isolate="MG5"
                /isolation_source="haemodialysis water distribution
                system"

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/db_xref="taxon:280864"
/country="Spain:Mallorca"
<1..>454
/gene="16S rRNA"
<1..>454
/gene="16S rRNA"
/product="16S ribosomal RNA"

ORIGIN
Query Match      91.6%;   Score 17.4;   DB 15;   Length 454;
Best Local Similarity 94.7%;   Pred. No. 1.8e+03;
Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  1 GAACGGAAGGCGCTTTCGG 19
    |||||
Db   30 GAACGGAAGGCGCTTTCGG 48

RESULT 93
AY358001
LOCUS      AY358001               456 bp    DNA          linear    BCT 19-AUG-2005
DEFINITION Actinobacterium irIII6 16S ribosomal RNA gene, partial sequence.
ACCESSION  AY358001
VERSION     AY358001.1 GI:34500642
KEYWORDS
SOURCE      actinobacterium irIII6
ORGANISM    actinobacterium irIII6
            Bacteria; Actinobacteria.
REFERENCE   1 (bases 1 to 456)
AUTHORS     Idris,R., Trifonova,R., Puschenreiter,M., Wenzel,W.W. and
            Sessitsch,A.
TITLE       Bacterial Communities Associated with Flowering Plants of the Ni
            Hyperaccumulator Thlaspi goesingense
JOURNAL     Appl. Environ. Microbiol. 70 (5), 2667-2677 (2004)
PUBMED     15128517
REFERENCE   2 (bases 1 to 456)
AUTHORS     Idris,R. and Sessitsch,A.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Environmental and Life Sciences, ARC
            Seibersdorf Research GmbH, Seibersdorf A-2444, Austria
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VERSION     AJ609008.1 GI:41033549
KEYWORDS    ENV; 16S ribosomal RNA; 16S rRNA gene.
SOURCE      uncultured bacterium
ORGANISM    Bacteria; environmental samples.
REFERENCE   1
AUTHORS     Schneider,B.A., Huettli,R.F. and Schneider,B.U.
TITLE       Evidence for a diverse bacterial consortium specialized to the
            degradation of aliphatic and aromatic hydrocarbons in lignite

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matter of a forest reclamation site

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 459)  
AUTHORS Schneider, B.A.  
TITLE Direct Submission  
JOURNAL Submitted (20-NOV-2003) Schneider B.A., Soil Protection and  
Reclamation, Brandenburg Technical University,  
Theodor-Neubauer-Str. 6, D-03046 Cottbus, GERMANY

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DEFINITION sequence.  
ACCESSION AY754884  
VERSION AY754884.1 GI:54065968  
KEYWORDS  
SOURCE Mycobacterium vaccae  
ORGANISM Mycobacterium vaccae  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS Tortoli, E., Mariottini, A. and Mazzarelli, G.  
TITLE Unusual mycobacteria isolated from clinical samples  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 459)  
AUTHORS Tortoli, E.  
TITLE Direct Submission  
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale  
Morgagni 85, Firenze, FI 50134, Italy

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ACCESSION AY754885  
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ORGANISM Mycobacterium sp. FI02139  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
REFERENCE 1 (bases 1 to 459)  
AUTHORS Tortoli, E., Mariottini, A. and Mazzarelli, G.  
TITLE Unusual mycobacteria isolated from clinical samples  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 459)  
AUTHORS Tortoli, E.  
TITLE Direct Submission  
JOURNAL Submitted (16-SEP-2004) Microbiology, Careggi Hospital, viale  
Morgagni 85, Firenze, FI 50134, Italy

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Db 30 GAACGGAAAGCCCTTTCGG 48

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DEFINITION sequence.  
ACCESSION AB118817  
VERSION AB118817.1 GI:66841148  
KEYWORDS  
SOURCE denitrifying bacterium W67a  
ORGANISM denitrifying bacterium W67a  
Bacteria; Actinobacteria.  
REFERENCE 1  
AUTHORS Hashimoto, T., Whang, K.S. and Nagaoka, K.  
TITLE A Quantitative Evaluation and Phylogenetic Characterization of  
Oligotrophic Denitrifying Bacteria Harbored in Subsurface Upland  
Soil Using Improved Culturability  
JOURNAL Biol. Fertil. Soils (2005) In press  
REFERENCE 2 (bases 1 to 464)  
AUTHORS Hashimoto, T. and Whang, K.  
TITLE Direct Submission  
JOURNAL Submitted (29-AUG-2003) Tomoyoshi Hashimoto, National Agricultural  
Research Center for Kyushu Okinawa Region, Department of  
Agro-Environmental Research, Nishigouhi-cho Suva 2421,  
Kikuchi-gun, Kumamoto, 861-1192, Japan  
(E-mail: hashimoto@affrc.go.jp, Tel: 0962427765, Fax: 0962491002)

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VERSION    DQ142669.1 GI:71912648
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ORGANISM   Mycobacterium sp. FI03023
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REFERENCE  1 (bases 1 to 464)
            Tortoli, E., Mariottini, A. and Mazzarelli, G.
            Unusual mycobacteria isolated from clinical specimens
            Unpublished
REFERENCE  2 (bases 1 to 464)
            Tortoli, E., Mariottini, A. and Mazzarelli, G.
            Direct Submission
            Submitted (18-JUL-2005) Microbiology, Careggi Hospital, Viale
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ACCESSION  DQ142672
VERSION    DQ142672.1 GI:71912651
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SOURCE     Mycobacterium sp. FI05244
ORGANISM   Mycobacterium sp. FI05244
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REFERENCE  1 (bases 1 to 464)
            Tortoli, E., Mariottini, A. and Mazzarelli, G.
            Unusual mycobacteria isolated from clinical specimens
            Unpublished
REFERENCE  2 (bases 1 to 464)
            Tortoli, E., Mariottini, A. and Mazzarelli, G.
            Direct Submission
            Submitted (25-JUL-2005) Microbiology, Careggi Hospital, Viale
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Db 30 GAACGGAAGGCCCTTCGG 48

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DEFINITION Mycobacterium sp. FI05038 16S ribosomal RNA gene, partial sequence.
ACCESSION  DQ067465
VERSION    DQ067465.1 GI:67528030
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SOURCE     Mycobacterium sp. FI05038
ORGANISM   Mycobacterium sp. FI05038
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REFERENCE  1 (bases 1 to 466)
            Tortoli, E., Mantella, A., Mariottini, A., Mazzarelli, G., Pecile, P.,
            Rogasi, P. G., Sterrantino, G., Fantoni, E. and Leoncini, F.
            Successfully treated spondylodiscitis due to a previously
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            J. Med. Microbiol. 55 (PT 1), 119-121 (2006)
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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Perfect score: 25

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Scoring table: IDENTITY NUC  
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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 104899840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 300 summaries

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5	24	96.0	24	10	ADG88353
6	24	96.0	24	14	AEA08228
7	23.4	93.6	500	13	ADZ20587 Formaldeh
8	23.4	93.6	1449	14	AEA22405
9	23.4	93.6	1455	14	AEA22412
10	23.4	93.6	1482	14	AEA22404
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12	21.8	87.2	166	2	AXX99199 M. kansas
13	21.8	87.2	460	8	ABZ76674 Microtetr
14	21.8	87.2	497	14	ABZ76674
15	21.8	87.2	500	14	ABZ76673 Streptosp
16	21.8	87.2	1343	12	ADG88356
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18	21.8	87.2	1403	12	ADJ38609 Micromono

19	21.8	87.2	1427	14	ADW16290
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25	21.8	87.2	1511	14	ADE11327
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Adc61232	Baeyer-Vi
Adf56671	YS-45494
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Adsl7269	Lechevali
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111	19.4	77.6	39	15	AEF95350	Aef95350 Nucleic a	c 184	17	68.0	110000	6	ABA03041_07	Continuation (8 of
112	19.4	77.6	41	14	ADU69960	Adue9960 LAMP reac	185	16.8	67.2	36538	10	ABV75558	Abv75558 Saccharop
113	19.4	77.6	41	14	ADU69958	Adue9958 LAMP reac	c 186	16.6	66.4	338	6	ABQ99174	Abq99174 Human ORF
114	19.4	77.6	42	14	ADU69959	Adue9959 LAMP reac	c 187	16.6	66.4	381	5	AAS77874	Asq77874 DNA encod
115	19.4	77.6	42	14	ADU69957	Adue9957 LAMP reac	c 188	16.6	66.4	479	4	AAK79949	Aak79949 Human imm
116	19.2	76.8	1158	14	ADW16249	Adw16249 DNA copy	c 189	16.6	66.4	479	4	AAK79948	Aak79948 Human imm
117	19	76.0	23	4	ADL11277	Adl11277 Mycobacte	c 190	16.6	66.4	508	5	AAS34274	Aas34274 Human cDN
118	19	76.0	23	10	ADG88358	Adg88358 Mycobacte	191	16.6	66.4	580	13	ADQ51208	Adq51208 Novel can
119	19	76.0	23	14	AEA08233	Aea08233 Mycobacte	c 192	16.6	66.4	671	13	ADQ79174	Adq79174 Novel can
120	19	76.0	50	2	AAX99197	Aax99197 M. sorofu	c 193	16.6	66.4	780	6	ABQ90469	Abq90469 M. capsul
121	18.8	75.2	1418	8	ABZ25595	Abz25595 Rhodococc	c 194	16.6	66.4	906	13	ADS61681	Ads61681 Bacterial
122	18.4	73.6	36	14	ADU69991	Adu69991 LAMP reac	c 195	16.6	66.4	1020	6	ABN74681	Abn74681 Bovine em
123	18.4	73.6	37	14	ADU69989	Adu69989 LAMP reac	196	16.6	66.4	1392	8	ACA23504	ACA23504 Prokaryot
124	18.4	73.6	1452	14	AEA22408	Aea22408 Mycobacte	197	16.6	66.4	1522	6	ABN89870	Abn89870 Clostridi
125	18	72.0	19	4	ADL11274	Adl11274 Mycobacte	c 198	16.6	66.4	2077	4	ABL04789	AbL04789 Drosophil
126	18	72.0	19	10	ADG88355	Adg88355 Mycobacte	c 199	16.6	66.4	3216	13	ADV97351	Adv97351 N tabacum
127	18	72.0	19	14	AEA08230	Aea08230 Mycobacte	c 200	16.6	66.4	4456	4	ABL04788	AbL04788 Drosophil
128	18	72.0	23	2	AAV59060	Aav59060 Primer KY	c 201	16.6	66.4	9591	14	AEC36640	Aec36640 Zucchini
129	18	72.0	23	10	ADF41650	Adf41650 Mycobacte	c 202	16.6	66.4	18900	13	ADW00484	Adw00484 Escherich
130	18	72.0	23	13	ADR90575	Adr90575 Mycobacte	c 203	16.6	66.4	41723	4	ABL23684	AbL23684 Drosophil
131	18	72.0	50	2	AAX99200	Aax99200 M. intrac	c 204	16.6	66.4	43572	12	ADQ97861	Adq97861 Mouse can
c 132	18	72.0	1137	9	ADS7239	Ads7239 Human CGD	205	16.4	65.6	18	ACC59438	Acc59438 T denticio	
133	18	72.0	1452	13	ADR90573	Adr90573 M intrace	206	16.4	65.6	18	ADD10217	Add10217 Probe #3	
134	17.8	71.2	1366	13	ADX59584	Adx59584 Plant ful	207	16.4	65.6	23	AAQ36781	Aaq36781 Mycobacte	
135	17.8	71.2	4540	6	ABK63777	Abk63777 Rat seque	208	16.4	65.6	25	AAV24418	Aav24418 Target se	
c 136	17.8	71.2	4540	10	ADB58396	Adb58396 Toxicity-	209	16.4	65.6	25	AAV13026	Aav13026 Mycobacte	
137	17.6	70.4	465	10	AB57680	Ab57680 Toxicity-	210	16.4	65.6	25	AAQ30718	Aas30718 Mycobacte	
138	17.6	70.4	960	11	ACN44517	Acn44517 Mouse mRN	211	16.4	65.6	25	AAQ30716	Aas30716 Mycobacte	
139	17.6	70.4	1436	14	ADW16288	Adw16288 DNA copy	212	16.4	65.6	549	4	ABL15533	AbL15533 Drosophil
140	17.6	70.4	1561	13	ADR07240	Adr07240 Full leng	213	16.4	65.6	1405	3	AAA15482	Aaa15482 16S rRNA
141	17.6	70.4	1763	15	AEb88040	Aeb88040 Human cDN	214	16.4	65.6	1413	3	AAA15478	Aaa15478 16S rRNA
142	17.6	70.4	1787	4	AAH14162	Aah14162 Human cDN	215	16.4	65.6	1432	12	ADK72438	Adk72438 Cyclocias
143	17.6	70.4	1792	12	ADQ84493	Adq84493 Human tum	216	16.4	65.6	1460	12	ADK72439	Adk72439 Cyclocias
144	17.6	70.4	1792	12	ADQ85308	Adq85308 Human tum	217	16.4	65.6	1462	3	AAA15480	Aaa15480 16S rRNA
145	17.6	70.4	43800	11	ACN44516	Acn44516 Mouse gen	218	16.4	65.6	1526	5	AAF76237	Aaf76237 Cyclocias
146	17.4	69.6	36	14	ADU69990	Adue69990 LAMP reac	219	16.4	65.6	1528	5	AAF76235	Aaf76235 Cyclocias
147	17.4	69.6	1456	15	AEg07725	Aeg07725 Nocardioi	220	16.4	65.6	1529	5	AAF76236	Aaf76236 Cyclocias
148	17.2	68.8	1417	12	ADJ87468	Adj87468 Tonato le	221	16.4	65.6	2274	13	ADX62498	Adx62498 Plant ful
149	17.2	68.8	1735	13	ADX33856	Adx33856 Plant ful	222	16.4	65.6	5503	4	ABL15532	AbL15532 Drosophil
150	17.2	68.8	1776	2	AAV59559	Aav59559 Human sec	223	16.2	64.8	587	8	ABZ53802	Abz53802 Aspergill
151	17.2	68.8	1776	6	AB573546	Ab573546 Human cDN	c 224	16.2	64.8	590	8	AQB83792	Aqb83792 Normal co
152	17.2	68.8	1776	9	ACD82689	AcD82689 cDNA sequ	c 225	16.2	64.8	637	3	AAF14590	Aaf14590 Aspergill
153	17.2	68.8	1776	10	ADI22774	Adi22774 cDNA enco	226	16.2	64.8	637	13	ADU58631	Adu58631 Aspergill
154	17.2	68.8	1776	12	ADH73776	Adh73776 Human sec	c 227	16.2	64.8	637	14	ADZ96634	Adz96634 Aspergill
155	17.2	68.8	1791	2	AAV59723	Aav59723 Human sec	c 228	16.2	64.8	665	14	AEb88183	Aeb88183 Human cDN
156	17.2	68.8	1791	6	AB573713	Ab573713 Human cDN	c 229	16.2	64.8	755	14	AEb88269	Aeb88269 Human DNA
157	17.2	68.8	1791	9	ACD82856	AcD82856 cDNA sequ	c 230	16.2	64.8	788	3	AAC33114	Aac33114 Arabidops
158	17.2	68.8	1791	10	ADI22941	Adi22941 cDNA enco	c 231	16.2	64.8	790	14	AEb88271	Aeb88271 Human DNA
159	17.2	68.8	1791	12	ADH73943	Adh73943 Human sec	c 232	16.2	64.8	813	14	AEb88267	Aeb88267 Human DNA
c 160	17.2	68.8	2919	13	ADS59960	Ads59960 Bacterial	c 233	16.2	64.8	972	6	ABK77386	Abk77386 Bacillus
161	17.2	68.8	3757	4	ABL14492	AbL14492 Drosophil	c 234	16.2	64.8	1049	13	ADS95257	Ads95257 Murine th
162	17.2	68.8	5656	4	ABL14490	AbL14490 Drosophil	c 235	16.2	64.8	1049	13	ADV68114	Adv68114 Biologica
163	17.2	68.8	13206	4	ABL14494	AbL14494 Drosophil	c 236	16.2	64.8	1393	3	AAC41244	Aac41244 Arabidops
164	17	68.0	260	6	AAL42509	Aal42509 Self-asse	c 237	16.2	64.8	1447	13	ADT15563	Adt15563 Plant cDN

C 238 16.2 64.8 1498 4 AAF63387  
 C 239 16.2 64.8 1588 4 AAF63423  
 C 240 16.2 64.8 1902 13 ADT48449  
 C 241 16.2 64.8 2226 13 ACN43714  
 C 242 16.2 64.8 2239 4 ABL02095  
 C 243 16.2 64.8 2294 4 AAF63419  
 C 244 16.2 64.8 2340 8 ACA04767  
 C 245 16.2 64.8 2371 4 AAF63416  
 C 246 16.2 64.8 2497 4 AAF63421  
 C 247 16.2 64.8 2597 13 ACN43713  
 C 248 16.2 64.8 2648 6 ABT05471  
 C 249 16.2 64.8 2693 4 AAF63418  
 C 250 16.2 64.8 2693 6 ABT05470  
 C 251 16.2 64.8 2729 12 ADQ87074  
 C 252 16.2 64.8 2736 6 ABL39778  
 C 253 16.2 64.8 2762 3 AAG96066  
 C 254 16.2 64.8 2762 4 AAF63422  
 C 255 16.2 64.8 2762 4 AAF63386  
 C 256 16.2 64.8 2762 6 AAD31693  
 C 257 16.2 64.8 2762 12 ADQ99441  
 C 258 16.2 64.8 2762 13 ADR69170  
 C 259 16.2 64.8 2762 13 ADR69004  
 C 260 16.2 64.8 2762 13 ACN40734  
 C 261 16.2 64.8 2762 13 ADR17884  
 C 262 16.2 64.8 2762 13 ADR87780  
 C 263 16.2 64.8 2762 13 ADR65838  
 C 264 16.2 64.8 2762 13 ADR65522  
 C 265 16.2 64.8 2762 13 ADS09773  
 C 266 16.2 64.8 2762 14 ADV16894  
 C 267 16.2 64.8 2762 14 ADZ66963  
 C 268 16.2 64.8 2762 14 ADZ74432  
 C 269 16.2 64.8 2805 4 AAF63420  
 C 270 16.2 64.8 2837 5 AAS87012  
 C 271 16.2 64.8 2882 4 AAF63424  
 C 272 16.2 64.8 2888 10 ADC14273  
 C 273 16.2 64.8 3200 4 ABL25250  
 C 274 16.2 64.8 3417 4 ABL02094  
 C 275 16.2 64.8 5498 4 ABL08702  
 C 276 16.2 64.8 110000 14 AEB35724\_2  
 C 277 16.2 64.8 110000 14 AEB35724\_3  
 C 278 16.2 64.8 110000 14 AEB39175\_23  
 C 279 16.2 64.8 110000 14 AEB39175\_24  
 C 280 16.2 64.8 110000 14 AEB42401\_23  
 C 281 16 64.0 17 14 ADU70004  
 C 282 16 64.0 20 2 AAG94743  
 C 283 16 64.0 24 2 AAV59061  
 C 284 16 64.0 24 12 ADP04297  
 C 285 16 64.0 24 14 AEA89585  
 C 286 16 64.0 26 4 AAD11278  
 C 287 16 64.0 26 10 ADG88359  
 C 288 16 64.0 26 14 AEA08234  
 C 289 16 64.0 121 12 ADK91427  
 C 290 16 64.0 161 6 ABK79321  
 C 291 16 64.0 171 12 ACH86554  
 C 292 16 64.0 330 4 AAS27929  
 C 293 16 64.0 330 10 ADG40833  
 C 294 16 64.0 330 11 ADI96607  
 C 295 16 64.0 360 6 ABO92667  
 C 296 16 64.0 455 3 AAC55929  
 C 297 16 64.0 455 3 AAC57218  
 C 298 16 64.0 465 11 ABD15057  
 C 299 16 64.0 496 5 AAS87009  
 C 300 16 64.0 506 12 ACH77915

## ALIGNMENTS

RESULT 1

AAD11271

ID AAD11271 standard; DNA; 25 BP.

XX

AC AAD11271;

XX 24-SEP-2001 (first entry)  
 DT Mycobacterium 16S rRNA amplifying primer #15.  
 DE Mycobacterium 16S rRNA; 16S ribosomal RNA; amplification;  
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.  
 XX Mycobacterium sp.  
 OS WO200144510-A2.  
 PN 21-JUN-2001.  
 XX 17-DEC-1999; 99WO-US030346.  
 PF 17-DEC-1999; 99WO-US030346.  
 PR (GENP-) GEN-PROBE INC.  
 XX (INNR) BIOMERIEUX SA.  
 PA Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodriguez M;  
 XX WPI; 2001-398170/42.  
 DR Detecting Mycobacterium species, involves in vitro amplification of 16S  
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
 PT specific primers, and detecting the amplified nucleic acid.  
 XX Claim 1; Page 36; 44pp; English.  
 PS The invention relates to a method of detecting Mycobacterium species,  
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
 CC comprising a polymerase, and at least two primers, and then detecting the  
 CC amplified nucleic acid. The method is relatively simple and useful for  
 CC detecting the presence of various Mycobacterium species in a biological  
 CC sample, and thus important for diagnosis of infections resulting from  
 CC them. The method is especially important for screening opportunistic  
 CC infections caused by M. tuberculosis or a Mycobacterium other than  
 CC tuberculosis (MOTT). The present sequence is a PCR primer used for  
 CC amplifying Mycobacterium 16S rRNA  
 SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 4; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.057; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0;  
 QY 1 GCAAGTCGACGAAAGGCTTTTCG 25  
 |||||  
 Db 1 GCAAGTCGACGAAAGGCTTTTCG 25  
 RESULT 2  
 ADG88352  
 ID ADG88352 standard; DNA; 25 BP.  
 XX  
 AC ADG88352;  
 DT 11-MAR-2004 (first entry)  
 DE Mycobacterium amplifying PCR primer #21.  
 XX  
 KW In vitro amplification; PCR; primer; ss.  
 OS Mycobacterium celatum.  
 XX US2003165824-A1.  
 PN 04-SEP-2003.  
 PD 15-DEC-2000; 2000US-00738274.  
 PF

```
XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Pi Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2003-898044/82.
XX
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX
XX PS Claim 1; SEQ ID NO 21; 20pp; English.
XX
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 25; DB 10; Length 25;
XX Best Local Similarity 100.0%; Pred. No. 0.057;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
XX | | | | | | | | | | | | | | | | | |
XX Db 1 GCAAGTCGAACGGAAGGCGCTTTCG 25
XX
XX RESULT 4
XX AAD11272
XX ID AAD11272 standard; DNA; 24 BP.
XX
XX AC AAD11272;
XX
XX XX 24-SEP-2001 (first entry)
XX DT
XX XX Mycobacterium 16S rRNA amplifying primer #16.
XX DE
XX XW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX OS Mycobacterium sp.
XX
XX XN WO200144510-A2.
XX PD
XX XX 21-JUN-2001.
XX
XX XX 17-DEC-1999; 99WO-US030346.
XX PF
XX XX 17-DEC-1999; 99WO-US030346.
XX PR
XX XX (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX DR WPI; 2001-398170/42.
XX
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX
XX PS Claim 1; Page 36; 44pp; English.
XX
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 96.0%; Score 24; DB 4; Length 24;
```

```
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 5
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
PN US2003165824-A1.
PD
PF 04-SEP-2003.
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
(BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 96.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 6
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX
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```
Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
PCR; primer; ss.
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
(BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 22; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S rRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 96.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCGCTTTTCG 25
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 7
ADZ20587
ID ADZ20587 standard; DNA; 500 BP.
XX
AC ADZ20587;
XX
DT 16-JUN-2005 (first entry)
DE Formaldehyde decomposition related Mycobacterium sp. DNA.
XX
KW decomposition; formaldehyde; ds.
XX
OS Mycobacterium sp.
XX
PN JP2003284548-A.
XX
PD 07-OCT-2003.
XX
PF 27-MAR-2002; 2002JP-00089307.
XX
PR 27-MAR-2002; 2002JP-00089307.
XX
(KUMO-) KUMOMOTO KEN PREFECTURE.
PA (MITS-) MITSUWA CORP YG.
PA
```

PA (MITS-) MITSUWA BIPRO KK.  
 XX  
 DR WPI; 2004-172963/17.  
 XX  
 PT Decomposing formaldehyde by Mycobacterium and/or growth medium of the  
 PT cells.  
 XX  
 PS Example 1; SEQ ID NO 1; 20pp; Japanese.  
 XX  
 CC The invention relates to a novel method for decomposing formaldehyde by  
 CC using microbial cells that belong to Mycobacterium sp. or Fusarium  
 CC oxysporum, and/or the growth medium of the microbial cells. The invention  
 CC further comprises: microbial cells which belong to Mycobacterium sp.  
 CC having the ability to decompose formaldehyde; a formaldehyde  
 CC decomposition agent comprising Mycobacterium sp. and/or the growth medium  
 CC of the microbial cells; and a formaldehyde decomposition agent comprising  
 CC F. oxysporum and/or its growth medium. The method is useful for  
 CC decomposing formaldehyde in sea water by Mycobacterium sp. or F.  
 CC oxysporum that is deposited under FERM P-S18690 or FERM P-18483,  
 CC respectively. This polynucleotide sequence represents the Mycobacterium  
 CC sp. DNA of the invention.  
 XX  
 SQ Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;  
 XX  
 Query Match 93.6%; Score 23.4; DB 13; Length 500;  
 Best\_Local\_Similarity 96.0%; Pred. No. 0.45; Length 500;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 Db 53 GCAAGTCGAACGGAAGGCGCTTCG 77  
 RESULT 8  
 AEA22405  
 ID AEA22405 standard; DNA; 1449 BP.  
 AC AEA22405;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.  
 XX  
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium fortuitum.  
 XX  
 FN US2005130168-A1.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 31-OCT-2003; 2003US-00697802.  
 XX  
 PR 31-OCT-2003; 2003US-00697802.  
 XX  
 PA (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 PI Han X, Pham AS;  
 XX  
 DR WPI; 2005-424597/43.  
 XX  
 PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 PS Disclosure; SEQ ID NO 6; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations; (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations; or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;  
 XX  
 Query Match 93.6%; Score 23.4; DB 14; Length 1449;  
 Best\_Local\_Similarity 96.0%; Pred. No. 0.51;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25  
 Db 20 GCAAGTCGAACGGAAGGCGCTTCG 44  
 RESULT 9  
 AEA22412  
 ID AEA22412 standard; DNA; 1455 BP.  
 AC AEA22412;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.  
 XX  
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium mucogenicum.  
 XX  
 FN US2005130168-A1.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 31-OCT-2003; 2003US-00697802.  
 XX  
 PR 31-OCT-2003; 2003US-00697802.  
 XX  
 PA (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 PI Han X, Pham AS;  
 XX  
 DR WPI; 2005-424597/43.  
 XX  
 PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 PS Disclosure; SEQ ID NO 13; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product

CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.

XX Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 1455;  
 Best Local Similarity 96.0%; Pred. No. 0.51;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCAGTCGACGGAAGGCCCTTCG 25  
 DB 30 GCAGTCGACGGAAGGCCCTTCG 54

RESULT 10  
 AEA22404  
 ID AEA22404 standard; DNA; 1482 BP.  
 XX AEA22404;  
 AC AEA22404;  
 DT 25-AUG-2005 (first entry)  
 XX Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.  
 DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 KW Mycobacterium farcinogenes.  
 OS Mycobacterium farcinogenes.  
 XX US2005130168-A1.  
 PN 16-JUN-2005.  
 PD 31-OCT-2003; 2003US-00697802.  
 PF 31-OCT-2003; 2003US-00697802.  
 XX (HANK/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX Han X, Pham AS;  
 PI WPI; 2005-424597/43.  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.  
 XX Disclosure; SEQ ID NO 5; 74pp; English.

CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.

XX Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 1482;  
 Best Local Similarity 96.0%; Pred. No. 0.51;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GCAGTCGACGGAAGGCCCTTCG 25  
 DB 28 GCAGTCGACGGAAGGCCCTTCG 52

RESULT 11  
 ADF94057  
 ID ADF94057 standard; DNA; 50 BP.  
 XX ADF94057;  
 AC ADF94057;  
 DT 11-MAR-2004 (first entry)  
 XX Microorganism detection probe, SEQ ID 150.  
 DE Probe; detection; identification; microorganism; food; drug;  
 KW 16S rRNA VI region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
 XX Mycobacterium gordonae.  
 OS WO2003106676-A1.  
 PN 24-DEC-2003.  
 PD 16-JUN-2003; 2003WO-JP007620.  
 PF 14-JUN-2002; 2002JP-00174564.  
 PR (HISF) HITACHI SOFTWARE ENG CO LTD.  
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
 PI Shimadzu M, Kobayashi I, Ishiko H;  
 XX WPI; 2004-071565/07.

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
 PT microorganism for specific detection and identification of the  
 PT microorganism in foods and drug compositions.

XX Claim 2; SEQ ID NO 150; 150pp; Japanese.

XX The present invention relates to probes (ADF93908-ADF94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADF94060 and ADF94061, labelling the amplification product (a  
 CC fluorescence label is preferred) and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,  
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*  
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*  
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*  
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*  
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*  
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*  
 CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,  
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Streptococcus faecium*,  
 CC *Streptococcus sanguinis*, *Streptococcus mitis*, *Streptococcus intermedius*,  
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*  
 CC *aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*  
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*  
 CC *caseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*  
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*  
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Bikenella*  
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*  
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,  
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*  
 CC *gordonae*.

SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 12; Length 50;  
 Best Local Similarity 92.0%; Pred. No. 2.1;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGACGGAAGGCGCTTCG 25  
 Db 3 GCAAGTCGACGCTGAGGCGCTTCG 27

RESULT 12

AA332481  
 ID AAX32481 standard; DNA; 166 BP.

XX AAX32481;

DT 22-JUN-1999 (first entry)

DE Preferred probe of the invention.

KW 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.

XX Synthetic.

OS Streptomyces ambofaciens.

XX WO9914361-A1.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-EP006038.

XX 18-SEP-1997; 97US-0059295P.

XX 16-DEC-1997; 97US-0069748P.

XX (MERI ) MERCK SHARP & DOHME ESPANA SAE.

XX Genilloud O, Mellado RP, Parro V, Rodriguez V;  
 XX WPI; 1999-229548/19.

PT New probes used for detection of maduromycetes bacteria and to  
 PT differentiate between maduromycetes and streptomycetes.

PS Disclosure; Fig 1; 22pp; English.

XX The invention relates to a novel nucleic acid probe hybridises to a  
 CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria  
 CC under hybridisation conditions, and does not hybridise to nucleic acids  
 CC encoding a portion of 16S rRNA of streptomycetes under identical  
 CC hybridisation conditions. The probes can be used for detecting the  
 CC presence of maduromycetes bacteria in a sample and for differentiating  
 CC between maduromycetes and streptomycetes bacteria in a sample. The  
 CC present sequence represents a preferred probe of the invention

SQ Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 2; Length 166;  
 Best Local Similarity 92.0%; Pred. No. 2.3;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGACGGAAGGCGCTTCG 25  
 Db 56 GCAAGTCGACGGAAGGCGCTTCG 80

RESULT 13

ABZ76674

ID ABZ76674 standard; DNA; 460 BP.

XX ABZ76674;

DT 30-APR-2003 (first entry)

DE Microtetrastpora recticatena IFO14525 DNA sequence SEQ ID NO:5.

KW Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;  
 KW antilipasemic; microorganism; gene; ds.

OS Nonomuraea recticatena.

XX WO200299109-A1.

XX 12-DEC-2002.

XX 30-MAY-2002; 2002WO-JP005252.

XX 01-JUN-2001; 2001JP-00166412.

XX (SAOC ) MERCIAN CORP.

XX Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Isshiki K;

XX WPI; 2003-148672/14.

XX Novel Streptomyces sp. produced polypeptide for hydroxylation of  
 PT compactin at 6beta-position and its encoded DNA, applicable in  
 PT constructing transformant microbes to synthesize pravastatin for treating  
 PT hyperlipidemia.

PS Disclosure; Page 50-51; 67pp; Japanese.

XX The present invention describes a DNA sequence which contains a base  
 CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,  
 CC or a DNA hybridisable with the DNA under stringent conditions and  
 CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-  
 CC position. Also described: (1) DNA containing base sequences from bases  
 CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA  
 CC hybridisable with the DNA under stringent conditions and encoding a



CC polypeptide with hydroxylase activity on compactin at the 6beta-position;  
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid  
CC sequence based on the polypeptide but with some amino acids deleted,  
CC substituted or added and having hydroxylase activity on compactin at the  
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of  
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a  
CC process for producing pravastatin by culturing the transformant  
CC microorganism before isolating the culture liquor or cells, and addition  
CC of compactin for reaction to give pravastatin for recovery; and (6)  
CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (I) has  
CC antilipaeamic activity. The polypeptide and its encoded DNA are applicable  
CC in constructing transformant microorganisms to synthesise pravastatin for  
CC treating hyperlipidaemia. With the recombinant microorganisms,  
CC pravastatin can be produced efficiently, with much less 6alpha  
CC hydroxylated epimer formed. The present sequence represents a  
CC Microtetraspora recticatenata IF014525 nucleotide sequence, which is given  
CC in the exemplification of the present invention  
XX  
SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;  
Query Match 87.2%; Score 21.8; DB 8; Length 460;  
Best Local Similarity 92.0%; Pred. No. 2.6;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCCTTTCG 25  
||||||| ||||||| ||||||| |||||  
Db 30 GCAAGTCGAGCGGAAGGCCCTTCG 54  
RESULT 14  
AEB72673  
ID AEB72673 standard; DNA; 497 BP.  
AC AEB72673;  
XX  
XX 06-OCT-2005 (first entry)  
DT  
DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.  
XX  
KW cyclosporin; cyclosporin A; ds.  
XX  
OS Streptosporangium sp.  
XX  
XX JP2005198543-A.  
XX  
XX 28-JUL-2005.  
XX  
PF 15-JAN-2004; 2004JP-00007488.  
XX  
PR 15-JAN-2004; 2004JP-00007488.  
XX  
XX (SAOC ) MERCIAN CORP.  
XX  
XX Ota K, Uematsu H, Kaneko K, Tsuchida T;  
PI  
XX WPI; 2005-537020/55.  
XX  
XX Producing cyclosporin derivative useful as reference standard for  
PT quantitative measurement of cyclosporin A in blood, by incubating  
PT cyclosporin A in presence of Dactylosporangium and extracting cyclosporin  
PT derivative.  
XX  
XX Disclosure; SEQ ID NO 2; 12pp; Japanese.  
PS  
XX The invention relates to a novel method for producing a cyclosporin  
CC derivative. The method involves incubating cyclosporin A in the presence  
CC of a strain belonging to Dactylosporangium, Streptomyces, Nocardia,  
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and  
CC extracting the cyclosporin derivative from the incubated liquid. The  
CC cyclosporin derivative is used as a reference standard for quantitative  
CC measurement of cyclosporin A and its metabolite in blood and urine. This  
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in  
CC the cyclosporin production method of the invention.

XX  
SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;  
Query Match 87.2%; Score 21.8; DB 14; Length 497;  
Best Local Similarity 92.0%; Pred. No. 2.6;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCCTTTCG 25  
||||||| ||||||| ||||||| |||||  
Db 53 GCAAGTCGAGCGGAAGGCCCTTCG 77  
RESULT 15  
AED64356  
ID AED64356 standard; DNA; 500 BP.  
XX  
XX AED64356;  
AC  
XX  
XX 12-JAN-2006 (first entry)  
DT  
XX Rhodococcus sp. 16S rDNA, SEQ ID 1.  
DE  
XX 16S ribosomal RNA; 16S rRNA; ds.  
KW  
XX Rhodococcus sp.; Z-35-1 strain.  
OS  
XX JP2005304498-A.  
PN  
XX 04-NOV-2005.  
PD  
XX 22-MAR-2005; 2005JP-00081977.  
PF  
XX 23-MAR-2004; 2004JP-00083956.  
PR  
XX (SANY-) SANYO FINE KK.  
PA  
XX Isobe K, Matsura A, Sakaguchi T;  
PI  
XX WPI; 2005-762911/78.  
DR  
XX Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its  
PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino  
PT protecting group of L- or D-lysine, by utilizing oxidase derived from  
PT Rhodococcus.  
XX  
XX Disclosure; SEQ ID NO 1; 30pp; Japanese.  
PS  
XX The present invention relates to a method (M1) for producing alpha-L- or  
CC -D-amino adipic acid semialdehyde derivatives. The method involves  
CC oxidatively deaminating the aminomethyl group of the alpha-amino  
CC protecting group of L- or D-lysine into an aldehyde group, by utilizing  
CC an oxidase derived from Rhodococcus. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;  
Query Match 87.2%; Score 21.8; DB 14; Length 500;  
Best Local Similarity 92.0%; Pred. No. 2.6;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCCTTTCG 25  
||||||| ||||||| ||||||| |||||  
Db 53 GCAAGTCGAGCGGTAAGGCCCTTCG 77  
RESULT 16  
ADO80217/c  
ID ADO80217 standard; DNA; 1343 BP.  
XX  
XX ADO80217;  
AC  
XX 29-JUL-2004 (first entry)  
DT  
XX

```

DE Rhodococcus sp. GR-002 strain 16S rDNA.
XX
KW cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;
KW catalase test positive; nitrate-reduction ability positive;
KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;
KW alkali phosphatase positive; beta-glucuronidase negative;
KW beta-galactosidase negative; alpha-glucosidase positive;
KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;
KW FERM P-18804; waste engine oil; aromatic hydrocarbon;
KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004113197-A.
XX
PD 15-APR-2004.
XX
XX
XX 27-SEP-2002; 2002JP-00284521.
XX
XX 27-SEP-2002; 2002JP-00284521.
XX
XX (GEIT-) GEITO KK.
XX
XX WPI; 2004-322544/30.
XX
XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain
XX having biochemical properties e.g. gram positive bacillus, catalase test
XX positive, pyrazinamidase negative, useful for degrading waste engine oil.
XX
XX Claim 2; SEQ ID NO 1; 13pp; Japanese.
XX
XX The invention relates to a novel cyclic hydrocarbon degrading agent from
XX the Rhodococcus genus. The cyclic hydrocarbon degrading agent having
XX biochemical properties such as: gram positive bacillus, catalase test
XX positive, nitrate-reduction ability positive, pyrazinamidase negative,
XX pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-
XX glucuronidase negative, beta-galactosidase negative, alpha-glucosidase
XX positive, N-acetyl-beta-glucosaminidase negative, urease positive. The
XX novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having
XX the accession number FERM P-18804. The cyclic hydrocarbon degrading agent
XX is useful for processing a cyclic hydrocarbon-containing substance, such
XX as a waste engine oil. The novel Rhodococcus microorganism is useful for
XX degrading cyclic hydrocarbons containing aromatic hydrocarbons,
XX cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.
XX This polynucleotide represents the novel Rhodococcus microorganism 16S
XX rDNA sequence of the invention.
XX
SQ Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;
Query Match 87.2%; Score 21.8; DB 12; Length 1343;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 1294 GCAAGTCGACGCGTAAGGCCCTTCG 1270
RESULT 17
ADW16264
ID ADW16264 standard; DNA; 1390 BP.
XX
XX AC ADW16264;
XX
XX 07-APR-2005 (first entry)
XX
XX DNA copy of the N_albus 16S ribosomal RNA EN46 isolate Seq 16.
XX
XX 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX

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OS Nocardioides albus.
XX
PN WO2005003328-A1.
XX
PD 13-JAN-2005.
XX
XX 07-JUL-2004; 2004WO-AU0000914.
XX
XX 07-JUL-2003; 2003US-0485241P.
XX
XX 22-SEP-2003; 2003US-0504703P.
XX
XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX
XX Franco CMW, Coombs JT;
XX
XX WPI; 2005-091806/10.
XX
XX Improving plant productivity comprises introducing into the plant or
XX propagation material an endophytic actinomycete that facilitates
XX induction of at least one characteristic related to improved
XX productivity.
XX
XX Claim 1; SEQ ID NO 16; 235pp; English.
XX
XX This invention relates to a novel method for improving plant
XX productivity. Specifically, it refers to introducing into the plant or
XX propagation material an endophytic actinomycetes or variant thereof,
XX where the actinomycetes facilitate induction of a characteristic related
XX to improved productivity. The present invention further describes
XX metabolites of the actinomycetes microorganism such as auxin, gibberellin
XX or cytokinin that are able to induce disease resistance in plants i.e.
XX provide disease bio-control capabilities against pathogen infection.
XX Accordingly, the method facilitates the improvement of cereal crop
XX productivity including increasing germination by up-regulating plant
XX growth promoting activities, as well as improving plant vigor or flower
XX and fruit yield. Furthermore, the new actinomycete or metabolite is
XX useful in the manufacture of a medicament for the therapeutic and/or
XX prophylactic treatment of a mammalian or non-mammalian subject i.e.
XX plant. As such, this method provides plant protectants and plant growth
XX stimulants that exhibit antibacterial, antimicrobial, fungicide,
XX insecticide and nematocide activities. This polynucleotide is the DNA
XX sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
XX
SQ Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;
Query Match 87.2%; Score 21.8; DB 14; Length 1390;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 3 GCAAGTCGACGCGTAAGGCCCTTCG 27
RESULT 18
ADJ38609
ID ADJ38609 standard; DNA; 1403 BP.
XX
XX AC ADJ38609;
XX
XX 06-MAY-2004 (first entry)
XX
XX Micromonospora sp. M42 16S rRNA, SEQ ID 1.
XX
XX Protozoacide; Tuberculostatic; Antitubercular; Antimalarial;
KW Cerebroprotective; Actinomycete; manzamine; 16S rRNA; antibiotic; ds.
XX
XX Micromonospora sp. M42.
XX
XX WO2004013297-A2.
XX
XX 12-FEB-2004.
XX

```

PF 01-AUG-2003; 2003WO-US024238.  
 XX  
 PR 01-AUG-2002; 2002US-0400330P.  
 XX  
 PA (UYNA-) UNIV MARYLAND BIOTECHNOLOGY.  
 PA (UMIS ) UNIV MISSISSIPPI.  
 PI Hill RT, Hamann MT, Peraud O, Kasanah N;  
 XX WPI; 2004-169330/16.  
 DR  
 XX New isolated actinomycete useful for producing antibiotics produces  
 PT manzamine having antituberculosis and antimalarial activity.  
 PT  
 XX Claim 19; SEQ ID NO 1; 46pp; English.  
 PS  
 XX The present invention relates to an isolated actinomycete (A1) producing  
 CC manzamine, which comprises a 16S rRNA (ADJ38609). (A1) is useful for  
 CC producing manzamine by fermentation, which involves culturing (A1) having  
 CC manzamine producing ability in a culture medium suitable for the growth  
 CC of manzamine compounds and production of manzamine and separating the  
 CC manzamine from the culturing medium. (A1) is useful for producing  
 CC antibiotics.  
 XX  
 CC Sequence 1403 BP; 304 A; 361 C; 484 G; 254 T; 0 U; 0 Other;  
 SQ Query Match 87.2%; Score 21.8; DB 12; Length 1403;  
 Best Local Similarity 92.0%; Pred. No. 2.9;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGACGGAAGGCTTCG 25  
 DB 25 GCAAGTCGACGGAAGGCTTCG 49  
 RESULT 19  
 ADW16290  
 ID ADW16290 standard; DNA; 1427 BP.  
 XX  
 AC ADW16290;  
 XX  
 DT 07-APR-2005 (first entry)  
 XX  
 DE DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.  
 XX  
 KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;  
 KW disease resistance; insect resistance; crop improvement;  
 KW plant growth factor; antibacterial; antimicrobial; fungicide;  
 KW insecticide; nematocide.  
 XX  
 OS Actinomycetales.  
 XX  
 PN WO2005003328-A1.  
 XX  
 PD 13-JAN-2005.  
 XX  
 PF 07-JUL-2004; 2004WO-AU000914.  
 XX  
 PR 07-JUL-2003; 2003US-0485241P.  
 PR 22-SEP-2003; 2003US-0504703P.  
 XX  
 PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.  
 XX  
 PI Franco CMM, Coombs JT;  
 XX  
 DR WPI; 2005-091806/10.  
 XX  
 XX Improving plant productivity comprises introducing into the plant or  
 PT propagation material an endophytic actinomycete that facilitates  
 PT induction of at least one characteristic related to improved  
 PT productivity.  
 XX  
 PS Example 18; Fig 19; 235pp; English.

XX This invention relates to a novel method for improving plant  
 CC productivity. Specifically, it refers to introducing into the plant or  
 CC propagation material an endophytic actinomycetes or variant thereof,  
 CC where the actinomycetes facilitate induction of a characteristic related  
 CC to improved productivity. The present invention further describes  
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin  
 CC or cytokinin that are able to induce disease resistance in plants i.e.  
 CC provide disease bio-control capabilities against pathogen infection.  
 CC Accordingly, the method facilitates the improvement of cereal crop  
 CC productivity including increasing germination by up-regulating plant  
 CC growth promoting activities, as well as improving plant vigor or flower  
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is  
 CC useful in the manufacture of a medicament for the therapeutic and/or  
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.  
 CC plant. As such, this method provides plant protectants and plant growth  
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,  
 CC insecticide and nematocide activities. This polynucleotide is the DNA  
 CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.  
 XX  
 SQ Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;  
 Query Match 87.2%; Score 21.8; DB 14; Length 1427;  
 Best Local Similarity 92.0%; Pred. No. 2.9;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGACGGAAGGCTTCG 25  
 DB 24 GCAAGTCGACGGAAGGCTTCG 48  
 RESULT 20  
 ADX38843  
 ID ADX38843 standard; DNA; 1443 BP.  
 XX  
 AC ADX38843;  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 DE Microbispora 16S rDNA.  
 XX  
 KW antibiotic; bacterial infection; animal growth; 16S rDNA; ds;  
 KW antibacterial; anabolic.  
 XX  
 OS Microbispora sp. ATCC PTA-5024.  
 XX  
 PN WO2005014628-A1.  
 XX  
 PD 17-FEB-2005.  
 XX  
 PF 12-JUL-2004; 2004WO-EP007658.  
 XX  
 PR 18-JUL-2003; 2003EP-00016306.  
 XX  
 PA (VICU-) VICURON PHARM INC.  
 XX  
 PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;  
 PI Marinelli F, Selva E, Parenti F;  
 XX  
 DR WPI; 2005-173079/18.  
 XX  
 XX New antibiotic 107891 complex comprising Factor A1 and Factor A2 and  
 PT having specified physico-chemical characteristics, used to form  
 PT medicament for the treatment or prevention of bacterial infections, or  
 PT used as animal growth promoter.  
 XX  
 XX Disclosure; SEQ ID NO 1; 85pp; English.  
 PS  
 XX The invention relates to an antibiotic 107891 complex comprising Factor  
 CC A1 and Factor A2. The antibiotic is used to form a pharmaceutical  
 CC composition used as medicament for the treatment or prevention of  
 CC bacterial infections, or as animal growth promoter. The present sequence  
 CC represents the Microbispora 16S rDNA.

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XX
SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

Query Match      87.2%; Score 21.8; DB 14; Length 1443;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCNAGTCGAACGGGAAGCCCTTCG 25
Db 30 GCAAGTCGAGCGGAAGCCCTTCG 54

RESULT 21
AEA22406
ID AEA22406 standard; DNA; 1461 BP.
XX
AC AEA22406;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium gordonae.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
XX (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
PS Disclosure; SEQ ID NO 7; 74pp; English.
XX
CC The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complimentary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complimentary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an APB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC APB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
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CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium gordonae 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
SQ Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;

Query Match      87.2%; Score 21.8; DB 14; Length 1461;
Best Local Similarity 92.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGGAAGCCCTTCG 25
Db 20 GCAAGTCGAACGGTAAGCCCTTCG 44

RESULT 22
AED35651
ID AED35651 standard; DNA; 1483 BP.
XX
AC AED35651;
XX
DT 15-DEC-2005 (first entry)
XX
DE Pseudonocardia sp. 727713 melanocortin receptor modulator WS727713.
XX
KW ds; melanocortin receptor; cosmetics; brain injury; cerebroprotective;
KW inflammation; renal disease; nephrotropic; ischemia;
KW cardiovascular disease; Vasotropic; reperfusion injury; inflammation;
KW hepatitis; Hepatotropic; Virucide; sepsis; septic shock; Antibacterial;
KW immunosuppressive; respiratory distress syndrome; Respiratory-Gen.;
KW respiratory disease; rheumatoid arthritis; arthritis; Antirheumatic;
KW Antiarthritic; immune disorder; gout; Antigout; osteoarthritis;
KW osteopathic; nephritis; genitourinary disease; nephrotropic;
KW hypersensitivity; Antiallergic; gastrointestinal disease; Endocrine-Gen.;
KW Gastrointestinal-Gen.; gastrointestinal disease; Endocrine-Gen.;
KW genitourinary disease; female sexual dysfunction;
KW male sexual dysfunction; Gynecological; transplant rejection; Analgesic;
KW pain; neurological disease; HIV infection; Anti-HIV; hypopigmentation;
KW Dermatological; dermatological disease; tinea; Fungicide;
KW diabetes mellitus; Antidiabetic; metabolic disorder; anorexia nervosa;
KW Eating-Disorder-General.; Cardiovascular-Gen.; Anorectic;
KW nutritional disorder; psychiatric disorder; fever; obesity; pancreatitis;
KW temperature disorder; functional bowel disorder; graft versus host disease;
KW fibroid; scar tissue; keloid; scleroderma; graft versus host disease;
KW liver cirrhosis; pulmonary fibrosis; nephropathy; Ophthalmological;
KW uveitis; Bence's disease; hematological disease; sarcoidosis; vasculitis;
KW infection; antimicrobial; celiac disease; melanoma; neoplasm; Cytostatic;
KW Anabolic.
XX
OS Pseudonocardia sp. 727713.
XX
PN WO2005097973-A1.
XX
PD 20-OCT-2005.
XX
PR 22-MAR-2005; 2005WO-JP005653.
XX
PA (FUJI ) FUJISAWA PHARM CO LTD.
XX
PI Otsuka T, Ueda H, Fujie K, Muramatsu H, Hashimoto M, Takase S;
XX
DR WPI; 2005-703551/72.
XX
PT New pure WS727713 compound which is a melanocortin receptor modulator
XX useful as antiinflammatory and for treating e.g. hypoxic shock, acute
XX respiratory distress syndrome, rheumatic arthritis and melanoma invasion.
XX
PS Disclosure; SEQ ID NO 1; 41pp; English.
XX
CC This invention describes a novel compound WS727713 isolated from
CC Pseudonocardia sp. 727713 in a leaf litter sample. The compound is
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CC capable of modulating the melanocortin receptor and has a potent anti-inflammatory effect. The compound can be used as a medicament or a cosmetic for treating or preventing ischemic or reperfusion injury, brain and renal inflammatory diseases, hepatitis, sepsis/septic shock, hypoxic shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis, gouty arthritis, aortic regurgitation, juvenile chronic arthritis, osteoarthritis, nephritis, induction of tolerance, contact hypersensitivity, inflammatory bowel disease, sexual dysfunction, transplantation, pain, disease progression of HIV, post inflammatory hypopigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever, functional bowel disease, obesity, satiety effect, diabetes mellitus, modulation of dermal exocrine function, canities (canities circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic scars, keloids, localized scleroderma, systemic sclerosis, sclerodermic graft versus host disease of the skin, cirrhosis of the liver, idiopathic and bleomycin induced lung fibrosis, cyclosporin induced nephropathy), uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis, microbial infections, celiac disease, vulvar vestibulitis syndrome, melanoma invasion or anorexia in human or an animal.

XX  
SQ Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;

Query Match 87.2%; Score 21.8; DB 14; Length 1483;  
Best Local Similarity 92.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
||||||| ||| |||||||||  
Db 31 GCAAGTCGAGCGGTAAGGCTTTTCG 55

RESULT 23  
ADR90327  
ID ADR90327 standard; DNA; 1511 BP.  
XX  
AC ADR90327;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.  
XX  
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.  
XX  
OS Rhodococcus sp.  
XX  
PN JP2004261126-A.  
XX  
PD 24-SEP-2004.  
XX  
PF 03-MAR-2003; 2003JP-00056155.  
XX  
PR 03-MAR-2003; 2003JP-00056155.  
XX  
PA (EBAR ) EBARA CORP.  
XX  
WPI; 2004-665486/65.  
XX  
PT Evaluating the ability of an environmental sample to degrade alkanes for providing alkane degrading bacteria, comprises measuring alkane degrading bacteria having high resolving power of alkane present in petroleum.  
XX  
PS Claim 1; SEQ ID NO 3; 33pp; Japanese.

CC The invention relates to a novel method for evaluating the ability of an environmental sample to degrade alkanes. The method comprises measuring the number of alkane-degrading bacteria present in the sample, where the bacteria have high resolving power of a type of alkane present in petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of the invention may be useful for evaluating the ability of an environmental sample to degrade alkanes and thus, for providing alkane-degrading bacteria to be utilized in bioremediation of an environment contaminated with petroleum. The method is rapid and simple. The current sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S

CC ribosomal RNA gene (rDNA) of the invention.  
XX  
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 13; Length 1511;  
Best Local Similarity 92.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
||||||| ||| |||||||||  
Db 50 GCAAGTCGAGCGGTAAGGCTTTTCG 74

RESULT 24  
ADR90325  
ID ADR90325 standard; DNA; 1511 BP.  
XX  
AC ADR90325;  
XX  
DT 16-DEC-2004 (first entry)  
XX  
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.  
XX  
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.  
XX  
OS Rhodococcus sp.  
XX  
PN JP2004261126-A.  
XX  
PD 24-SEP-2004.  
XX  
PF 03-MAR-2003; 2003JP-00056155.  
XX  
PR 03-MAR-2003; 2003JP-00056155.  
XX  
PA (EBAR ) EBARA CORP.  
XX  
WPI; 2004-665486/65.  
XX  
PT Evaluating the ability of an environmental sample to degrade alkanes for providing alkane degrading bacteria, comprises measuring alkane degrading bacteria having high resolving power of alkane present in petroleum.  
XX  
PS Claim 1; SEQ ID NO 1; 33pp; Japanese.

CC The invention relates to a novel method for evaluating the ability of an environmental sample to degrade alkanes. The method comprises measuring the number of alkane-degrading bacteria present in the sample, where the bacteria have high resolving power of a type of alkane present in petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of the invention may be useful for evaluating the ability of an environmental sample to degrade alkanes and thus, for providing alkane-degrading bacteria to be utilized in bioremediation of an environment contaminated with petroleum. The method is rapid and simple. The current sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S ribosomal RNA gene (rDNA) of the invention.

XX  
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match 87.2%; Score 21.8; DB 13; Length 1511;  
Best Local Similarity 92.0%; Pred. No. 2.9;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
||||||| ||| |||||||||  
Db 50 GCAAGTCGAGCGGTAAGGCTTTTCG 74

RESULT 25  
AED11327  
ID AED11327 standard; DNA; 1511 BP.  
XX  
AC AED11327;

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XX 01-DEC-2005 (first entry)
XX Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
XX degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
XX pollutant; degradation; groundwater decontamination; 16S rRNA;
XX 16S ribosomal RNA; gene; ds.
XX Rhodococcus erythropolis.
XX JP2005261218-A.
XX 29-SEP-2005.
XX 16-MAR-2004; 2004JP-00074370.
XX 16-MAR-2004; 2004JP-00074370.
XX (EBAR ) EBARA CORP.
XX Karube M, Tamatsubo K, Miya A;
XX WPI; 2005-678804/70.
XX Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic
XX hydrocarbon, useful for bioremediation of oil-polluted environment such
XX as river water, underground water, ocean, sea cost.
XX Claim 1; SEQ ID NO 1; 14pp; Japanese.
XX The invention relates to a novel Rhodococcus erythropolis M-13 strain
XX capable of degrading aliphatic hydrocarbons. The invention further
XX provides the 16S rRNA gene of the novel strain showing 98% or more
XX homology with a nucleotide sequence of a fully defined 1511 nucleotide
XX (AED11327) sequence given in specification. The novel strain is useful
XX for the bioremediation of an oil-polluted environment, such as river
XX water, underground water, ocean, sea cost, etc. The novel strain degrades
XX linear or branched aliphatic hydrocarbons efficiently. This
XX polynucleotide sequence represents the DNA of the novel Rhodococcus
XX erythropolis M-13 strain 16S rRNA gene of the invention.
XX Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;
XX
XX Query Match 87.2%; Score 21.8; DB 14; Length 1511;
XX Best Local Similarity 92.0%; Pred. No. 2.9;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GCAAGTCGACGCGGTAAGCCCTTCG 25
XX 50 GCAAGTCGACGCGGTAAGCCCTTCG 74
XX
XX RESULT 26
XX ADE41084
XX ID ADE41084 standard; rRNA; 1584 BP.
XX
XX AC ADE41084;
XX
XX 29-JAN-2004 (first entry)
XX . corallina partial 16S rRNA sequence.
XX Antibiotic; ss; 16S rRNA; MF-BA-1768alpal; MF-BA-1768betal;
XX Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;
XX bacterial infection.
XX Microbispora corallina; strain NRRL 30420.
XX US5551591-B1.
XX 22-APR-2003.
XX

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PF 07-SEP-2001; 2001US-00949230.
XX
XX 07-SEP-2001; 2001US-00949230.
XX
XX (ESSE-) ESSENTIAL THERAPEUTICS INC.
XX
XX Lee MD;
XX
XX WPI; 2003-895156/82.
XX
XX Novel antibiotics isolated from fermentation broth of novel strain of
XX Microbispora corallina, useful for treating a wide range of bacterial
XX infections.
XX
XX Disclosure; SEQ ID NO 1; 20pp; English.
XX
XX The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal
XX or its pharmaceutically acceptable salt, having physicochemical
XX characteristics in the non-salt form as detailed in the specification.
XX The antibiotics are isolated from a novel strain of Microbispora
XX corallina designated NRRL 30420. Also included are producing the above
XX antibiotic (by cultivating Microbispora corallina NRRL 30420, or an
XX antibiotic MF- BA-1768alpal or MF-BA-1768betal -producing mutant,
XX variant or its recombinant form, in a culture medium containing
XX assimilable sources of carbon, nitrogen and inorganic salts under aerobic
XX fermentation conditions until the antibiotic is produced and then
XX recovering the antibiotic) and a composition comprising the above
XX antibiotic or its salt. The antibiotics are useful for treating a
XX bacterial infection caused by Staphylococcus (e.g. S.aureus , S.epidermis
XX , S.haemolyticus ), Enterococcus (e.g. E.faecalis , E.faecium ),
XX Streptococcus (e.g. S.pneumoniae , S.pyrogenes ), Haemophilus (e.g.
XX H.influenzae ) or Escherichia (e.g. E.coli ) in a patient. The present
XX sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which
XX identifies the strain.
XX
XX Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;
XX
XX Query Match 87.2%; Score 21.8; DB 10; Length 1584;
XX Best Local Similarity 92.0%; Pred. No. 3;
XX Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 GCAAGTCGACGCGGTAAGCCCTTCG 25
XX 124 GCAAGTCGACGCGGTAAGCCCTTCG 148
XX
XX RESULT 27
XX AED48445/c
XX ID AED48445 standard; DNA; 84222 BP.
XX
XX AC AED48445;
XX
XX 15-DEC-2005 (first entry)
XX
XX M. echinospora gentamycin biosynthetic gene cluster DNA.
XX
XX ds; gene; antibiotic; virucide; aminoglycoside; bacterial infection;
XX viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; genM1; gmrA;
XX genS1; genC; genD2; genM2; genD1; genS2; genW; genB4; genB3; genK;
XX genB2; genX; genU; genT; genE; genY; genA; genF; genG; genH; genI; genJ;
XX genL; genN; DNA polymerase beta chain; integral membrane protein;
XX agglutinin; esterase; Trp-trNA ligase;
XX guanine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;
XX gentamicin (hexosaminyl-6-)aminotransferase I; gentamicin oxidoreductase;
XX (N-acetyl-) hexosaminyltransferase; ribosomal methyltransferase;
XX L-glutamine:ketoacylitol; 2-deoxy-scyllo-inosose synthase;
XX gentamicin glycosyltransferase II; gentamicin aminotransferase II;
XX gentamicin production protein; gentamicin aminotransferase IV;
XX aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;
XX gentamicin C-methyltransferase; gentamicin aminotransferase II;
XX gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;
XX gentamicin methyltransferase; two-component system histidine kinase;
XX two-component system response regulator; serine protease;

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KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;  
 KW subtilase; transcriptional regulator; acetyltransferase;  
 KW ATP-binding protein; ABC-transporter, permease component.  
 XX Micromonospora echinospora.

XX Key Location/Qualifiers  
 FH 191..1264  
 FT CDS /tag= a  
 FT /product= "putative DNA polymerase beta chain"  
 FT /note= "ORF MecP21.15"  
 FT complement(1347..2321)  
 FT /tag= b  
 FT /product= "putative integral membrane protein"  
 FT /note= "ORF MecP21.16c"  
 FT 2374..2847  
 FT /tag= c  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecP21.17"  
 FT 2847..4517  
 FT /tag= d  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecP21.18"  
 FT complement(4571..5590)  
 FT /tag= e  
 FT /product= "putative plus agglutinin"  
 FT /note= "ORF MecP21.19c"  
 FT complement(5628..6206)  
 FT /tag= f  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecP21.20c"  
 FT complement(6297..6899)  
 FT /tag= g  
 FT /product= "putative esterase"  
 FT /note= "ORF MecP21.21c"  
 FT 7683..9389  
 FT /tag= h  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecP21.22"  
 FT complement(9518..10144)  
 FT /tag= i  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecP21.23c"  
 FT 16081..16620  
 FT /tag= j  
 FT /product= "hypothetical protein"  
 FT /note= "ORF MecE04.1"  
 FT 16711..17790  
 FT /tag= k  
 FT /product= "putative Trp-tRNA ligase"  
 FT /note= "ORF MecE04.2"  
 FT 17857..19014  
 FT /tag= l  
 FT /product= "guanine/archaeosine tRNA-ribosyltransferase"  
 FT /gene= "genP"  
 FT 19121..19939  
 FT /tag= m  
 FT /gene= "gm-B"  
 FT /product= "putative ribosomal methyltransferase"  
 FT complement(19953..21206)  
 FT /tag= n  
 FT /product= "gentamicin (hexosaminy-6-)aminotransferase I"  
 FT /gene= "genB1"  
 FT complement(21238..22761)  
 FT /tag= o  
 FT /gene= "genQ"  
 FT /product= "gentamicin (hexosaminy-6-)aminotransferase I"  
 FT complement(22934..23743)  
 FT /tag= p  
 FT /product= "putative gentamicin oxidoreductase"  
 FT /gene= "genB3"  
 FT complement(23758..25005)  
 FT /tag= q

FT /gene= "genM1"  
 FT /product= "putative (N-acetyl-) hexosaminytransferase"  
 FT complement(25042..25866)  
 FT /tag= r  
 FT /product= "putative ribosomal methyltransferase"  
 FT /gene= "gmrA"  
 FT 26161..27423  
 FT /tag= s  
 FT /gene= "genS1"  
 FT /product= "putative L-glutamine:ketocyclitol"  
 FT 27538..28751  
 FT /tag= t  
 FT /product= "2-deoxy-scylo-inosose synthase"  
 FT /gene= "genC"  
 FT 28744..29769  
 FT /tag= u  
 FT /gene= "genD2"  
 FT /product= "putative gentamicin oxidoreductase"  
 FT 29858..31030  
 FT /tag= v  
 FT /product= "putative gentamicin glycosyltransferase II"  
 FT /gene= "genM2"  
 FT 31032..33011  
 FT /tag= w  
 FT /gene= "genD1"  
 FT /product= "putative gentamicin oxidoreductase"  
 FT 33011..34267  
 FT /tag= x  
 FT /product= "putative gentamicin aminotransferase II"  
 FT /gene= "genS2"  
 FT 34275..34646  
 FT /tag= y  
 FT /gene= "genW"  
 FT /product= "putative gentamicin production protein"  
 FT complement(34741..36078)  
 FT /tag= z  
 FT /product= "putative gentamicin aminotransferase IV"  
 FT /gene= "genB4"  
 FT complement(36137..36943)  
 FT /tag= aa  
 FT /gene= "genJ"  
 FT /product= "biosynthetic aminoglycoside 3'-  
 FT phosphotransferase"  
 FT complement(36981..38453)  
 FT /tag= ab  
 FT /product= "putative gentamicin aminotransferase III"  
 FT /gene= "genB3"  
 FT complement(38969..40885)  
 FT /tag= ac  
 FT /gene= "genK"  
 FT /product= "putative gentamicin C-methyltransferase"  
 FT 41135..42379  
 FT /tag= ad  
 FT /product= "putative gentamicin aminotransferase II"  
 FT /gene= "genB2"  
 FT complement(42465..42977)  
 FT /tag= ae  
 FT /gene= "genX"  
 FT /product= "putative gentamicin production protein"  
 FT complement(43032..43967)  
 FT /tag= af  
 FT /product= "putative gentamicin production protein"  
 FT /gene= "genU"  
 FT complement(44162..45568)  
 FT /tag= ag  
 FT /gene= "genT"  
 FT /product= "putative gentamicin exporter"  
 FT complement(45861..46883)  
 FT /tag= ah  
 FT /product= "putative aminocyclitol 1-dehydrogenase"  
 FT /gene= "genE"  
 FT 47364..48878  
 FT /tag= ai

```

FT FT /gene= "genY"
FT FT /product= "putative cation antiporter"
FT FT 49000. .49737
FT FT /*tag= aj
FT FT /product= "putative gentamicin production protein"
FT FT /gene= "genA"
FT FT 49734. .50381
FT FT /*tag= ak
FT FT /gene= "genF"
FT FT /product= "putative gentamicin production protein"
FT FT 50381. .50734
FT FT /*tag= al
FT FT /product= "putative gentamicin production protein"
FT FT /gene= "genG"
FT FT complement(50813. .54229)
FT FT /*tag= am
FT FT /product= "putative gentamicin exporter "
FT FT /gene= "genH"
FT FT complement(54226. .56163)
FT FT /*tag= an
FT FT /gene= "genI"
FT FT /product= "putative gentamicin exporter "
FT FT complement(56689. .57627)
FT FT /*tag= ao
FT FT /gene= "genJ"
FT FT /product= "putative gentamicin production protein"
FT FT 58121. .58741
FT FT /*tag= ap
FT FT /product= "putative gentamicin production protein"

Query Match 87.2%; Score 21.8; DB 14; Length 84222;
Best Local Similarity 92.0%; Pred. No. 4.5;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTCG 25
Db 15396 GCAAGTCGACGGAAGGCCTTCG 15372

RESULT 29
AAD11024/c
ID AAD11024 standard; DNA; 32 BP.
AC AAD11024;
XX
XX
XX
DT 24-SEP-2001 (first entry)
XX
XX
XX
DE Probe #4 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
XX
KW Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; probe; ss.
XX
OS Mycobacterium sp.
XX
XX WO200144511-A2.
XX
XX PD 21-JUN-2001.
XX
XX PF 15-DEC-2000; 2000WO-US033872.
XX
XX PR 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX
XX PI Brentano ST, Lankford RL;
XX
XX DR WPI; 2001-398171/42.
XX
XX PF 15-DEC-2000; 2000WO-US033872.
XX
XX PR 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX
XX PI Brentano ST, Lankford RL;
XX
XX DR WPI; 2001-398171/42.
XX
XX PF Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX nucleic acid amplification with amplification oligonucleotides specific
XX for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial

```

```

PT species.
XX Claim 11; Page 27; 27pp; English.
XX
CC The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified
CC nucleic acid and detecting amplified nucleic acid. The method is useful
CC for in vitro diagnostic detection of pathogenic bacteria, particularly
CC detecting infections caused by MAC organisms, distinguished from other
CC closely-related Mycobacterium species. The present sequence is a probe
CC used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
SQ Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 85.6%; Score 21.4; DB 4; Length 32;
Best Local Similarity 95.7%; Pred. No. 3;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTT 23
Db 32 GCAAGTCGACGGAAGGCCTTCT 10

RESULT 29
AAD11017
ID AAD11017 standard; DNA; 32 BP.
XX
XX AAD11017;
AC
XX
XX
DT 24-SEP-2001 (first entry)
XX
XX
XX
DE PCR primer #4 used for in vitro amplification of MAC rRNA.
XX
XX Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW in vitro amplification; MAC infection; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
XX WO200144511-A2.
XX
XX PD 21-JUN-2001.
XX
XX PF 15-DEC-2000; 2000WO-US033872.
XX
XX PR 15-DEC-1999; 99US-0171202P.
XX
XX (GENP-) GEN-PROBE INC.
XX (BREN/) BRENTANO S T.
XX (LANK/) LANKFORD R L.
XX
XX PI Brentano ST, Lankford RL;
XX
XX DR WPI; 2001-398171/42.
XX
XX PF Detecting Mycobacterium avium complex organisms, comprises using in vitro
XX nucleic acid amplification with amplification oligonucleotides specific
XX for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
XX species.
XX
XX Claim 1; Page 12; 27pp; English.
XX
XX
CC The present invention relates to a method for detecting Mycobacterium
CC avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC tuberculosis, M. paratuberculosis) present in a biological sample. The
CC method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC 16S rRNA obtained from a biological sample containing nucleic acid from a
CC MAC species in an in vitro nucleic acid amplification mixture comprising
CC a polymerase activity and a pair of primers to produce an amplified

```



CC nucleic acid and detecting amplified nucleic acid. The method is useful  
 CC for in vitro diagnostic detection of pathogenic bacteria, particularly  
 CC detecting infections caused by MAC organisms, distinguished from other  
 CC closely-related Mycobacterium species. The present sequence is a PCR  
 CC primer used for in vitro amplification of MAC rRNA

XX  
 SQ Sequence 32 BP; 9 A; 7 C; 11 G; 5 T; 0 U; 0 Other;

Query Match 85.6%; Score 21.4; DB 4; Length 32;  
 Best Local Similarity 95.7%; Pred. No. 3;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 |||||  
 Db 1 GCAAGTCGAACGGAAGGCCTCT 23

## RESULT 30

AA99195  
 ID AAX99195 standard; DNA; 50 BP.

XX  
 AC AAX99195;

XX  
 DT 28-SEP-1999 (first entry)

XX  
 DE M. avium 16S rRNA gene fragment.

XX  
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX  
 OS Mycobacterium avium.

XX  
 PN WO9935284-A1.

XX  
 PD 15-JUL-1999.

XX  
 PF 30-DEC-1997; 97WO-BR000087.

XX  
 PR 30-DEC-1997; 97WO-BR000087.

XX  
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.

XX  
 PI Peregrino Ferreira PC, Geessien Kroon E;

XX  
 PI Bernardes Margutti Pinto ME, Aleixo AW;

XX  
 DR WPI; 1999-444201/37.

XX  
 PT Detection of mycobacteria by shift mobility assay.

XX  
 PS Disclosure; Fig 7; 20pp; English.

XX The invention describes a new method for diagnosis, identification and  
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
 CC DNA amplification and shift mobility assay. The method is based on  
 CC divergence in sequences found in 16S rRNA to identify mycobacteria  
 CC species, since a remarkable shift of heteroduplex bands are obtained  
 CC between single stranded and homoduplex bands in UPAGE. The method is  
 CC fast, simple and can produce information not easily obtained when  
 CC compared with other detection methods. The sensitivity of other assays  
 CC suffer due to the tendency of the denatured PCR product strands to  
 CC reassociate and exclude oligonucleotide probes, and steric interference  
 CC between the bound oligonucleotides and the solid support which impede  
 CC hybridization to nucleic acids in solution. Sequences AAX99193-237  
 CC represent 16S rRNA gene regions of some mycobacterial species

XX  
 SQ Sequence 50 BP; 15 A; 12 C; 14 G; 9 T; 0 U; 0 Other;

Query Match 85.6%; Score 21.4; DB 2; Length 50;  
 Best Local Similarity 95.7%; Pred. No. 3.2;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 |||||  
 Db 9 GCAAGTCGAACGGAAGGCCTCT 31

## RESULT 31

AA99196  
 ID AAX99196 standard; DNA; 50 BP.

XX  
 AC AAX99196;

XX  
 DT 28-SEP-1999 (first entry)

XX  
 DE M. fortuitum 16S rRNA gene fragment.

XX  
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX  
 OS Mycobacterium fortuitum.

XX  
 PN WO9935284-A1.

XX  
 PD 15-JUL-1999.

XX  
 PF 30-DEC-1997; 97WO-BR000087.

XX  
 PR 30-DEC-1997; 97WO-BR000087.

XX  
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.

XX  
 PI Peregrino Ferreira PC, Geessien Kroon E;

XX  
 PI Bernardes Margutti Pinto ME, Aleixo AW;

XX  
 DR WPI; 1999-444201/37.

XX  
 PT Detection of mycobacteria by shift mobility assay.

XX  
 PS Disclosure; Fig 7; 20pp; English.

XX The invention describes a new method for diagnosis, identification and  
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
 CC DNA amplification and shift mobility assay. The method is based on  
 CC divergence in sequences found in 16S rRNA to identify mycobacteria  
 CC species, since a remarkable shift of heteroduplex bands are obtained  
 CC between single stranded and homoduplex bands in UPAGE. The method is  
 CC fast, simple and can produce information not easily obtained when  
 CC compared with other detection methods. The sensitivity of other assays  
 CC suffer due to the tendency of the denatured PCR product strands to  
 CC reassociate and exclude oligonucleotide probes, and steric interference  
 CC between the bound oligonucleotides and the solid support which impede  
 CC hybridization to nucleic acids in solution. Sequences AAX99193-237  
 CC represent 16S rRNA gene regions of some mycobacterial species

XX  
 SQ Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;

Query Match 85.6%; Score 21.4; DB 2; Length 50;  
 Best Local Similarity 95.7%; Pred. No. 3.2;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 |||||  
 Db 9 GCAAGTCGAACGGAAGGCCTCT 31

## RESULT 32

ADF94050  
 ID ADF94050 standard; DNA; 50 BP.

XX  
 AC ADF94050;

XX  
 DT 11-MAR-2004 (first entry)



```

PN WO2002101042-A1.
XX
XX 19-DEC-2002.
XX
XX 12-JUN-2002; 2002WO-JP005832.
XX
XX 12-JUN-2001; 2001JP-00177737.
XX
XX 20-AUG-2001; 2001JP-00249689.
XX
XX (TAKI ) TAKARA BIO INC.
XX
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
XX Enoki T, Asada K, Kato I;
XX WPI; 2003-148805/14.
XX
XX Method for stabilizing and storing reaction reagents for specific
XX amplification and detection of nucleic acids particularly in e.g.
XX identifying pathogenic microorganisms or viruses in sample.
XX
XX Example 15; Page 109; 177pp; Japanese.
XX
XX The invention relates to a novel stabilising reaction reagent for use in
XX the amplification and/or detection of a target nucleic acid comprising:
XX preparing a reaction mixture with e.g. a nucleic acid as template, at
XX least 1 primer and RNaseH; and incubation of the reaction mixture for a
XX defined period of time to form a reaction product during the
XX amplification of such target nucleic acid. The method is useful for
XX stabilising and long-term storage of reaction reagents for highly
XX sensitive and specific amplification and detection of nucleic acids
XX particularly in identifying pathogenic microorganisms or viruses in a
XX sample using chimeric oligonucleotide primers, which is useful in genetic
XX engineering and clinical medicine. This polynucleotide sequence
XX represents an oligo relating to the novel stabilising reaction reagent
XX method of the invention
XX
XX Sequence 560 BP; 117 A; 134 C; 198 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 85.6%; Score 21.4; DB 10; Length 560;
XX Best Local Similarity 95.7%; Pred. No. 4.1;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GCAAGTCGAACGAAAGGCCTTT 23
Db 30 GCAAGTCGAACGAAAGGCCTCT 52
RESULT 35
AEA22411
XX AEA22411 standard; DNA; 1421 BP.
XX
XX AEA22411;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mycobacterium lentiflavum 16S rRNA sequence SEQ ID NO:12.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium lentiflavum.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANX/) HAN X.
XX
XX (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX
XX WO2002101042-A1.
XX
XX 19-DEC-2002.
XX
XX 12-JUN-2002; 2002WO-JP005832.
XX
XX 12-JUN-2001; 2001JP-00177737.
XX
XX 20-AUG-2001; 2001JP-00249689.
XX
XX (TAKI ) TAKARA BIO INC.
XX
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
XX Enoki T, Asada K, Kato I;
XX WPI; 2003-148805/14.
XX
XX Method for stabilizing and storing reaction reagents for specific
XX amplification and detection of nucleic acids particularly in e.g.
XX identifying pathogenic microorganisms or viruses in sample.
XX
XX Example 15; Page 109; 177pp; Japanese.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complementary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22489)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium lentiflavum 16S rRNA nucleotide
XX sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1421 BP; 306 A; 344 C; 487 G; 284 T; 0 U; 0 Other;
XX
XX Query Match 85.6%; Score 21.4; DB 14; Length 1421;
XX Best Local Similarity 95.7%; Pred. No. 4.5;
XX Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 1 GCAAGTCGAACGAAAGGCCTTT 23
Db 20 GCAAGTCGAACGAAAGGCCTCT 42
RESULT 36
ADK66476
XX ADK66476 standard; RNA; 1431 BP.
XX
XX ADK66476;
XX
XX 06-MAY-2004 (first entry)
XX
XX Corynebacterium 16S rRNA sequence.
XX
XX ss; 16S rRNA; microorganism detection; clinical sample;
XX pharmaceutical composition.
XX
XX Corynebacterium sp.
XX
XX WO2004009839-A2.
XX
XX 29-JAN-2004.
XX
XX 16-JUL-2003; 2003WO-EP007717.
XX
XX 18-JUL-2002; 2002DE-01032776.
XX
XX 14-FEB-2003; 2003DE-01007732.
XX

```

XX (HENK ) HENKEL KGAA.  
PA (VERM-) VERMICON AG.  
XX  
PI Saettler A, Jassoy C, Scholtyssek R, Maienschein V, Nieveler S;  
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;  
PI Mueller S, Adomat C, Bergmaier I;  
XX  
DR WPI; 2004-123402/12.  
XX  
XX New oligonucleotides for specific detection of microorganisms, useful  
PT e.g. for detecting or quantifying microbes on the skin, in foods,  
PT clinical samples or water, by in situ hybridization.  
XX  
XX Disclosure; Page 66-67; 67pp; German.  
XX  
XX The present invention provides a number of oligonucleotides for the  
CC specific detection of microorganisms. The oligonucleotides are used to  
CC detect and/or quantify microorganisms, especially on the skin, in foods  
CC or the environment (water, soil and air), from waste waters or biofilms,  
CC in clinical samples (body fluids or tissues), and in pharmaceutical or  
CC cosmetic compositions. The present sequence is a *Corynebacterium* 16S rRNA  
CC sequence.  
XX  
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;  
SQ

Query Match 85.6%; Score 21.4; DB 12; Length 1431;  
Best Local Similarity 82.6%; Pred. No. 4.5;  
Matches 19; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCTTT 23  
||||:|||||: :  
DB 30 GCAAGUCGACGGAAGGCCUCU 52

RESULT 37  
ADK66445  
ID ADK66445 standard; RNA; 1431 BP.  
XX  
AC ADK66445;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX *Corynebacterium* 16S rRNA sequence.  
DE  
XX ss; 16S rRNA; microorganism detection; skin; acne.  
XX  
XX *Corynebacterium* sp.  
XX  
XX WO2004009843-A2.  
XX  
XX 29-JAN-2004.  
XX  
XX 16-JUL-2003; 2003WO-EP007718.  
XX  
XX 18-JUL-2002; 2002DE-01032775.  
XX  
XX 14-FEB-2003; 2003DE-01006616.  
XX  
XX (HENK ) HENKEL KGAA.  
XX  
XX Saettler A, Jassoy C, Scholtyssek R, Maienschein V, Nieveler S;  
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;  
PI Mueller S, Adomat C, Bergmaier I;  
XX  
DR WPI; 2004-123405/12.  
XX  
XX Kit for detection of microorganisms on skin, useful e.g. for diagnosis of  
PT infection, comprises specific oligonucleotides for in situ hybridization.  
XX  
XX Disclosure; Page 62-63; 63pp; German.  
XX  
XX The present invention relates to a kit for detecting microorganisms that  
CC contains at least one oligonucleotide specific for at least one species,

CC or group of species, that is present on the skin. The kit is used to  
CC detect and/or quantify microorganisms that are present on the skin; e.g.  
CC for early diagnosis of secondary infection in cases of acne. The present  
CC sequence is a *Corynebacterium* 16S rRNA sequence.  
XX  
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;  
SQ

Query Match 85.6%; Score 21.4; DB 12; Length 1431;  
Best Local Similarity 82.6%; Pred. No. 4.5;  
Matches 19; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCTTT 23  
||||:|||||: :  
DB 30 GCAAGUCGACGGAAGGCCUCU 52

RESULT 38  
AAQ37639  
ID AAQ37639 standard; rRNA; 1449 BP.  
XX  
XX AAQ37639;  
AC  
XX 25-MAR-2003 (revised)  
DT 18-JUN-1993 (first entry)  
DE  
XX *Mycobacterium* genavense 16S rRNA.  
XX  
XX Detection; rapid; immunosuppressed patients; AIDS; ss.  
XX  
XX *Mycobacterium* genavense.  
XX  
XX EP529985-A1.  
XX  
XX 03-MAR-1993.  
XX  
XX 21-AUG-1992; 92EP-00307690.  
XX  
XX 23-AUG-1991; 91GB-00018262.  
XX  
XX 09-JUL-1992; 92GB-00014601.  
XX  
XX (PINA/) CHANG PINARES H R.  
PA (BOET/) BOETTGER E C.  
PA (HIRS/) HIRSCHHEL B J.  
XX  
XX Chang Pinares HR, Boettger EC, Hirschhel BJ;  
XX  
XX WPI; 1993-068993/09.  
XX  
XX New 16S ribosomal RNA sequence of new *Mycobacterium* genavense - also  
PT probes and primers specific for the sequence, for detecting *M. genavense*  
PT infections in AIDS patients.  
XX  
XX Claim 1; Page 17; 21pp; English.  
XX  
XX The sequence is that of the 16S rRNA of *Mycobacterium* genavense sp. nov.  
XX from which nucleic acid sequences can be obtd. for use in a method for  
XX the reliable and rapid detection and identification of *M. genavense*,  
XX partic. opportunistic *M. genavense* infections in highly immunosuppressed  
XX patients suffering from AIDS. It was isolated by PCR amplification of DNA  
XX from liver, spleen, lymph nodes and polymorphonuclear leukocytes (PMNs,  
XX buffy coats) from AIDS patients. (Updated on 25-MAR-2003 to correct PN  
XX field.)  
XX  
XX Sequence 1449 BP; 316 A; 345 C; 495 G; 289 T; 0 U; 4 Other;  
SQ

Query Match 85.6%; Score 21.4; DB 2; Length 1449;  
Best Local Similarity 95.7%; Pred. No. 4.5;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGGCCTTT 23  
||||:|||||: :  
DB 47 GCAAGTCGAACGGAAGGCCTTCT 69

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RESULT 39
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
XX
PI (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX
PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
PS Disclosure; SEQ ID NO 2; 74pp; English.
XX
CC The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complimentary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complimentary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an AFB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 21.4; DB 14; Length 1454;
Best Local Similarity 95.7%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTTT 23

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```

Db 30 GCAAGTCGAACGGAAGGCTCT 52
RESULT 40
ADB61680
ID ADB61680 standard; DNA; 1465 BP.
XX
AC ADB61680;
XX
DT 04-DEC-2003 (first entry)
XX
DE 16S rRNA of Mycobacterium avium DNA sequence.
XX
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
KW poly-A tail; mRNA purification; oligo-dT capture;
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX
OS Mycobacterium avium.
XX
PN WO2003054162-A2.
XX
PD 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US041014.
XX
PR 20-DEC-2001; 2001US-00029397.
XX
PA (AMBI-) AMBION INC.
XX
PI Murphy GL, Whitley JP;
XX
DR WPI; 2003-663255/62.
XX
PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
PT bridging oligonucleotide comprising bridging region and a targeting
PT region complementary to a targeted nucleic acid, and a capture
PT oligonucleotide.
XX
PS Claim 4; Page 168; 208pp; English.
XX
CC This invention relates to a novel method for isolating, depleting or
CC separating a targeted nucleic acid, such as rRNA, from a sample
CC comprising targeted and non-targeted nucleic acids. It effects a way of
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating
CC sufficient quantities of high quality bacterial mRNA is a demanding
CC process which impedes analysis of bacterial gene expression in the
CC presence of host cells. A small percentage of bacterial mRNAs may be poly
CC -A tailed, but these are targeted for degradation and tend to be
CC unstable. As a result, the commonly employed method for mRNA purification
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present
CC invention provides an alternative, more suitable method for mRNA
CC purification from prokaryotes. The method of the invention comprises the
CC incubation of a sample with a bridging oligonucleotide (containing a
CC targeting region) and subsequently incubating with a capture
CC oligonucleotide allowing the isolation of the target from the sample. The
CC method is useful for depleting or isolating targeted nucleic acid, for
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may
CC comprise any one of 64 fully defined sequences as given in the
CC specification. The present sequence is that of a DNA sequence which
CC represents the sequence of 16S rRNA of Mycobacterium avium related to the
CC invention.
XX
SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;
XX
Query Match 85.6%; Score 21.4; DB 10; Length 1465;
Best Local Similarity 95.7%; Pred. No. 4.5;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Oy 1 GCAAGTCGACGGAAGGCGCTTT 23
Db 20 GCAAGTCGACGGAAGGCGCTCT 42

RESULT 41
ADR90572
ID ADR90572 standard; DNA; 1472 BP.
XX
AC ADR90572;
XX
XX 02-DEC-2004 (first entry)
XX
DE M avium 16S rRNA gene sequence SeqID1.
XX
KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
XX
XX Mycobacterium avium.
XX
XX Key Location/Qualifiers
FT variation 893
FT /*tag= a
FT variation 1312
FT /*tag= b
FT variation 1393
FT /*tag= c
XX
XX JP2004254591-A.
XX
XX 16-SEP-2004.
XX
XX 26-FEB-2003; 2003JP-00048654.
XX
XX 26-FEB-2003; 2003JP-00048654.
XX
XX (M1TP ) MITSUBISHI YUKA BCL KK.
XX
XX WPI; 2004-664464/65.
XX
XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex,
XX useful for detecting mutant of M.avium complex, and for grouping strains
XX of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
XX bacterium.
XX
XX Claim 3; SEQ ID NO 1; 23pp; Japanese.
XX
XX This invention relates to a novel method of differentiating acid-fast
XX bacterium, which involves detecting a mutation in the 16S rRNA gene of
XX the acid-fast bacterium. The method is useful for differentiating acid-
XX fast bacterium such as M avium complex (MAC) or M kansasii in particular
XX for detecting mutants of MAC, and for grouping strains of M kansasii. The
XX method is also useful for carrying out taxonomic-tree analysis of
XX atypical-mycobacteria and enables detection of MAC accurately and
XX reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
XX which may be used in the method of the invention.
XX
XX Sequence 1472 BP; 323 A; 348 C; 500 G; 298 T; 0 U; 3 Other;

Query Match 85.6%; Score 21.4; DB 13; Length 1472;
Best Local Similarity 95.7%; Pred. No. 4.6;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCGCTTT 23
Db 30 GCAAGTCGACGGAAGGCGCTCT 52

RESULT 42
AAD11273
ID AAD11273 standard; DNA; 22 BP.
XX
XX AAD11273;

us-10-665-708-21.rng

24-SEP-2001 (first entry)
Mycobacterium 16S rRNA amplifying primer #17.
Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
Mycobacterium sp.
WO200144510-A2.
21-JUN-2001.
17-DEC-1999; 99WO-US030346.
17-DEC-1999; 99WO-US030346.
(GENP-) GEN-PROBE INC.
(INMR ) BIOMERIEUX SA.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2001-398170/42.
Detecting Mycobacterium species, involves in vitro amplification of 16S
rRNA or DNA encoding RNA in nucleic acid amplification mixture using
specific primers, and detecting the amplified nucleic acid.
Claim 1; Page 36; 44pp; English.
The invention relates to a method of detecting Mycobacterium species,
that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
encoding 16S rRNA in an in vitro nucleic acid amplification mixture
comprising a polymerase, and at least two primers, and then detecting the
amplified nucleic acid. The method is relatively simple and useful for
detecting the presence of various Mycobacterium species in a biological
sample, and thus important for diagnosis of infections resulting from
them. The method is especially important for screening opportunistic
infections caused by M. tuberculosis or a Mycobacterium other than
tuberculosis (MOTT). The present sequence is a PCR primer used for
amplifying Mycobacterium 16S rRNA
Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 84.0%; Score 21; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GTCGACGGAAGGCGCTTTCG 25
Db 1 GTCGACGGAAGGCGCTTTCG 21

RESULT 43
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX
AC ADG88354;
XX
XX 11-MAR-2004 (first entry)
XX
XX Mycobacterium amplifying PCR primer #23.
XX
XX In vitro amplification; PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX
XX 15-DEC-2000; 2000US-00738274.

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```
XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 23; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 84.0%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 GTCGAACGGAAGGCGCTTTTCG 25
Db 1 GTCGAACGGAAGGCGCTTTTCG 21
XX
RESULT 44
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX
AC AEA08229;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.
KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
```

```
XX Claim 8; SEQ ID NO 23; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 84.0%; Score 21; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 5 GTCGAACGGAAGGCGCTTTTCG 25
Db 1 GTCGAACGGAAGGCGCTTTTCG 21
XX
RESULT 45
AEB98771
ID AEB98771 standard; DNA; 39 BP.
XX
AC AEB98771;
XX
DT 06-OCT-2005 (first entry)
DE Mycobacterium avium identification LAMP primer, SEQ ID 13.
KW microorganism detection; mycobacterium infection; antibacterial; primer;
KW PCR; ss; LAMP.
XX
OS Mycobacterium avium.
OS Synthetic.
XX
PN JP2005204582-A.
XX
PD 04-AUG-2005.
XX
PF 23-JAN-2004; 2004JP-00015195.
XX
PR 23-JAN-2004; 2004JP-00015195.
XX
PA (ASAH ) ASahi KASEI KK.
XX
PI Oda N;
XX
PW WPI; 2005-526965/54.
XX
PT New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
PS Claim 1; SEQ ID NO 13; 14pp; Japanese.
XX
CC The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This oligo sequence represents a loop-mediated
CC isothermal amplification (LAMP) primer used in the exemplification of the
CC invention.
XX
SQ Sequence 39 BP; 10 A; 11 C; 10 G; 8 T; 0 U; 0 Other;
```

```
Query Match      84.0%; Score 21; DB 14; Length 39;
Best Local Similarity 100.0%; Pred.No. 4.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCCT 21
    |||||:|||||
Db 19 GCAAGTCGAACGGAAGGCCT 39

RESULT 46
ID AAT45276
AC AAT45276;
DT 12-SEP-1997 (first entry)
DE Corynebacterium diphtheriae 16S rRNA.
KW Ribosomal RNA; species specific; detection; reverse transcription;
KW primer; hybridisation probe; identification; ss.
XX Corynebacterium diphtheriae.
OS
XX Key Location/Qualifiers
FH misc_feature 38..59
FT /tag= a
FT /note= "Defined as nucleotides 72-100"
FT misc_feature 153..170
FT /tag= b
FT /note= "Defined as nucleotides 195-215"
FT misc_feature 415..431
FT /tag= c
FT /note= "Defined as nucleotides 466-494"
FT misc_feature 544..567
FT /tag= d
FT /note= "Defined as nucleotides 544-567"
FT misc_feature 773..787
FT /tag= e
FT /note= "Defined as nucleotides 838-853"
FT misc_feature 793..808
FT /tag= f
FT /note= "Defined as nucleotides 859-875"
FT misc_feature 946..965
FT /tag= g
FT /note= "Defined as nucleotides 1013-1032"
XX
XX FR2733755-A1.
XX
XX 08-NOV-1996.
XX
XX 03-MAY-1995; 95FR-00005494.
XX
XX 03-MAY-1995; 95FR-00005494.
XX
XX (INNR ) BIO MERIEUX.
XX
XX Mabilat C, Ruimy R;
XX WPI; 1997-001738/01.
XX
XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for
XX identifying Corynebacterium spp.
XX
XX Claim 1; Fig 1; 60pp; French.
XX
XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were
XX amplified from 28 strains of 25 different species of Corynebacterium by
XX PCR using primers specific for eubacteria. The amplification products
XX were sequenced and the sequences were aligned for comparison. It was
XX found that certain regions, i.e. those corresponding to nucleotides 72-
XX 100, 195-215, 466-494, 608-853, 838-853, 859-875 and 1013-1033 in the 16S
XX ribosomal RNA of C. diphtheriae (refer to features table for the present
XX

CC sequence), vary considerably between different species. Probes and
CC primers comprising at least 5 nucleotides from one of these species-
CC specific sequences, including the present sequence, or their complements,
CC are useful to distinguish between different Corynebacterium species. DNA
CC versions of the probes and primers are also included
XX
SQ Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match      84.0%; Score 21; DB 2; Length 1391;
Best Local Similarity 90.5%; Pred.No. 7;
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCCT 21
    |||||:|||||
Db 29 GCAAGUCGAACGGAAAGGCCU 49

RESULT 47
ADZ35975
ID ADZ35975 standard; DNA; 1440 BP.
XX
XX AC ADZ35975;
XX
XX 30-JUN-2005 (first entry)
XX
XX Verrucosisspora sp. AB-18-032 16S rRNA gene.
XX
XX ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
XX polycyclic macrolactone; abysomicin; p-Aminobenzoic acid; folic acid;
XX vitamin; abysomicin B; abysomicin C; abysomicin D;
XX Staphylococcus aureus infection; protozoal infection;
XX Plasmodium infection; Leishmania infection; chagas disease;
XX Gram positive bacteria infection; mrsa infection .
XX
XX Verrucosisspora sp. AB-18-032.
XX
XX WO2005033114-A1.
XX
XX 14-APR-2005.
XX
XX 23-SEP-2004; 2004WO-EP010661.
XX
XX 01-OCT-2003; 2003DE-01047472.
XX
XX 11-NOV-2003; 2003DE-01053300.
XX
XX (UYTU-) UNIV TUEBINGEN.
XX
XX Fiedler H, Suesmuth R, Zaehner H, Bull A;
XX WPI; 2005-296122/30.
XX
XX New abysomicin polycyclic macrolactone compounds, useful as antibiotics
XX and antiprotozoal agents effective against multiresistant strains,
XX prepared using bacteria of genus Verrucosisspora.
XX
XX Disclosure; SEQ ID NO 1; 47pp; German.
XX
XX This invention describes novel polycyclic macrolactones and their
XX derivatives , prepared using bacteria of genus Verrucosisspora and
XX designated abysomicins. The polycyclic macrolactones have at least one
XX oxa-bicyclo system as a partial structure and at least one Michael system
XX as double bond system. The polycyclic macrolactones are prepared by
XX culturing Verrucosisspora strain AB 18-032, recovering a culture
XX supernatant from the culture, optionally preparing a culture filtrate and
XX optionally isolating one or more polycyclic macrolactones from the
XX supernatant and/or filtrate. Alternatively the microorganism is cultured
XX followed by isolating one or more polycyclic macrolactones from the
XX microorganism. The Verrucosisspora strain AB 18-032 was isolated from
XX marine sediment collected at a depth of 1000m in Sagami bay in the
XX Japanese Sea and is deposited as DSM No. 15899. The polycyclic
XX macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
XX essential component in the biosynthesis of folic acid) from chorismic
XX acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is
```



CC essential to the life of microorganisms, especially prokaryotes and  
 CC protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of  
 CC folic acid in mammals (including humans), and thus have no adverse  
 CC effects on mammalian cells. Three polycyclic macrolactones are  
 CC specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin  
 CC D. Abyssomicin C strongly inhibited growth of methicillin-resistant  
 CC *Staphylococcus aureus* strain N35 and vancomycin-resistant *Staphylococcus*  
 CC *aureus* strain Mu50. The products of the invention are useful as  
 CC antibiotics (especially effective against Gram positive bacteria) and  
 CC antiprotzoal agents, specifically effective against bacteria and  
 CC protozoa resistant (especially multi-resistant) to conventional  
 CC antibiotics. Typically polycyclic macrolactones are useful for combating  
 CC tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping  
 CC sickness and Chagas disease) and infections caused by resistant Gram  
 CC positive bacteria such as methicillin- and vancomycin-resistant  
 CC *Staphylococcus aureus* strains. Polycyclic macrolactones are also useful  
 CC as disinfectants (especially in hospitals and other medical  
 CC establishments) and as lead structures for the development of further  
 CC active agents. This sequence represents the *Verrucosipora* strain AB 18-  
 CC 032 16S rRNA DNA which is used to phylogenically classify the bacterial  
 CC strain.

SQ Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match 83.2%; Score 20.8; DB 14; Length 1440;  
 Best Local Similarity 91.7%; Pred. No. 8.8;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGACGGAAGGCGCTTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 1 CAAGTCGACGGAAGGCGCTTTCG 24

## RESULT 48

ABN86276  
 ID ABN86276 standard; DNA; 1457 BP.

XX AC ABN86276;

XX DT 08-OCT-2002 (first entry)

XX DE G. polyisoprenivorans P8219 16S rDNA sequence #2.

XX KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.

XX OS Gordonia polyisoprenivorans.

XX PN JP2002142754-A.

XX PD 21-MAY-2002.

XX PF 08-NOV-2000; 2000JP-00341214.

XX PR 08-NOV-2000; 2000JP-00341214.

XX PA (IMBI-) IMB KK.

XX DR WPI; 2002-561124/60.

XX A Gordonia sp. microorganism, useful in the eradication of the  
 PT environmental hormone of phthalic acid esters for environmental  
 PT protection.

XX PS Disclosure; Fig 2A-D; 21pp; Japanese.

XX The invention relates to a Gordonia sp. microorganism, capable of  
 CC eradication of the environmental hormone of phthalic acid alkyl esters.  
 CC The microorganism is used in the eradication of phthalic acid esters for  
 CC environmental protection. The present sequence represents an alternate G.  
 CC polyisoprenivorans P8219 16S rDNA sequence

XX SQ Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

Query Match 83.2%; Score 20.8; DB 6; Length 1457;  
 Best Local Similarity 91.7%; Pred. No. 8.8;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCGCTTTC 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 40 GCAAGTCGACGGAAGGCGCTTTC 63

## RESULT 49

ABN86275  
 ID ABN86275 standard; DNA; 1457 BP.

XX AC ABN86275;

XX DT 08-OCT-2002 (first entry)

XX DE G. polyisoprenivorans P8219 16S rDNA sequence.

XX KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.

XX OS Gordonia polyisoprenivorans.

XX PN JP2002142754-A.

XX PD 21-MAY-2002.

XX PF 08-NOV-2000; 2000JP-00341214.

XX PR 08-NOV-2000; 2000JP-00341214.

XX PA (IMBI-) IMB KK.

XX DR WPI; 2002-561124/60.

XX A Gordonia sp. microorganism, useful in the eradication of the  
 PT environmental hormone of phthalic acid esters for environmental  
 PT protection.

XX PS Disclosure; Fig 2A-D; 21pp; Japanese.

XX The invention relates to a Gordonia sp. microorganism, capable of  
 CC eradication of the environmental hormone of phthalic acid alkyl esters.  
 CC The microorganism is used in the eradication of phthalic acid esters for  
 CC environmental protection. The present sequence represents a G.  
 CC polyisoprenivorans P8219 16S rDNA sequence

XX SQ Sequence 1457 BP; 322 A; 349 C; 496 G; 290 T; 0 U; 0 Other;

Query Match 83.2%; Score 20.8; DB 6; Length 1457;  
 Best Local Similarity 91.7%; Pred. No. 8.8;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAGGCGCTTTC 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 40 GCAAGTCGACGGAAGGCGCTTTC 63

## RESULT 50

AAS59540/c  
 ID AAS59540 standard; DNA; 2743 BP.

XX AC AAS59540;

XX DT 13-FEB-2002 (first entry)

XX DE Propionibacterium acnes immunogenic protein encoding DNA #35.

XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant; ds.

XX

```

OS      Propionibacterium acnes.
XX      WO200181581-A2.
XX      PD      01-NOV-2001.
XX      PF      20-APR-2001; 2001WO-US012865.
XX      PR      21-APR-2000; 2000US-0199047P.
XX      PR      02-JUN-2000; 2000US-0208841P.
XX      PR      07-JUL-2000; 2000US-0216747P.
XX      PA      (CORI-) CORIXA CORP.
XX      PI      Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX      PI      L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX      DR      WPI; 2001-616774/71.
XX      PT      Propionibacterium acnes polypeptides and nucleic acids useful for
XX      PT      vaccinating against and diagnosing infections, especially useful for
XX      PT      treating acne vulgaris.
XX      PS      Claim 1; SEQ ID NO 35; 1069pp; English.
XX      CC      Sequences AAS59506-AAS59804 represent DNA molecules encoding
XX      CC      Propionibacterium acnes immunogenic polypeptides. The proteins and their
XX      CC      associated DNA sequences are used in the treatment, prevention and
XX      CC      diagnosis of medical conditions caused by P. acnes. The disorders include
XX      CC      SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
XX      CC      osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
XX      CC      infections of bone, joints and the central nervous system, however it is
XX      CC      particularly involved in the inflammatory lesions associated with acne
XX      CC      vulgaris. A method for detecting the presence or absence of P. acnes in a
XX      CC      patient comprises contacting a sample with a binding agent that binds to
XX      CC      the proteins of the invention and determining the amount of bound protein
XX      CC      in the sample. The polypeptides may be used as antigens in the production
XX      CC      of antibodies specific for P. acnes proteins. These antibodies can be
XX      CC      used to downregulate expression and activity of P. acnes polypeptides and
XX      CC      therefore treat P. acnes infections. The antibodies may also be used as
XX      CC      diagnostic agents for determining P. acnes presence, for example, by
XX      CC      enzyme linked immunosorbent assay (ELISA). This sequence encodes the
XX      CC      polypeptides shown in AAU47822-AAU47846. Note: The sequence data for this
XX      CC      patent did not form part of the printed specification, but was obtained
XX      CC      in electronic format directly from WIPO at
XX      CC      ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;

Query Match      83.2%; Score 20.8; DB 4; Length 2743;
Best Local Similarity 91.7%; Pred. No. 9.4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCGCTTTC 24
      |||||
Db      2593 GCAAGTCGAACGGAAGGCGCTGCG 2570

RESULT 51
ACF64469/c
ID      ACF64469 standard; DNA; 2743 BP.
XX      AC      ACF64469;
XX      DT      17-OCT-2003 (first entry)
XX      DE      Propionibacterium acnes DNA contig sequence #35.
XX      KW      Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX      KW      immunostimulant; immune response; vaccine; ds.
XX      OS      Propionibacterium acnes.
XX

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PN      WO2003033515-A1.
XX      PD      24-APR-2003.
XX      PF      11-OCT-2002; 2002WO-US032727.
XX      PR      15-OCT-2001; 2001US-00978825.
XX      PA      (CORI-) CORIXA CORP.
XX      PI      Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX      PI      Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX      PI      Barth B, Vallieue-Douglas J;
XX      DR      WPI; 2003-361789/36.
XX      PT      New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX      PT      polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX      PT      or for stimulating an immune response specific for a P. acnes protein.
XX      PS      Claim 1; SEQ ID NO 35; 1481pp; English.
XX      CC      The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX      CC      encoding a Propionibacterium acnes protein. The invention also relates to
XX      CC      polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX      CC      immunogenic fragments of P. acnes polypeptides. The invention
XX      CC      additionally encompasses expression vectors and host cells comprising a
XX      CC      polynucleotide of the invention; antibodies against polypeptides of the
XX      CC      invention; fusion proteins comprising a polypeptide of the invention; a
XX      CC      method for stimulating an immune response specific for a P. acnes
XX      CC      polypeptide and an isolated T cell population comprising T cells prepared
XX      CC      via this method; a vaccine composition (comprising P. acnes polypeptides,
XX      CC      polynucleotides, antibodies, fusion proteins, T cell populations, or
XX      CC      antigen-presenting cells that express the polypeptide); a method and kit
XX      CC      for detecting or determining the presence or absence of P. acnes in a
XX      CC      patient; and a method for inhibiting the development of P. acnes in a
XX      CC      patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX      CC      proteins, T cell populations or antigen-presenting cells that express the
XX      CC      polypeptides are useful for diagnosing, preventing or treating acne
XX      CC      vulgaris, or for stimulating an immune response specific for a P. acnes
XX      CC      protein. The polynucleotides can also be used as probes or primers for
XX      CC      nucleic acid hybridisation. The vaccine composition is useful for the
XX      CC      stimulation of an immune response against P. acnes, or for treating acne,
XX      CC      and the kit is useful for performing a diagnostic assay. The present
XX      CC      sequence represents a P. acnes DNA contig which is specifically claimed
XX      CC      in the invention. Note: The sequence data for this patent did not form
XX      CC      part of the printed specification, but was obtained in electronic format
XX      CC      directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX      SQ      Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;

Query Match      83.2%; Score 20.8; DB 8; Length 2743;
Best Local Similarity 91.7%; Pred. No. 9.4;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCGCTTTC 24
      |||||
Db      2593 GCAAGTCGAACGGAAGGCGCTGCG 2570

RESULT 52
AAX99198
ID      AAX99198 standard; DNA; 50 BP.
XX      AC      AAX99198;
XX      DT      28-SEP-1999 (first entry)
XX      DE      M. smegmatis 16S rRNA gene fragment.
XX      KW      Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX      KW      shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX

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OS Mycobacterium smegmatis.
XX WO9935284-A1.
XX
XX
PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
XX CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX CC DNA amplification and shift mobility assay. The method is based on
XX CC divergence in sequences found in 16S rRNA to identify mycobacteria
XX CC species, since a remarkable shift of heteroduplex bands are obtained
XX CC between single stranded and homoduplex bands in UPAGE. The method is
XX CC compared with other detection methods. The sensitivity of other assays
XX CC suffer due to the tendency of the denatured PCR product strands to
XX CC reassociate and exclude oligonucleotide probes, and stearic interference
XX CC between the bound oligonucleotides and the solid support which impede
XX CC hybridization to nucleic acids in solution. Sequences AAX99193-237
XX CC represent 16S rRNA gene regions of some mycobacterial species
XX CC
XX SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
    Query Match      81.6%; Score 20.4; DB 2; Length 50;
    Best Local Similarity 91.3%; Pred. No. 9.5;
    Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 9 GCAAGTCGAACGGAAGGCGCTT 31

RESULT 53
AAX99201
ID AAX99201 standard; DNA; 50 BP.
XX
XX AC AAX99201;
XX
XX DT 27-AUG-2003 (revised)
XX DT 28-SEP-1999 (first entry)
XX
XX DE M. simium 16S rRNA gene fragment.
XX
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
XX OS Mycobacterium simiae.
XX
XX PN WO9935284-A1.
XX
XX PD 15-JUL-1999.
XX
XX PF 30-DEC-1997; 97WO-BR000087.
XX
XX PR 30-DEC-1997; 97WO-BR000087.
XX
XX PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX PI Peregrino Ferreira PC, Geessien Kroon E;
XX PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX DR WPI; 1999-444201/37.
XX
XX PT Detection of mycobacteria by shift mobility assay.
XX
XX PS Disclosure; Fig 7; 20pp; English.
XX
XX CC The invention describes a new method for diagnosis, identification and
XX CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX CC DNA amplification and shift mobility assay. The method is based on
XX CC divergence in sequences found in 16S rRNA to identify mycobacteria
XX CC species, since a remarkable shift of heteroduplex bands are obtained
XX CC between single stranded and homoduplex bands in UPAGE. The method is
XX CC compared with other detection methods. The sensitivity of other assays
XX CC suffer due to the tendency of the denatured PCR product strands to
XX CC reassociate and exclude oligonucleotide probes, and stearic interference
XX CC between the bound oligonucleotides and the solid support which impede
XX CC hybridization to nucleic acids in solution. Sequences AAX99193-237
XX CC represent 16S rRNA gene regions of some mycobacterial species
XX CC
XX SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
    Query Match      81.6%; Score 20.4; DB 2; Length 50;
    Best Local Similarity 91.3%; Pred. No. 9.5;
    Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 9 GCAAGTCGAACGGAAGGCGCTT 31

RESULT 54
ADS75567
ID ADS75567 standard; DNA; 535 BP.
XX
XX AC ADS75567;
XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE Rhodococcus equi TB-60 16S rDNA sequence, SEQ ID 1.
XX
XX KW Urethane; polyurethane; 16S rDNA; ds.
XX
XX OS Rhodococcus equi; TB-60.
XX
XX PN WO2004078952-A1.
XX
XX PD 16-SEP-2004.
XX
XX PF 03-MAR-2004; 2004WO-JP002691.
XX
XX PR 03-MAR-2003; 2003JP-00055421.
XX
XX PA (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
XX
XX PI Kambe T, Shigeno Y;
XX
XX DR WPI; 2004-728402/71.
XX
XX PT Novel microorganism or its mutant belonging to Rhodococcus genus and
XX PT having ability to cleave urethane bond, useful for plastic disposal and
XX PT recycling of urethane compounds.
XX
XX PS Example 2; SEQ ID NO 1; 26pp; Japanese.
XX
XX CC The present invention relates to a novel Rhodococcus equi TB-60 strain

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CC microorganism (I) or its mutant, which can cleave urethane bonds. (I) is
CC useful for decomposing urethane compounds which involves contacting (I)
CC with urethane compound. The urethane compound is a raw material of
CC polyurethane or is polyurethane. (I) is useful in plastic disposal and
CC recycling of urethane compounds by decomposing urethane compounds. The
CC present sequence is a 16S rDNA sequence from the microorganism of the
CC invention.
XX
SQ Sequence 535 BP; 118 A; 131 C; 191 G; 95 T; 0 U; 0 Other;

Query Match      80.8%; Score 20.2; DB 13; Length 535;
Best Local Similarity 88.0%; Pred. No. 15;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGGAAGGCCCTTCG 25
Db 51 GCAAGTCGACGCGGTAAGGCCCTTCG 75

RESULT 55
ADFS6670
ID ADFS6670 standard; DNA; 1437 BP.
XX
XX ADFS6670;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
DE YS-44442 16S rDNA, SEQ ID 1.
XX
XX Pravastatin; HMG-CoA reductase inhibitor;
KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
XX
XX Saccharothrix sp.
OS
XX JP2003250532-A.
FN
XX
XX 09-SEP-2003.
PD
XX
XX 22-FEB-2002; 2002JP-00046750.
PF
XX
XX 22-FEB-2002; 2002JP-00046750.
PR
XX
XX (YUNG-) YUNG SHIN PHARM IND CO LTD.
PA
XX
XX WPI; 2004-046768/05.
DR
XX
XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
PT mutants useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 18pp; Japanese.
PS
XX
XX The present invention relates to microorganisms (I) Saccharothrix genus
CC YS-44442 and YS-45494 strains and their mutants. Also claimed is a method
CC (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match      80.8%; Score 20.2; DB 12; Length 1437;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGGAAGGCCCTTCG 25
Db 30 GCAAGTCGACGCGGTAAGGCCCTTCG 54

RESULT 56
ADG64519
ID ADG64519 standard; DNA; 1437 BP.
XX
XX ADG64519;
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.
DE

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DT 11-MAR-2004 (first entry)
XX
DE Saccharothrix strain YS-44442 16S rDNA sequence.
XX
XX Microorganism; Saccharothrix; YS-44442; YS-45494;
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
KW pravastatin; fermentation; compactin; lovastatin;
KW blood cholesterol level; antilipemic; 16S rDNA; ds.
XX
OS Saccharothrix sp.
XX
XX US2003199047-A1.
PN
XX
XX 23-OCT-2003.
PD
XX
XX 27-FEB-2002; 2002US-00085871.
PF
XX
XX 27-FEB-2002; 2002US-00085871.
PR
XX
XX (LEEF/) LEE F.
PA (LEEM/) LEE M.
PA (HONG/) HONG A C.
PA (CHIU/) CHIU S.
XX
XX Lee F, Lee M, Hong AC, Chiu S;
PI
XX WPI; 2004-041353/04.
XX
XX Novel microorganism strains YS-44442 and YS-45494 of Saccharothrix,
DR useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 16pp; English.
PS
XX
XX The present invention relates to the isolation of novel microorganism
CC strains of Saccharothrix designated YS-44442 and YS-45494. Also disclosed
CC is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
CC inhibitors such as pravastatin. The Saccharothrix strains YS-44442 and YS
CC -45494 are useful for producing pravastatin. The method involves
CC cultivating the strains at a suitable condition to generate a
CC fermentation broth, feeding compactin into the broth, fermenting the
CC broth for a period of time to convert the compactin to pravastatin, and
CC isolating the pravastatin from the broth. The fermentation broth is
CC cultivated for less than 2 days, preferably for 18 hours. The
CC fermentation broth is derived from a seed culture of the microorganism
CC which is cultivated at a suitable condition for 18-48 hours before
CC inoculation into the broth. The broth is fermented for less than 5 days,
CC preferably 3 days, most preferably less than 24 hours. The method of the
CC invention is useful for isolating HMG-CoA reductase inhibitor such as
CC pravastatin, compactin or lovastatin, preferably pravastatin. The
CC pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
CC cholesterol levels. The present sequence represents Saccharothrix strain
CC YS-44442 16S rDNA sequence.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;
SQ

Query Match      80.8%; Score 20.2; DB 12; Length 1437;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGGAAGGCCCTTCG 25
Db 30 GCAAGTCGACGCGGTAAGGCCCTTCG 54

RESULT 57
ADY86147
ID ADY86147 standard; DNA; 1437 BP.
XX
XX ADY86147;
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.
DE

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XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;  
 KW metabolic disorder; ds.  
 XX  
 OS Saccharothrix; YS-44442.  
 XX  
 PN US2005064566-A1.  
 XX  
 XX 24-MAR-2005.  
 XX  
 XX 03-DEC-2003; 2003US-00727643.  
 XX  
 XX 27-FEB-2002; 2002US-00085871.  
 XX  
 XX (LEEF/) LEE F.  
 PA (LEEM/) LEE M.  
 PA (HONG/) HONG A. C.  
 PA (CHIU/) CHIU S.  
 XX  
 PI Lee F, Lee M, Hong AC, Chiu S;  
 XX  
 XX WPI; 2005-252680/26.  
 XX  
 XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises  
 PT adding ammonium sulfate into a first solution to form precipitate,  
 PT isolating and dissolving the precipitate to form a second solution and  
 PT followed by extracting.  
 XX  
 XX Example 1; SEQ ID NO 1; 19pp; English.  
 XX  
 XX The present invention relates to two new microorganism strains of  
 CC Saccharothrix, designated as YS-44442 and YS-45494. The invention also  
 CC provides a method of isolating pravastatin from Saccharothrix sp and an  
 CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A  
 CC (HMG CoA) reductase inhibitor. The invention is useful for the  
 CC preparation of pravastatin which is useful in the treatment of  
 CC hypercholesterolemia. The present sequence is the Saccharothrix YS-44442  
 CC 16s rDNA.  
 XX  
 XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;  
 SQ  
 Query Match 80.8%; Score 20.2; DB 14; Length 1437;  
 Best Local Similarity 88.0%; Pred. No. 17;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54  
 RESULT 58  
 ADC61232  
 ID ADC61232 standard; DNA; 1439 BP.  
 XX  
 XX ADC61232;  
 AC  
 XX 18-DEC-2003 (first entry)  
 DT  
 XX Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.  
 DE  
 XX Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;  
 KW 16s rDNA; ds.  
 KW  
 XX Rhodococcus erythropolis.  
 OS  
 XX WO2003020890-A2.  
 PN  
 XX 13-MAR-2003.  
 PD  
 XX 29-AUG-2002; 2002WO-US027549.  
 PF  
 XX 29-AUG-2001; 2001US-0315546P.  
 PR  
 XX

PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX  
 PI Bramucci MG, Brzosowicz PC, Kostichka KN, Nagarajan V;  
 PI Rouviere PB, Thomas SM,  
 XX  
 XX WPI; 2003-313085/30.  
 XX  
 XX Novel nucleic acid fragment useful for converting ketone substrates to  
 PT the corresponding lactone or ester, is isolated from Rhodococcus,  
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase  
 PT polypeptide.  
 XX  
 XX Claim 54; SEQ ID NO 6; 225pp; English.  
 XX  
 XX The invention relates to a novel isolated nucleic acid fragment  
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase  
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 523, 493, 539,  
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;  
 CC a nucleic acid molecule that hybridises with the above sequence under the  
 CC hybridisation conditions; or their complements. The BV monooxygenase  
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV  
 CC monooxygenase polypeptide, by probing a genomic library with the  
 CC fragment, identifying a DNA clone that hybridises with the fragment, and  
 CC sequencing the genomic fragment that comprises the above identified  
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase  
 CC polypeptide. The genes and their products are useful for converting  
 CC suitable ketone substrates to the corresponding lactone or ester. This  
 CC polynucleotide sequence represents the 16s rDNA gene from Arthrobacter  
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.  
 XX  
 XX Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;  
 SQ  
 Query Match 80.8%; Score 20.2; DB 10; Length 1439;  
 Best Local Similarity 88.0%; Pred. No. 17;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 31 GCAATTCGAGCGGTAAGGCCCTTCG 55  
 RESULT 59  
 ADF56671  
 ID ADF56671 standard; DNA; 1471 BP.  
 XX  
 XX ADF56671;  
 AC  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX YS-45494 16s rDNA, SEQ ID 2.  
 DE  
 XX Pravastatin; HMG-CoA reductase inhibitor;  
 KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16s rDNA; ds.  
 KW  
 XX Saccharothrix sp.  
 OS  
 XX JP2003250532-A.  
 PN  
 XX 09-SEP-2003.  
 PD  
 XX 22-FEB-2002; 2002JP-00046750.  
 PF  
 XX 22-FEB-2002; 2002JP-00046750.  
 PR  
 XX (YUNG-) YUNG SHIN PHARM IND CO LTD.  
 PA  
 XX WPI; 2004-046768/05.  
 DR  
 XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their  
 PT mutants useful for producing pravastatin.  
 PT  
 XX Example 1; SEQ ID NO 2; 18pp; Japanese.  
 PS  
 XX

CC The present invention relates to microorganisms (I) Saccharothrix genus  
CC YS-4442 and YS-45494 strains and their mutants. Also claimed is a method  
CC (M1) for producing pravastatin by using (I), and isolating (M2) 3-hydroxy-  
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.

XX Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;  
SQ

Query Match 80.8%; Score 20.2; DB 12; Length 1471;  
Best Local Similarity 88.0%; Pred. No. 17;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25  
||||||| ||||| ||||| ||||| |||||  
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 60  
ADG64520  
ID ADG64520 standard; DNA; 1471 BP.

XX AC ADG64520;

XX DT 11-MAR-2004 (first entry)

XX DE Saccharothrix strain YS-45494 16s rDNA sequence.

XX KW Microorganism; Saccharothrix; YS-4442; YS-45494;  
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;  
KW pravastatin; fermentation; compactin; lovastatin;  
KW blood cholesterol level; antilipemic; 16s rDNA; ds.

XX OS Saccharothrix sp.

XX PN US2003199047-A1.

XX PD 23-OCT-2003.

XX PF 27-FEB-2002; 2002US-00085871.

XX PR 27-FEB-2002; 2002US-00085871.

XX PA (LEEF/) LEE F.  
PA (LEEM/) LEE M.  
PA (HONG/) HONG A C.  
PA (CHIU/) CHIU S.

XX PI Lee F, Lee M, Hong AC, Chiu S;

XX DR WPI; 2004-041353/04.

XX PT Novel microorganism strains YS-4442 and YS-45494 of Saccharothrix,  
XX useful for producing pravastatin.

XX PS Example 1; SEQ ID NO 2; 16pp; English.

XX CC The present invention relates to the isolation of novel microorganism  
CC strains of Saccharothrix designated YS-4442 and YS-45494. Also disclosed  
CC is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase  
CC inhibitors such as pravastatin. The Saccharothrix strains YS-4442 and YS  
CC -45494 are useful for producing pravastatin. The method involves  
CC cultivating the strains at a suitable condition to generate a  
CC fermentation broth, feeding compactin into the broth, fermenting the  
CC broth for a period of time to convert the compactin to pravastatin, and  
CC isolating the pravastatin from the broth. The fermentation broth is  
CC cultivated for less than 2 days, preferably for 18 hours. The  
CC fermentation broth is derived from a seed culture of the microorganism  
CC which is cultivated at a suitable condition for 18-48 hours before  
CC inoculation into the broth. The broth is fermented for less than 5 days,  
CC preferably 3 days, most preferably less than 24 hours. The method of the  
CC invention is useful for isolating HMG-CoA reductase inhibitor such as  
CC pravastatin, compactin or lovastatin, preferably pravastatin. The  
CC pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood  
CC cholesterol levels. The present sequence represents Saccharothrix strain

CC YS-45494 16s rDNA sequence.

XX Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

SQ Query Match 80.8%; Score 20.2; DB 12; Length 1471;  
Best Local Similarity 88.0%; Pred. No. 17;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25  
||||||| ||||| ||||| ||||| |||||  
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 61  
ADY86148

ID ADY86148 standard; DNA; 1471 BP.

XX AC ADY86148;

XX DT 02-JUN-2005 (first entry)

XX DE Saccharothrix YS-45494 16s rDNA, SEQ ID NO: 2.

XX KW Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;  
KW metabolic disorder; ds.

XX OS Saccharothrix; YS-45494.

XX PN US2005064566-A1.

XX PD 24-MAR-2005.

XX PF 03-DEC-2003; 2003US-00727643.

XX PR 27-FEB-2002; 2002US-00085871.

XX PA (LEEF/) LEE F.

XX PA (LEEM/) LEE M.

XX PA (HONG/) HONG A C.

XX PA (CHIU/) CHIU S.

XX PI Lee F, Lee M, Hong AC, Chiu S;

XX DR WPI; 2005-252680/26.

XX PT Isolation of pravastatin, used to treat hypercholesterolemia, comprises  
XX adding ammonium sulfate into a first solution to form precipitate,  
XX isolating and dissolving the precipitate to form a second solution and  
XX followed by extracting.

XX PS Example 1; SEQ ID NO 2; 19pp; English.

XX CC The present invention relates to two new microorganism strains of  
CC Saccharothrix, designated as YS-4442 and YS-45494. The invention also  
CC provides a method for isolating pravastatin from Saccharothrix sp and an  
CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A  
CC (HMG CoA) reductase inhibitor. The invention is useful for the  
CC preparation of pravastatin which is useful in the treatment of  
CC hypercholesterolemia. The present sequence is the Saccharothrix YS-45494  
CC 16s rDNA.

SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 14; Length 1471;  
Best Local Similarity 88.0%; Pred. No. 17;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCTTCG 25  
||||||| ||||| ||||| ||||| |||||  
Db 30 GCAAGTCGAGCGGTAAAGCCCTTCG 54

RESULT 62

```

AED47485
ID AED47485 standard; DNA; 1477 BP.
XX
AC AED47485;
XX
DT 15-DEC-2005 (first entry)
XX
DE Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.
XX
KW Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.;
KW Uropathic; binding inhibitor; muscarinic acetylcholine receptor;
KW analgesic; Parkinsons disease; asthma;
KW chronic obstructive pulmonary disease; bladder disease;
KW micturition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.
XX
OS Nocardia sp.
XX
PN JP2005289890-A.
XX
PD 20-OCT-2005.
XX
PF 31-MAR-2004; 2004JP-00107929.
XX
PR 31-MAR-2004; 2004JP-00107929.
XX
PA (YOSH ) YOSHITOMI PHARM IND KK.
XX
PI Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;
XX
DR WPI; 2005-738172/76.
XX
PT Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3
PT useful for treating diseases e.g. asthma, contains chelate having TP
PT 0052A-F compound derived from Nocardia species TP-A0674 and metal ion.
XX
PS Disclosure; SEQ ID NO 1; 22pp; Japanese.
XX
CC The invention relates to a novel binding inhibitor of muscarinic
CC acetylcholine receptor subtype 4 or 3, comprising a chelate having a TP
CC 0052A-F compound or its salt and a metal ion. The invention further
CC comprises a method and a microorganism for producing the novel binding
CC inhibitor. The binding inhibitor and compound are useful as central
CC analgesics and memory improving drugs, for treating Parkinson's disease,
CC asthma, chronic obstructive pulmonary disease, overactive bladder,
CC frequent urination and urinary incontinence. This polynucleotide sequence
CC represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674
CC microorganism, useful in producing a muscarinic acetylcholine receptor
CC binding inhibitor compound of the invention.
XX
SQ Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 14; Length 1477;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 47 GCAAGTCGACGCGTAAGGCCCTTCG 71

RESULT 63
ADS17269
ID ADS17269 standard; DNA; 1498 BP.
XX
AC ADS17269;
XX
DT 02-DEC-2004 (first entry)
XX
DE Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
KW Plant protectant; antibiotic; thiobutacin; antifungal; antiomycete;
KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX

OS Lechevalieria aerocolonigenes.
XX
PN US2004180960-A1.
XX
PD 16-SEP-2004.
XX
PF 13-JAN-2004; 2004US-00756683.
XX
PR 13-MAR-2003; 2003KR-00015628.
XX
PA (HWAN)/ HWANG B K.
PA (LEEJ)/ LEE J Y.
XX
PI Hwang BK, Lee JY;
XX
DR WPI; 2004-661528/64.
DR EMBL; AY196703.
XX
PT New antibiotic compound, thiobutacin, is used to treat plant disease e.g.
PT phytophthora blight and to control plant diseases caused by pathogens
PT e.g. Phytophthora capsici and Botrytis cinerea.
XX
PS Example 2; SEQ ID NO 1; 17pp; English.
XX
CC The invention relates to an antibiotic compound thiobutacin and
CC antifungal and antiomycete compositions comprising thiobutacin.
CC Thiobutacin is used to treat plant disease such as phytophthora blight
CC and to control plant diseases caused by pathogens e.g. Phytophthora
CC capsici and Botrytis cinerea. The present sequence is the Lechevalieria
CC aerocolonigenes strain VK-A9 16S ribosomal DNA (rDNA). L. aerocolonigenes
CC strain VK-A9 has strong antifungal and antimicrobial activity and it can
CC inhibit the growth of Phytophthora capsici.
XX
SQ Sequence 1488 BP; 339 A; 369 C; 508 G; 272 T; 0 U; 0 Other;

Query Match 80.8%; Score 20.2; DB 13; Length 1488;
Best Local Similarity 88.0%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGCGTAAGGCCCTTCG 25
Db 42 GCAAGTCGACGCGTAAGGCCCTTCG 66

RESULT 64
ADW12667
ID ADW12667 standard; DNA; 1514 BP.
XX
AC ADW12667;
XX
DT 07-APR-2005 (first entry)
XX
DE Rhodococcus opacus 16S rDNA, SEQ ID NO:2.
XX
KW Stereoselective synthesis; enantiomeric enrichment;
KW beta-amino acid synthesis; cell culture; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus opacus.
XX
PN US2005009151-A1.
XX
PD 13-JAN-2005.
XX
PF 22-JUN-2004; 2004US-00875161.
XX
PR 10-JUL-2003; 2003US-0486032P.
PR 02-SEP-2003; 2003US-0499622P.
XX
PA (PHAA ) PHARMACIA CORP.
XX
PI Chase M, Clayton R, Landis B, Banerjee A;
XX

```





CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADP94060 and ADP94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,  
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*  
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*  
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*  
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*  
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*  
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*  
 CC *aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*,  
 CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,  
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*,  
 CC *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*,  
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*  
 CC *aquaticum*, *Streptococcus oralis*, *Staphylococcus aureus*, *Neisseria*  
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*  
 CC *casseliflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*  
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*  
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*  
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*  
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,  
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*  
 CC *gordonae*.

SQ Sequence 50 BP; 11 A; 12 C; 20 G; 7 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 12; Length 50;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20

DB 1 GCAAGTCGAACGGAAGGCC 20

RESULT 67

ADU66542

ID ADU66542 standard; DNA; 80 BP.

XX

AC ADU66542;

XX

DT 27-JAN-2005 (first entry)

XX

DE Cut base A amplicon fragment.

XX

KW ds; mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.

XX

OS Unidentified.

XX

PN WO2004097369-A2.

XX

PD 11-NOV-2004.

XX

PF 22-APR-2004; 2004WO-US012520.

XX

PR 25-APR-2003; 2003US-0466006P.

XX

PA (SEQU-) SEQUENOM INC.

PA (BOBC/) BOECKER S.

XX

PI Boecker S, Van Den Boom D;

XX

XX WPI; 2005-012656/01.

DR

PT Obtaining sequence information from target biomolecule, by fragmenting  
 PT target biomolecule by partial cleavage, performing mass spectrometry,  
 PT extracting information from mass spectra, constructing sequencing graph  
 PT and traversing graphs.

XX

PS Disclosure; SEQ ID NO 11; 133bp; English.

XX

CC This invention describes a novel method for obtaining sequence  
 CC information from a target biomolecule and involves fragmenting the target  
 CC biomolecule into several fragments by partial cleavage, performing mass  
 CC spectrometry on fragments to produce mass spectra, extracting peak  
 CC information from the produced mass spectra, constructing sequencing graph  
 CC using the extracted peak information and traversing the sequencing graphs  
 CC to reconstruct sequence information of the target biomolecule. The target  
 CC biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein  
 CC and the compositions of the two fragments are the base compositions or  
 CC amino acid compositions. This method preferably involves subjecting the  
 CC nucleic acid molecule to partial cleavage reactions with one or more  
 CC specific cleavage reagents, thus generating two or more fragments that  
 CC are specific cleavage products, determining the molecular weights of the  
 CC two or more fragments, determining the possible base compositions of the  
 CC two or more fragments, ordering the possible base compositions of the two  
 CC or more fragments according to the number of specific cleavage sites that  
 CC are not cleaved in each fragment, constructing one or more sequencing  
 CC graphs that are a graph theoretical representation of the ordered base  
 CC compositions for the two or more fragments, and traversing the one or  
 CC more sequencing graph to reconstruct one or more underlying sequence  
 CC candidates, where each sequencing graph corresponds to the ordered base  
 CC compositions derived from a partial cleavage reaction with one base-  
 CC specific cleavage reagent. This method further involves scoring the one  
 CC or more underlying sequence candidates and determining the rank order of  
 CC fitness, where the scoring is done by statistical analysis or maximum  
 CC likelihood statistical analysis. This method determines epigenetic  
 CC changes in a target nucleic acid molecule relative to reference nucleic  
 CC acid molecule and allows the sequencing of large biomolecules. The  
 CC invention also describes a method of producing a candidate sequence of a  
 CC biomolecule which involves receiving several sequencing graphs having  
 CC several vertices and edges, where each vertex represents a compomer of  
 CC the biomolecule and each edge represents a cut base of the sequencing  
 CC graph and generating the candidate sequence by traversing several  
 CC sequencing graphs. This second method further involves traversing several  
 CC sequencing graphs by tracing through each sequencing graph, starting at a  
 CC source vertex. The results of each method can be read by a program  
 CC product for use in a computer that executes program instructions recorded  
 CC in a computer-readable media to produce a candidate sequence of a  
 CC biomolecule or to obtain sequence information in a target biomolecule.  
 CC The target biomolecule contains a sequence variation, which is a mutation  
 CC or a polymorphism. The target is a target nucleic acid molecule from an  
 CC organism chosen from eukaryotes, prokaryotes and viruses, preferably a  
 CC bacterium. The specific cleavage reagent is an RNase chosen from RNase  
 CC T1, RNase U2, RNase PhY, RNase A, chicken liver RNase (RNase CL3) and  
 CC cusavatin, or a glycosylase. The sequence variations in the target  
 CC biomolecule permit genotyping a subject, forensic analysis, disease  
 CC diagnosis or disease prognosis. The novel methods are useful for de novo  
 CC sequencing, to identify genetic disease or chromosome abnormality,  
 CC identifying a predisposition to a disease, or condition including  
 CC obesity, atherosclerosis, or cancer, to identify an infection by an  
 CC infectious agent, to identify a pathogen, determine haplotypes, analyze  
 CC microsatellite sequences, and short tandem repeat (STR) loci, determine  
 CC allelic variation and/or frequency, and analyze cellular methylation  
 CC patterns. This sequence represents an amplicon used to illustrate the  
 CC sequencing technique described in the invention.

SQ Sequence 80 BP; 18 A; 20 C; 27 G; 15 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 14; Length 80;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20

DB 50 GCAAGTCGAACGGAAGGCC 69

RESULT 68

AEB98763

ID AEB98763 standard; DNA; 209 BP.

XX

AC AEB98763;

XX

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DT 06-OCT-2005 (first entry)
XX Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.
DE microorganism detection; mycobacterium infection; antibacterial; ds.
KW Mycobacterium intracellulare.
OS JP2005204582-A.
XX 04-AUG-2005.
XX 23-JAN-2004; 2004JP-00015195.
XX 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
PA Oda N;
XX WPI; 2005-526965/54.
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX Example 1; SEQ ID NO 5; 14pp; Japanese.
PS The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This polynucleotide represents a Mycobacterium
CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of
CC the invention.
XX Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;
SQ Query Match 80.0%; Score 20; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 17; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
Qy 1 GCAAGTCGACGGAAGGCC 20
Db 39 GCAAGTCGACGGAAGGCC 58
RESULT 69
ABT23572
ID ABT23572 standard; DNA; 560 BP.
XX AC ABT23572;
XX 22-MAY-2003 (first entry)
DT Stabilising reagent method related oligo SEQ ID No 24.
DE Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;
KW specific amplification; pathogenic microorganism; chimeric;
KW genetic engineering; clinical medicine; ss.
XX Mycobacterium avium.
OS WO2002101042-A1.
XX 19-DEC-2002.
XX 12-JUN-2002; 2002WO-JP005832.
PF Determining a bacterium species comprises providing oligonucleotide
primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
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XX 12-JUN-2001; 2001JP-00177737.
PR 20-AUG-2001; 2001JP-00249689.
XX (TAKI ) TAKARA BIO INC.
XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
XX WPI; 2003-149805/14.
DR Method for stabilizing and storing reaction reagents for specific
XX amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX Example 15; Page 110; 177pp; Japanese.
XX The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly
CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention
XX Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;
SQ Query Match 80.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GCAAGTCGACGGAAGGCC 20
Db 42 GCAAGTCGACGGAAGGCC 61
RESULT 70
AEA22410
ID AEA22410 standard; DNA; 1321 BP.
XX AC AEA22410;
XX 25-AUG-2005 (first entry)
DT Mycobacterium kubicae 16S rRNA sequence SEQ ID NO:11.
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
KW Mycobacterium kubicae.
OS US2005130168-A1.
XX 16-JUN-2005.
XX 31-OCT-2003; 2003US-00697802.
XX 31-OCT-2003; 2003US-00697802.
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX Han X, Pham AS;
PI WPI; 2005-424597/43.
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
PT
```

XX PS Disclosure; SEQ ID NO 11; 74pp; English.

XX CC The invention relates to a method (M1) for determining a bacterium

XX CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)

XX CC extracting a genomic nucleotide from the bacterium to provide a

XX CC nucleotide template; (c) annealing a region of a nucleotide template to a

XX CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a

XX CC complementary fashion, the primer set designed to provide a product

XX CC having a predetermined size dictated by a complementary primer set; (d)

XX CC amplifying the region of the nucleotide template to produce the product;

XX CC and (e) determining a species of a bacterium in a nucleotide sequence of

XX CC the product. Also described is an alternative method (M2) for determining

XX CC a bacterium species comprising: (a) providing a specimen or a sample

XX CC having a template; (b) providing a pair of primers selected from: (i) a

XX CC first forward primer having consecutive bases of an AFB-f comprising any

XX CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments

XX CC or variations; and a first reverse primer having consecutive bases of an

XX CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)

XX CC or their fragments or variations; (ii) a second forward primer having

XX CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21

XX CC bp (AEA22489-AEA22516) or their fragments or variations; and a second

XX CC reverse primer having consecutive bases of an UB-r comprising any of the

XX CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or

XX CC variations; or (iii) a first forward primer having consecutive bases of

XX CC an AFB-f of AEA22417-AEA22452 or their fragments or variations; and a

XX CC second reverse primer having consecutive bases of an UB-r of AEA22517-

XX CC AEA22544 or their fragments or variations; (c) the specimen; and (d)

XX CC comparing the product from the specimen with a nucleotide sequence from a

XX CC database to determine the bacterium species present in the specimen. The

XX CC methods are useful for determining a bacterium species. The present

XX CC sequence represents a Mycobacterium kubaecae 16S rRNA nucleotide sequence,

XX CC which is used in the exemplification of the present invention.

XX SQ Sequence 1321 BP; 287 A; 314 C; 457 G; 263 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 14; Length 1321;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAGTGCAGCGAAGGCC 20

DB 14 GCAAGTCGACGAAAGGCC 33

RESULT 71

AD085868/c

ID AD085868 standard; DNA; 1344 BP.

XX AC AD085868;

XX DT 29-JUL-2004 (first entry)

XX DE Gordonia sp. bacterium 16S rDNA.

XX KW microorganism; Gordonia genus; gram-positive bacillus; catalase;

XX KW nitrate reduction; alkali phosphatase; beta-galactosidase;

XX KW pyrazinamidase; pyrolidonyl allyl amidase; beta-glucuronidase;

XX KW alpha-glucosidase; urease; gelatin-liquefaction; esculin; glucose;

XX KW ribose; GR-004 strain; FERM P-18806;

XX KW cyclic hydrocarbon degradation agent; waste engine oil; 16S rDNA; ds.

XX OS Gordonia sp.

XX XX JP2004121068-A.

XX PN 22-APR-2004.

XX PD 01-OCT-2002; 2002JP-00288714.

XX PF 01-OCT-2002; 2002JP-00288714.

XX PR 01-OCT-2002; 2002JP-00288714.

XX PS (GEIT-) GEITO KK.

XX CC The invention relates to a method (M1) for determining a bacterium

XX DR WPI; 2004-322761/30.

XX PT Novel microorganism of Gordonia genus having biochemical properties

XX PT positive for catalase, approximately beta-galactosidase, nitrate reduction

XX PT ability, is useful as cyclic hydrocarbon degradation agent in waste-oil

XX PT treatment.

XX PS Claim 2; SEQ ID NO 1; 12pp; Japanese.

XX CC The invention relates to a novel microorganism belonging to the Gordonia

XX CC genus, a gram-positive bacillus. The novel microorganism having

XX CC biochemical properties positive for catalase, nitrate reduction ability,

XX CC alkali phosphatase, and beta-galactosidase, and negative for

XX CC pyrazinamidase, pyrolidonyl allyl amidase, beta-glucuronidase, alpha-

XX CC glucosidase, urease, gelatin-liquefaction ability, and esculin, glucose

XX CC and ribose utilisation ability. The invention further comprises: a GR-004

XX CC strain of Gordonia sp. having the accession number FERM P-18806; and a

XX CC cyclic hydrocarbon degradation agent containing the novel microorganism.

XX CC The Gordonia genus microorganism is useful for processing a cyclic

XX CC hydrocarbon-containing substance, which involves using the cyclic

XX CC hydrocarbon degradation agent, where the cyclic hydrocarbon-containing

XX CC substance is a waste engine oil. The Gordonia genus microorganism is

XX CC useful as a cyclic hydrocarbon degradation agent for waste-oil treatment.

XX CC This polynucleotide sequence represents the Gordonia sp. bacterium 16S

XX CC rDNA of the invention.

XX SQ Sequence 1344 BP; 276 A; 447 C; 315 G; 306 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 12; Length 1344;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCAGTGCAGCGAAGGCC 20

DB 1299 GCAAGTCGACGAAAGGCC 1280

RESULT 72

AD22413

ID AEA22413 standard; DNA; 1415 BP.

XX AC AEA22413;

XX DT 25-AUG-2005 (first entry)

XX DE Mycobacterium paraffinicum 16S rRNA sequence SEQ ID NO:14.

XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX OS Mycobacterium paraffinicum.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

XX PF 31-OCT-2003; 2003US-00697802.

XX PR 31-OCT-2003; 2003US-00697802.

XX PA (HANX/) HAN X.

XX PA (PHAM/) PHAM A S.

XX PI Han X, Pham AS;

XX DR WPI; 2005-424597/43.

XX PT Determining a bacterium species comprises providing oligonucleotide

XX PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.

XX PS Disclosure; SEQ ID NO 14; 74pp; English.

XX CC The invention relates to a method (M1) for determining a bacterium

species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion, the primer set designed to provide a product having a predetermined size dictated by a complementary primer set; (d) amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments or variations and a first reverse primer having consecutive bases of an AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488) or their fragments or variations, (ii) a second forward primer having consecutive bases of an AFB-f of AEA22417-AEA22452 or their fragments or variations and a second reverse primer having consecutive bases of an UB-r of AEA22517-AEA22544 or their fragments or variations; (c) the specimen; and (d) comparing the product from the specimen with a nucleotide sequence from a database to determine the bacterium species present in the specimen. The methods are useful for determining a bacterium species. The present sequence represents a *Mycobacterium paraffinicum* 16S rRNA nucleotide sequence, which is used in the exemplification of the present invention.

XX SQ Sequence 1415 BP; 307 A; 343 C; 480 G; 285 T; 0 U; 0 Other;

Query Match 80.0%; Score 20; DB 14; Length 1415;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCC 20  
 |||||  
 Db 15 GCAAGTCGAACGGAAGGCC 34  
 |||||

RESULT 73  
 AA222765  
 ID AA222765 standard; DNA; 1460 BP.  
 AC AA222765;  
 XX 15-MAR-2000 (first entry)  
 DT Corynebacterium sp. NK-1 16S rRNA gene.  
 XX  
 KW Seasoning liquor; flavour; vegetable; pickling; salted rice bran paste;  
 KW microorganism; gamma-dodecalactone; gamma-dodecelactone; lactic acid;  
 KW propionic acid; 16S rRNA; pickle; ss.  
 XX  
 OS Corynebacterium sp.  
 XX WO9962347-A1.  
 FN 09-DEC-1999.  
 XX 28-MAY-1999; 99WO-JP002854.  
 XX 29-MAY-1998; 98JP-00166226.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Saitoh C, Yoshiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;  
 PI Ochiai K, Ando K, Katahira H;  
 XX WPI; 2000-062809/05.  
 DR Production of seasoning liquors with the flavor of vegetables pickled in

PT salted rice bran.  
 XX Disclosure; Page 41-43; 45pp; Japanese.  
 XX The invention relates to a method of producing seasoning liquors with the flavour of vegetables pickled in salted rice bran paste by culturing a microorganism in a rice bran dispersion to produce gamma-dodecalactone and/or gamma-dodecelactone. The microorganism produces lactic acid, propionic acid, gamma-dodecalactone and/or gamma-dodecelactone. The microorganism is especially a novel strain of *Corynebacterium* (strain NK-1, FERM BP-6329) with properties defined in the specification. This sequence represents the 16S rRNA gene from the novel *Corynebacterium* strain. The seasoning liquor is used for preparing a salted rice bran pickle bed which provides pickles

XX SQ Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;  
 Query Match 80.0%; Score 20; DB 3; Length 1460;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GCAAGTCGAACGGAAGGCC 20  
 |||||  
 Db 38 GCAAGTCGAACGGAAGGCC 57  
 |||||

RESULT 74  
 AEA22415  
 ID AEA22415 standard; DNA; 1462 BP.  
 XX AC AEA22415;  
 XX 25-AUG-2005 (first entry)  
 DT Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.  
 XX DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 KW Mycobacterium szulgai.  
 OS Mycobacterium szulgai.  
 XX US2005130168-A1.  
 FN 16-JUN-2005.  
 XX 31-OCT-2003; 2003US-00697802.  
 XX 31-OCT-2003; 2003US-00697802.  
 XX (HANK/) HAN X.  
 XX (PHAM/) PHAM A S.  
 XX Han X, Pham AS;  
 XX WPI; 2005-424597/43.  
 DR Determining a bacterium species comprises providing oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 PT Disclosure; SEQ ID NO 16; 74pp; English.  
 XX The invention relates to a method (M1) for determining a bacterium species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion, the primer set designed to provide a product having a predetermined size dictated by a complementary primer set; (d) amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any

CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium szulgai 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1462 BP; 314 A; 350 C; 507 G; 291 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 20; DB 14; Length 1462;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGAACGAAAGGCC 20  
 Db 20 GCAAGTCGAACGAAAGGCC 39  
 RESULT 75  
 ID AEA22414 standard; DNA; 1484 BP.  
 XX AEA22414;  
 AC  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 KW Mycobacterium simiae.  
 OS  
 XX US2005130168-A1.  
 PN 16-JUN-2005.  
 PD  
 XX 31-OCT-2003; 2003US-00697802.  
 PF 31-OCT-2003; 2003US-00697802.  
 PR (HANK/) HAN X.  
 XX (PHAM/) PHAM A S.  
 PA  
 XX Han X, Pham AS;  
 PI  
 XX WPI; 2005-424597/43.  
 DR  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 PS Disclosure; SEQ ID NO 15; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining

CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium simiae 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1484 BP; 320 A; 362 C; 509 G; 293 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 20; DB 14; Length 1484;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCAAGTCGAACGAAAGGCC 20  
 Db 20 GCAAGTCGAACGAAAGGCC 39  
 RESULT 76  
 ADM92517  
 ID ADM92517 standard; DNA; 1517 BP.  
 XX ADM92517;  
 AC  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Gordonia genus Actinomycetes DNA sequence SeqID1.  
 XX  
 DE Gordonia genus; Actinomycetes; ammonia; nitrous acid oxidation;  
 KW purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;  
 KW gold fish; ds.  
 XX  
 OS Gordonia.  
 XX  
 XX JP2004081109-A.  
 PN 18-MAR-2004.  
 PD  
 XX 27-AUG-2002; 2002JP-00247166.  
 PF 27-AUG-2002; 2002JP-00247166.  
 XX  
 PR (KANM-) KANMONKAI KK.  
 XX  
 XX WPI; 2004-233309/22.  
 DR  
 XX Gordonia genus Actinomycetes for purifying fresh water and seawater useful  
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia  
 PT utilizing ability and nitrous acid oxidation ability.  
 XX  
 PS Disclosure; SEQ ID NO 1; 16pp; Japanese.  
 XX  
 CC This invention relates to a novel Gordonia genus Actinomycetes which has  
 CC ammonia utilizing ability and nitrous acid oxidation ability. The  
 CC invention may be useful for purifying fresh water and seawater, of  
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The  
 CC Gordonia genus actinomycetes effectively suppresses concentration of  
 CC ammonia and nitrous acid in fresh water and seawater, and provides  
 CC purified water that is favourable for raising fishes.

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XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
Query Match      80.0%; Score 20; DB 12; Length 1517;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
Db 53 GCAAGTCGAACGGAAGGCC 72

RESULT 77
AD071823
ID AD071823 standard; DNA; 1517 BP.
XX AC
XX AD071823;
XX DT
XX 15-JUL-2004 (first entry)
XX DE DNA of RNA isolated from Gordonia sp. Kanmonkai-1129 SeqID 1.
XX KW astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;
XX KW ds.
XX OS Gordonia sp.
XX PN JP2004089015-A.
XX XX
XX PD 25-MAR-2004.
XX PF 29-AUG-2002; 2002JP-00251165.
XX XX
XX PR 29-AUG-2002; 2002JP-00251165.
XX XX
XX PA (KANM-) KANMONKAI KK.
XX XX
XX DR WPI; 2004-253025/24.
XX XX
XX PT Production of astaxanthin and canthaxanthine useful as fodder and feed
XX PT for livestock, domestic fowl and fish, involves cultivating Actinomyces
XX PT belonging to Gordonia genus.
XX PS Disclosure; SEQ ID NO 1; 13pp; Japanese.
XX XX
XX CC This invention relates to a novel method for producing astaxanthin and
XX CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces
XX CC microbial cells belonging to the Gordonia genus using a fresh water or
XX CC sea water mineral nutrition containing culture medium. The present
XX CC invention describes producing astaxanthin and canthaxanthine for use as a
XX CC fodder for livestock and domestic fowl, as well as a feed for fish
XX CC breeding. The production method uses natural products and is efficient at
XX CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated
XX CC from the Gordonia sp. Kanmonkai-1129 microorganism of the invention.
XX SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;
Query Match      80.0%; Score 20; DB 12; Length 1517;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
Db 53 GCAAGTCGAACGGAAGGCC 72

RESULT 78
AEA22407
ID AEA22407 standard; DNA; 1527 BP.
XX AC
XX AEA22407;
XX DT 25-AUG-2005 (first entry)
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XX DE Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.
XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX OS Mycobacterium heckeshornense.
XX XX
XX PN US2005130168-A1.
XX PD 16-JUN-2005.
XX XX
XX PF 31-OCT-2003; 2003US-00697802.
XX PR 31-OCT-2003; 2003US-00697802.
XX XX
XX PA (HANX/) HAN X.
XX PA (PHAM/) PHAM A S.
XX XX
XX PI Han X, Pham AS;
XX XX
XX DR WPI; 2005-424597/43.
XX PT
XX PT Determining a bacterium species comprises providing oligonucleotide
XX PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
XX PS Disclosure; SEQ ID NO 8; 74pp; English.
XX CC
XX CC The invention relates to a method (M1) for determining a bacterium
XX CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX CC extracting a genomic nucleotide from the bacterium to provide a
XX CC nucleotide template; (c) annealing a region of a nucleotide template to a
XX CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX CC complementary fashion, the primer set designed to provide a product
XX CC having a predetermined size dictated by a complementary primer set; (d)
XX CC amplifying the region of the nucleotide template to produce the product;
XX CC and (e) determining a species of a bacterium in a nucleotide sequence of
XX CC the product. Also described is an alternative method (M2) for determining
XX CC a bacterium species comprising: (a) providing a specimen or a sample
XX CC having a template; (b) providing a pair of primers selected from: (i) a
XX CC first forward primer having consecutive bases of an AFB-f comprising any
XX CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX CC or variations and a first reverse primer having consecutive bases of an
XX CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX CC or their fragments or variations, (iii) a second forward primer having
XX CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX CC bp (AEA22489-AEA22516) or their fragments or variations and a second
XX CC reverse primer having consecutive bases of an UB-r comprising any of the
XX CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX CC variations, or (iii) a first forward primer having consecutive bases of
XX CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX CC second reverse primer having consecutive bases of an UB-r of AEA22517-
XX CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX CC comparing the product from the specimen with a nucleotide sequence from a
XX CC database to determine the bacterium species present in the specimen. The
XX CC methods are useful for determining a bacterium species. The present
XX CC sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide
XX CC sequence, which is used in the exemplification of the present invention.
XX SQ Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;
Query Match      80.0%; Score 20; DB 14; Length 1527;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCC 20
Db 44 GCAAGTCGAACGGAAGGCC 63

RESULT 79
AAD11264
ID AAD11264 standard; DNA; 32 BP.
XX XX
```

```

AC AAD11264;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #8.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INNR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2001-398170/42.
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 35; 44pp; English.
XX
CC The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 4; Length 32;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 80
ADG88345
ID ADG88345 standard; DNA; 32 BP.
XX
AC ADG88345;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #14.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium sp.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX

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PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIA P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 14; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 32;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23

RESULT 81
AEA08220
ID AEA08220 standard; DNA; 32 BP.
XX
AC AEA08220;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium tuberculosis 16SrRNA amplifying PCR primer, SEQ ID NO: 14.
XX
KW Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium tuberculosis; ATCC 27294.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIA P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid

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PT amplification and detection of amplified products.

PS Example 1; SEQ ID NO 14; 21pp; English.

XX The present invention relates to a method of detecting Mycobacterium species present in a biological sample. The method involves using in CC vitro nucleic acid amplification and detection of amplified products. The CC invention is useful for diagnostic detection of pathogenic bacteria such CC as Mycobacterium species. The present sequence is the Mycobacterium CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16S rRNA) amplifying PCR CC primer.

XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 32;  
Best Local Similarity 91.3%; Pred. No. 17;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||

Db 1 GCAAGTCGAACGGAAGGTCTCT 23  
|||||

RESULT 82

AAAX99199  
ID AAX99199 standard; DNA; 50 BP.

AC AAX99199;

XX 28-SEP-1999 (first entry)

DE M. kansasii 16S rRNA gene fragment.

XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX Mycobacterium kansasii.

PN WO9935284-A1.

XX 15-JUL-1999.

PD 30-DEC-1997; 97WO-BR000087.

XX 30-DEC-1997; 97WO-BR000087.

XX (UWMI-) UNIV FEDERAL MINAS GERAIS.

XX Peregrino Ferreira PC, Geessien Kroon E;  
PI Bernardes Margutti Pinto ME, Aleixo AW;

XX WPI; 1999-444201/37.

XX Detection of mycobacteria by shift mobility assay.

XX Disclosure; Fig 7; 20pp; English.

XX The invention describes a new method for diagnosis, identification and CC characterisation of Mycobacterium tuberculosis or any other mycobacteria CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA) CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction, CC DNA amplification and shift mobility assay. The method is based on CC divergence in sequences found in 16S rRNA to identify mycobacteria CC species, since a remarkable shift of heteroduplex bands are obtained CC between single stranded and homoduplex bands in UPAGE. The method is CC fast, simple and can produce information not easily obtained when CC compared with other detection methods. The sensitivity of other assays CC suffer due to the tendency of the denatured PCR product strands to CC reassociate and exclude oligonucleotide probes, and steric interference CC between the bound oligonucleotides and the solid support which impede CC hybridization to nucleic acids in solution. Sequences AAX99193-237 CC represent 16S rRNA gene regions of some mycobacterial species

XX

SQ Sequence 50 BP; 14 A; 12 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 2; Length 50;  
Best Local Similarity 91.3%; Pred. No. 18;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||

Db 9 GCAAGTCGAACGGAAGGTCTCT 31  
|||||

RESULT 83

AAAX99194  
ID AAX99194 standard; DNA; 50 BP.

XX AAX99194;

XX 28-SEP-1999 (first entry)

DE M. bovis 16S rRNA gene fragment.

XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.

XX Mycobacterium bovis.

XX WO9935284-A1.

XX 15-JUL-1999.

XX 30-DEC-1997; 97WO-BR000087.

XX 30-DEC-1997; 97WO-BR000087.

XX (UWMI-) UNIV FEDERAL MINAS GERAIS.

XX Peregrino Ferreira PC, Geessien Kroon E;  
PI Bernardes Margutti Pinto ME, Aleixo AW;

XX WPI; 1999-444201/37.

XX Detection of mycobacteria by shift mobility assay.

XX Disclosure; Fig 7; 20pp; English.

XX The invention describes a new method for diagnosis, identification and CC characterisation of Mycobacterium tuberculosis or any other mycobacteria CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA) CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction, CC DNA amplification and shift mobility assay. The method is based on CC divergence in sequences found in 16S rRNA to identify mycobacteria CC species, since a remarkable shift of heteroduplex bands are obtained CC between single stranded and homoduplex bands in UPAGE. The method is CC fast, simple and can produce information not easily obtained when CC compared with other detection methods. The sensitivity of other assays CC suffer due to the tendency of the denatured PCR product strands to CC reassociate and exclude oligonucleotide probes, and steric interference CC between the bound oligonucleotides and the solid support which impede CC hybridization to nucleic acids in solution. Sequences AAX99193-237 CC represent 16S rRNA gene regions of some mycobacterial species

SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 2; Length 50;  
Best Local Similarity 91.3%; Pred. No. 18;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||

Db 9 GCAAGTCGAACGGAAGGTCTCT 31  
|||||

RESULT 84



```

AAX99193
ID AAX99193 standard; DNA; 50 BP.
XX
AC AAX99193;
XX
DT 28-SEP-1999 (first entry)
XX
DE M. tuberculosis 16S rRNA gene fragment.
XX
KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9935284-A1;
XX
PD 15-JUL-1999.
XX
PF 30-DEC-1997; 97WO-BR000087.
XX
PR 30-DEC-1997; 97WO-BR000087.
XX
PA (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
PI Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
DR WPI; 1999-444201/37.
XX
PT Detection of mycobacteria by shift mobility assay.
XX
PS Disclosure; Fig 7; 20pp; English.
XX
CC The invention describes a new method for diagnosis, identification and
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
CC DNA amplification and shift mobility assay. The method is based on
CC divergence in sequences found in 16S rRNA to identify mycobacteria
CC species, since a remarkable shift of heteroduplex bands are obtained
CC between single stranded and homoduplex bands in UPAGE. The method is
CC fast, simple and can produce information not easily obtained when
CC compared with other detection methods. The sensitivity of other assays
CC suffer due to the tendency of the denatured PCR product strands to
CC reassociate and exclude oligonucleotide probes, and steric interference
CC between the bound oligonucleotides and the solid support which impede
CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species
XX
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 2; Length 50;
Best Local Similarity 91.3%; Pred No. 18;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 9 GCAAGTCGAACGGAAGGCTCT 31
RESULT 85
ID ADF94055
ID ADF94055 standard; DNA; 50 BP.
XX
AC ADF94055;
XX
DT 11-MAR-2004 (first entry)
XX
DE Microorganism detection probe, SEQ ID 148.
XX
KW Probe; detection; identification; microorganism; food; drug;
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX

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OS Mycobacterium kansasii.
XX
PN WO2003106676-A1.
XX
PD 24-DEC-2003.
XX
PF 16-JUN-2003; 2003WO-JP007620.
XX
PR 14-JUN-2002; 2002JP-00174564.
XX
PA (HISF) HITACHI SOFTWARE ENG CO LTD.
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
PI Shimadzu M, Kobayashi I, Ishiko H;
XX
DR WPI; 2004-071565/07.
XX
PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
PT microorganism for specific detection and identification of the
PT microorganism in foods and drug compositions.
XX
PS Claim 2; SEQ ID NO 148; 150pp; Japanese.
XX
CC The present invention relates to probes (ADF93908-ADF94059) for the
CC specific detection and identification of harmful microorganisms in
CC samples of foods and drug compositions. The probe sequences are derived
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,
CC or its complementary sequence. Detection and identification of the
CC microorganism is by amplification of the complete 16S rRNA gene using
CC primers ADF94060 and ADF94061, labelling the amplification product (a
CC fluorescence label is preferred), and hybridising to the probe or probes
CC of the invention. The probes may be immobilised on a DNA chip. The
CC microorganism is selected from Actinobacillus actinomycetemcomitans,
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium
CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium
CC Gordonae.
XX
SQ Sequence 50 BP; 13 A; 11 C; 18 G; 8 T; 0 U; 0 Other;
Query Match 79.2%; Score 19.8; DB 12; Length 50;
Best Local Similarity 91.3%; Pred No. 18;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCTTT 23
Db 1 GCAAGTCGAACGGAAGGCTCT 23
RESULT 86
ID ADF94047
ID ADF94047 standard; DNA; 50 BP.
XX
AC ADF94047;
XX
DT 11-MAR-2004 (first entry)

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XX Microorganism detection probe, SEQ ID 140.  
DE Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
XX Mycobacterium tuberculosis.  
XX WO2003106676-A1.  
XX 24-DEC-2003.  
XX 16-JUN-2003; 2003WO-JP007620.  
XX 14-JUN-2002; 2002JP-00174564.  
XX (HISF ) HITACHI SOFTWARE ENG CO LTD.  
XX (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimadzu M, Kobayashi I, Ishiko H;  
XX WPI; 2004-071565/07.  
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.  
XX Claim 2; SEQ ID NO 140; 150pp; Japanese.  
PS The present invention relates to probes (ADF93908-ADF94059) for the  
CC specific detection and identification of harmful microorganisms in  
CC samples of foods and drug compositions. The probe sequences are derived  
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
CC or its complementary sequence. Detection and identification of the  
CC microorganism is by amplification of the complete 16S rRNA gene using  
CC primers ADF94060 and ADF94061, labelling the amplification product (a  
CC fluorescence label is preferred), and hybridising to the probe or probes  
CC of the invention. The probes may be immobilised on a DNA chip. The  
CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella  
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
CC Gordonae.  
XX SQ Sequence 50 BP; 13 A; 10 C; 18 G; 9 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 12; Length 50;  
Best Local Similarity 91.3%; Pred. No. 18;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 1 GCAAGTCGAACGGAAGGCCTCT 23  
|||||

RESULT 87

AAQ94742  
ID AAQ94742 standard; DNA; 203 BP.  
XX  
AC AAQ94742;  
XX  
DT 26-FEB-1996 (first entry)  
XX  
XX DNA fragment of 16S rRNA gene of M. tuberculosis.  
XX hybridisation; Mycobacteria; acid-fast; 16S rRNA; ribosomal RNA; probe;  
KW detection; identification; ss.  
XX Mycobacterium tuberculosis.  
XX  
FH Key Location/Qualifiers  
FT misc\_binding complement(1..20)  
FT FT /\*tag= a  
FT /\*note= "probe binding (see AAQ94743)"  
FT misc\_binding 41..60  
FT FT /\*tag= b  
FT /\*note= "probe binding (see AAQ94745)"  
FT misc\_binding 92..113  
FT FT /\*tag= c  
FT /\*note= "probe binding (see AAQ94746)"  
FT misc\_binding 183..203  
FT FT /\*tag= d  
FT /\*note= "probe binding (see AAQ94744)"  
XX  
PN JP07155200-A.  
XX  
PD 20-JUN-1995.  
XX  
PF 10-DEC-1993; 93JP-00310665.  
XX  
PR 10-DEC-1993; 93JP-00310665.  
XX (TOYM ) TOYOCO KK.  
XX  
XX WPI; 1995-250746/33.  
XX Novel oligo-nucleotide(s) which hybridise with the 16S rRNA gene of  
PT bacteria - used for detection and identification of acid-fast bacteria,  
PT eg. Mycobacterium.  
XX  
PS Claim 1; Page 10; 13pp; Japanese.  
XX  
CC AAQ94743-46 are oligonucleotides used for the detection and  
CC identification of acid-fast bacteria (pref. Mycobacterium) by hybridising  
CC with the base sequence of the 16S rRNA gene of the bacteria. The  
CC oligonucleotides can be represented by all or a part of the 203 base  
CC sequence shown here. Mycobacteria are gram-positive bacteria which grow  
CC very slowly and require a lot of time for culture for detection (longer  
CC than one month). The probes provide a simple, rapid and exact method for  
CC detection and identification of the bacteria. The method can be applied  
CC directly to sputum or blood samples and the result obtd. within one day.  
CC AAQ94747-60 are specific probes for different Mycobacteria species  
XX  
SQ Sequence 203 BP; 44 A; 42 C; 72 G; 45 T; 0 U; 0 Other;  
Query Match 79.2%; Score 19.8; DB 2; Length 203;  
Best Local Similarity 91.3%; Pred. No. 21;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 5 GCAAGTCGAACGGAAGGCCTCT 27  
|||||  
RESULT 88  
AEB98764  
ID AEB98764 standard; DNA; 209 BP.  
XX  
AC AEB98764;

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XX 06-OCT-2005 (first entry)
XX Mycobacterium kansasii partial 16S rDNA sequence, SEQ ID 6.
XX microorganism detection; mycobacterium infection; antibacterial; ds.
XX Mycobacterium kansasii.
XX JP2005204582-A.
XX 04-AUG-2005.
XX 23-JAN-2004; 2004JP-00015195.
XX 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
XX Oda N;
XX WPI; 2005-526965/54.
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX Example 1; SEQ ID NO 6; 14pp; Japanese.
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This polynucleotide represents a Mycobacterium
XX kansasii partial 16S rDNA sequence amplified by the LAMP method of the
XX invention.
XX Sequence 209 BP; 47 A; 49 C; 72 G; 41 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 14; Length 209;
XX Best Local Similarity 91.3%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCTTT 23
Db 39 GCAAGTCGAACGGAAGGCTCT 61
RESULT 89
AEB98761
ID AEB98761 standard; DNA; 211 BP.
XX AC AEB98761;
XX 06-OCT-2005 (first entry)
XX Mycobacterium tuberculosis partial 16S rDNA sequence, SEQ ID 3.
XX microorganism detection; mycobacterium infection; antibacterial; ds.
XX Mycobacterium tuberculosis.
XX JP2005204582-A.
XX 04-AUG-2005.
XX 23-JAN-2004; 2004JP-00015195.
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This polynucleotide represents a Mycobacterium
XX kansasii partial 16S rDNA sequence amplified by the LAMP method of the
XX invention.
XX Sequence 209 BP; 47 A; 49 C; 72 G; 41 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 14; Length 209;
XX Best Local Similarity 91.3%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCTTT 23
Db 39 GCAAGTCGAACGGAAGGCTCT 61

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PR 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
XX Oda N;
XX WPI; 2005-526965/54.
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX Example 1; SEQ ID NO 3; 14pp; Japanese.
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This polynucleotide represents a Mycobacterium
XX tuberculosis partial 16S rDNA sequence amplified by the LAMP method of
XX the invention.
XX Sequence 211 BP; 48 A; 45 C; 74 G; 44 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 14; Length 211;
XX Best Local Similarity 91.3%; Pred. No. 21;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GCAAGTCGAACGGAAGGCTTT 23
Db 39 GCAAGTCGAACGGAAGGCTCT 61
RESULT 90
ADV99481
ID ADV99481 standard; DNA; 349 BP.
XX AC ADV99481;
XX 24-FEB-2005 (first entry)
XX Meningitis causing bacteria DNA fragment #9.
XX ds; antibacterial; antiinflammatory; inflammation; neurological disease;
XX diagnosis; meningitis; biochip.
XX Mycobacterium tuberculosis.
XX CNI420123-A.
XX 28-MAY-2003.
XX 16-NOV-2001; 2001CN-00137478.
XX 16-NOV-2001; 2001CN-00137478.
XX (JING-) JINGQI BIO CHEM SCI & TECH CO LTD.
XX Xu B, Jiang Y, Huang X;
XX WPI; 2004-044307/05.
XX A nucleic acid sequence useful for diagnosing pathogenic bacteria for
XX meningitides.
XX Disclosure; Page 18; 24pp; Chinese.
XX The invention relates to a nucleic acid sequence group for quickly

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CC diagnosing 20 kinds of pathogenic bacteria for meningitis. Its method  
CC includes comparing the DNA sequences of different pathogenic bacteria,  
CC choosing special fragments, finding out common primer, designing 3  
CC specific probe fragments for each pathogenic bacterium, dotting them on  
CC high-molecular polymer to obtain chip, sampling the DNA of pathogenic  
CC bacterium of patient, labeling, amplification, and reacting with said  
CC chip for visually recognizing the pathogenic bacterium. Its advantages are  
CC high speed and low cost. The present sequence represents a meningitis  
CC causing bacteria DNA fragment.

XX SQ Sequence 349 BP; 75 A; 82 C; 125 G; 67 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 13; Length 349;  
Best Local Similarity 91.3%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 52 GCAAGTCGAACGGAAGGCTCT 74

RESULT 91

AAV24293  
ID AAV24293 standard; DNA; 1271 BP.

XX AC AAV24293;

XX DT 14-SEP-1998 (first entry)

XX DE Mycobacterium tuberculosis 16S ribosomal RNA gene.

XX KW Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;  
XX KW ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic fibrosis;  
XX KW tuberculosis; ss.

XX OS Mycobacterium tuberculosis.

XX PN WO9814567-A2.

XX PD 09-APR-1998.

XX PF 30-SEP-1997; 97WO-US018094.

XX PR 01-OCT-1996; 96US-0027729P.

XX PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

XX PI Martin WJ, Wisniewski P;

XX DR WPI; 1998-240079/21.

XX PT Use of oligo:nucleotide(s) corresponding to bacterial 16S rRNA - for  
XX PT inhibiting bacterial protein expression and treating bacterial infection.

XX PS Claim 26; Page 60-61; 73pp; English.

XX CC This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of  
XX CC Mycobacterium tuberculosis. The invention relates to methods and  
XX CC compositions for the treatment of Gram-negative bacterial infections  
XX CC employing novel oligonucleotides as antimicrobial agents. The  
XX CC oligonucleotides are targeted to the Shine-Dalgarno (SD) region of  
XX CC prokaryotes to inhibit bacterial expression and hence inhibit bacterial  
XX CC infection. They preferably comprise 10-35 consecutive bases of the 3' end  
XX CC of a bacterial 16S rRNA (see also AAV24291-95). An oligonucleotide may  
XX CC also include a transport moiety and may have DNA phosphate modifications  
XX CC to increase nuclease resistance, or may be formulated in a liposome. A  
XX CC claimed method for treating a bacterial infection of a patient comprises  
XX CC administering a liposomal formulation of such an oligonucleotide. The  
XX CC oligonucleotides can be used particularly for treating bacterial  
XX CC infections in pulmonary diseases such as cystic fibrosis or tuberculosis.  
XX CC Since the SD sequence is not present in eukaryotic cells, the  
XX CC oligonucleotides provide a pathogen-specific therapeutic method

SQ Sequence 1271 BP; 260 A; 281 C; 430 G; 300 T; 0 U; 0 Other;  
Query Match 79.2%; Score 19.8; DB 2; Length 1271;  
Best Local Similarity 91.3%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 442 GCAAGTCGAACGGAAGGCTCT 464

RESULT 92

AEA22416  
ID AEA22416 standard; DNA; 1416 BP.

XX AC AEA22416;

XX DT 25-AUG-2005 (first entry)

XX DE Mycobacterium tuberculosis 16S rRNA sequence SEQ ID NO:17.

XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX OS Mycobacterium tuberculosis.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

XX PF 31-OCT-2003; 2003US-00697802.

XX PR 31-OCT-2003; 2003US-00697802.

XX PA (HANX/) HAN X.

XX PA (PHAM/) PHAM A S.

XX PI Han X, Pham AS;

XX DR WPI; 2005-424597/43.

XX PT Determining a bacterium species comprises providing oligonucleotide  
XX PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX PS Disclosure; SEQ ID NO 17; 74pp; English.

XX CC The invention relates to a method (M1) for determining a bacterium  
XX CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
XX CC extracting a genomic nucleotide from the bacterium to provide a  
XX CC nucleotide template; (c) annealing a region of a nucleotide template to a  
XX CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
XX CC complimentary fashion, the primer set designed to provide a product  
XX CC having a predetermined size dictated by a complementary primer set; (d)  
XX CC amplifying the region of the nucleotide template to produce the product; and  
XX CC (e) determining a species of a bacterium in a nucleotide sequence of  
XX CC the product. Also described is an alternative method (M2) for determining  
XX CC a bacterium species comprising: (a) providing a specimen or a sample  
XX CC having a template; (b) providing a pair of primers selected from: (i) a  
XX CC first forward primer having consecutive bases of an AFB-f comprising any  
XX CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
XX CC or variations and a first reverse primer having consecutive bases of an  
XX CC AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
XX CC or their fragments or variations, (ii) a second forward primer having  
XX CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
XX CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
XX CC reverse primer having consecutive bases of an UB-r comprising any of the  
XX CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
XX CC variations, or (iii) a first forward primer having consecutive bases of  
XX CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
XX CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
XX CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
XX CC comparing the product from the specimen with a nucleotide sequence from a  
XX CC database to determine the bacterium species present in the specimen. The  
XX CC methods are useful for determining a bacterium species. The present

CC sequence represents a Mycobacterium tuberculosis 16S rRNA nucleotide  
CC sequence, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 1416 BP; 309 A; 341 C; 481 G; 285 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 1416;  
Best Local Similarity 91.3%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTT 23  
|||||  
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 93  
AEA22402

ID AEA22402 standard; DNA; 1421 BP.

XX  
AC AEA22402;

XX 25-AUG-2005 (first entry)

XX Mycobacterium bovis 16S rRNA sequence SEQ ID NO:3.

XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX Mycobacterium bovis.

XX OS

XX Mycobacterium bovis.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HAXX/) HAN X.

XX (PHAM/) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide  
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX Disclosure; SEQ ID NO 3; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium  
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
XX extracting a genomic nucleotide from the bacterium to provide a  
XX nucleotide template; (c) annealing a region of a nucleotide template to a  
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
XX complimentary fashion, the primer set designed to provide a product  
XX having a predetermined size dictated by a complementary primer set; (d)  
XX amplifying the region of the nucleotide template to produce the product;  
XX and (e) determining a species of a bacterium in a nucleotide sequence of  
XX the product. Also described is an alternative method (M2) for determining  
XX a bacterium species comprising: (a) providing a specimen or a sample  
XX having a template; (b) providing a pair of primers selected from: (i) a  
XX first forward primer having consecutive bases of an AFB-f comprising any  
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
XX or variations and a first reverse primer having consecutive bases of an  
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
XX or their fragments or variations, (ii) a second forward primer having  
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
XX bp (AEA22489-AEA22516) or their fragments or variations and a second  
XX reverse primer having consecutive bases of an UB-r comprising any of the  
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
XX variations, or (iii) a first forward primer having consecutive bases of  
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
XX second reverse primer having consecutive bases of an UB-r of AEA22517-  
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)

CC comparing the product from the specimen with a nucleotide sequence from a  
CC database to determine the bacterium species present in the specimen. The  
CC methods are useful for determining a bacterium species. The present  
CC sequence represents a Mycobacterium bovis 16S rRNA nucleotide sequence,  
CC which is used in the exemplification of the present invention.

XX  
SQ Sequence 1421 BP; 310 A; 341 C; 484 G; 286 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 1421;  
Best Local Similarity 91.3%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTT 23  
|||||  
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 94

AEA22409

ID AEA22409 standard; DNA; 1463 BP.

XX  
AC AEA22409;

XX 25-AUG-2005 (first entry)

XX Mycobacterium kansasii 16S rRNA sequence SEQ ID NO:10.

XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX Mycobacterium kansasii.

XX OS

XX Mycobacterium kansasii.

XX PN US2005130168-A1.

XX PD 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HAXX/) HAN X.

XX (PHAM/) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide  
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.

XX Disclosure; SEQ ID NO 10; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium  
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
XX extracting a genomic nucleotide from the bacterium to provide a  
XX nucleotide template; (c) annealing a region of a nucleotide template to a  
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
XX complimentary fashion, the primer set designed to provide a product  
XX having a predetermined size dictated by a complementary primer set; (d)  
XX amplifying the region of the nucleotide template to produce the product;  
XX and (e) determining a species of a bacterium in a nucleotide sequence of  
XX the product. Also described is an alternative method (M2) for determining  
XX a bacterium species comprising: (a) providing a specimen or a sample  
XX having a template; (b) providing a pair of primers selected from: (i) a  
XX first forward primer having consecutive bases of an AFB-f comprising any  
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
XX or variations and a first reverse primer having consecutive bases of an  
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
XX or their fragments or variations, (ii) a second forward primer having  
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
XX bp (AEA22489-AEA22516) or their fragments or variations and a second  
XX reverse primer having consecutive bases of an UB-r comprising any of the  
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
XX variations, or (iii) a first forward primer having consecutive bases of  
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
XX second reverse primer having consecutive bases of an UB-r of AEA22517-  
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA23517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium kansasii 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 XX Sequence 1463 BP; 318 A; 354 C; 500 G; 291 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 14; Length 1463;  
 Best Local Similarity 91.3%; Pred. No. 26;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 Db 19 GCAAGTCGAACGGAAGGTCCT 41

RESULT 95  
 AAZ35571  
 ID AAZ35571 standard; DNA; 1464 BP.

AC AAZ35571;

DT 28-JAN-2000 (first entry)

DE Mycobacterium tuberculosis 16S rRNA gene.

KW 16S rRNA gene; oligonucleotide primer; amplify; genus specific;  
 diagnosis; Mycobacterium; ss.

OS Mycobacterium tuberculosis.

PN US985569-A.

PD 16-NOV-1999.

PF 26-SEP-1997; 97US-00938858.

PR 26-SEP-1997; 97US-00938858.

PA (BECT ) BECTON DICKINSON & CO.

PI Foxall PA, Kumar H;

XX WPI; 2000-012779/01.

XX Oligonucleotide primers useful for detecting microorganisms of the genus  
 PT Mycobacterium.

PS Example; Fig 3; 2lpp; English.

CC This sequence is the Mycobacterium tuberculosis 16S rRNA gene. This  
 CC sequence is used in an example of a method using oligonucleotide primers  
 CC for amplification of a genus specific sequence of the 16S rRNA gene. The  
 CC method of the invention consists of using primers AAZ35572-235586 to  
 CC amplify M. tuberculosis DNA and then detecting the amplified nucleic  
 CC acids. The oligonucleotides are useful for the detection of species of  
 CC medical interest of the genus Mycobacterium. In particular the detection  
 CC can be used for human and veterinary diagnosis from samples of biological  
 CC fluids or tissue e.g. sputum, bronchial washings, gastric washings,  
 CC blood, milk, lymph, skin and soft tissues. Identifying the mycobacterium  
 CC using the nucleic acid based diagnostic assay reduces the time required  
 CC for an accurate diagnosis as cultivation of the organisms is not required  
 XX

XX Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 3; Length 1464;  
 Best Local Similarity 91.3%; Pred. No. 26;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 96

AAZ11027  
 ID AAS11027 standard; DNA; 1464 BP.

XX AAS11027;

AC AAS11027;

DT 24-OCT-2001 (first entry)

DE Mycobacterium tuberculosis 16S ribosomal RNA gene.

XX Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human;

KW food grain supplement; livestock; poultry; therapeutic; ds.

OS Mycobacterium tuberculosis.

PN WO200142457-A2.

PD 14-JUN-2001.

PF 29-NOV-2000; 2000WO-US042391.

PR 29-NOV-1999; 99US-0168150P.

XX (AVIB-) AVI BIOPHARMA INC.

PI Iversen PL;

XX WPI; 2001-457295/49.

XX Antibacterial compound, useful for treating bacterial infections and as  
 PT livestock and poultry food supplement, comprises antisense  
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.

PS Disclosure; Page; 62pp; English.

XX AAS11021-AAS11034 represent the coding sequences of bacterial 16S  
 CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-  
 CC bacterial compounds comprising substantially uncharged antisense  
 CC oligomers containing 8-40 nucleotide subunits, including a targeting  
 CC nucleic acid sequence at least 10 nucleotides in length which is  
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The  
 CC antisense oligomers are used for treating a bacterial infection in a  
 CC human or a mammalian animal produced by Escherichia coli, Salmonella  
 CC typhimurium, Pseudomonas aeruginosa, Vibrio cholera, Neisseria  
 CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus  
 CC influenza, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium  
 CC tuberculosis, Streptococcus pneumoniae, Treponema pallidum and Chlamydia  
 CC trachomatis. The antibacterial compound may be used as a food grain  
 CC supplement in livestock and poultry food composition. Note: The present  
 CC sequence is not shown in the specification but has been accessed from  
 CC GenBank using the appropriate accession number given in the specification

XX Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 5; Length 1464;  
 Best Local Similarity 91.3%; Pred. No. 26;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 97

ADR90574  
 ID ADR90574 standard; DNA; 1469 BP.

XX ADR90574;

```
XX 02-DEC-2004 (first entry)
XX M kansasii 16S rRNA gene sequence SeqID3.
XX acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;
XX taxonomic-tree analysis; atypical-mycobacteria; gene; ds.
XX Mycobacterium kansasii.
XX JP2004254591-A.
XX 16-SEP-2004.
XX 26-FEB-2003; 2003JP-00048654.
XX 26-FEB-2003; 2003JP-00048654.
XX (M1TP ) MITSUBISHI YUKA BCL KK.
XX WPI; 2004-664464/65.
XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex,
XX useful for detecting mutant of M.avium complex, and for grouping strains
XX of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
XX bacterium.
XX Claim 3; SEQ ID NO 3; 23pp; Japanese.
XX This invention relates to a novel method of differentiating acid-fast
XX bacterium, which involves detecting a mutation in the 16S rRNA gene of
XX the acid-fast bacterium. The method is useful for differentiating acid-
XX fast bacterium such as M avium complex (MAC) or M kansasii, in particular
XX for detecting mutants of MAC, and for grouping strains of M kansasii. The
XX method is also useful for carrying out taxonomic-tree analysis of
XX atypical-mycobacteria and enables detection of MAC accurately and
XX reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
XX which may be used in the method of the invention.
XX Sequence 1469 BP; 321 A; 355 C; 502 G; 291 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 13; Length 1469;
XX Best Local Similarity 91.3%; Pred. No. 26;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GCAAGTCGAACGGAAGGCTTT 23
DB 30 GCAAGTCGAACGGAAGGCTCT 52
RESULT 98
AAS30719
ID AAS30719 standard; DNA; 1524 BP.
XX AC AAS30719;
XX 04-DEC-2001 (first entry)
XX Mycobacterium tuberculosis 16S ribosomal gene partial sequence.
XX Mycobacterium; species-specific bacterial identification;
XX 16S ribosomal gene; ds.
XX Mycobacterium tuberculosis.
XX WO200166797-A2.
XX 13-SEP-2001.
XX 01-MAR-2001; 2001WO-US006731.
XX 03-MAR-2000; 2000US-0186840P.
XX
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PA (BECI ) BECKMAN COULTER INC.
PA PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX (USSH ) US NAT INST OF HEALTH.
XX Fischer SH, Rampal JB, Fahle GA, Conville PS;
XX WPI; 2001-514847/56.
XX Species-specific bacterial identification, used particularly to identify
XX Mycobacterium species, involves hybridizing bacterial genus-selective or
XX specific primers to a sample.
XX Example 2; Page 42-43; 43pp; English.
XX The invention relates to a method of species-specific bacterial
XX identification, comprising hybridising a bacterial genus-selective or
XX specific primer to a sample and amplifying nucleic acids. This is
XX followed by hybridising the amplified nucleic acid to a solid phase array
XX comprising bacterial species specific probe oligonucleotides chemically
XX linked to a polymeric support in a predetermined pattern. This method is
XX used for species-specific identification of a bacterium, particularly a
XX Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.
XX tuberculosis, M. marinum, or M. kansasii. The method provides rapid
XX identification of multiple species of Mycobacterium. AAS30686-AAS30720
XX represent Mycobacterium species-specific primers and probes used in the
XX method of the invention. The present sequence may be used in the
XX invention as a target sequence for amplification
XX Sequence 1524 BP; 333 A; 365 C; 520 G; 306 T; 0 U; 0 Other;
XX Query Match 79.2%; Score 19.8; DB 4; Length 1524;
XX Best Local Similarity 91.3%; Pred. No. 26;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 GCAAGTCGAACGGAAGGCTTT 23
DB 50 GCAAGTCGAACGGAAGGCTCT 72
RESULT 99
ADB61681
ID ADB61681 standard; DNA; 1536 BP.
XX AC ADB61681;
XX 04-DEC-2003 (first entry)
XX 16S rRNA of Mycobacterium tuberculosis DNA sequence.
XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;
XX poly-A tail; mRNA purification; oligo-dt capture;
XX prokaryote mRNA purification; bridging oligonucleotide; targeting region;
XX capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;
XX eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;
XX 28S eukaryotic rRNA bridging oligonucleotide; ds.
XX Mycobacterium tuberculosis.
XX WO2003054162-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US041014.
XX 20-DEC-2001; 2001US-00029397.
XX (AMBI-) AMBION INC.
XX Murphy GL, Whitley JP;
XX WPI; 2003-663255/62.
XX Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a
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PT bridging oligonucleotide comprising bridging region and a targeting  
PT region complementary to a targeted nucleic acid, and a capture  
XX oligonucleotide.  
XX  
XX Claim 4; Page 168-169; 208pp; English.  
XX  
CC This invention relates to a novel method for isolating, depleting or  
CC separating a targeted nucleic acid, such as rRNA, from a sample  
CC comprising targeted and non-targeted nucleic acids. It effects a way of  
CC enriching for non-targeted nucleic acids such as mRNAs. Isolating  
CC sufficient quantities of high quality bacterial mRNA is a demanding  
CC process which impedes analysis of bacterial gene expression in the  
CC presence of host cells. A small percentage of bacterial mRNAs may be poly  
CC -A tailed, but these are targeted for degradation and tend to be  
CC unstable. As a result, the commonly employed method for mRNA purification  
CC with eukaryotic cells, oligo-dT capture, is ineffective. The present  
CC invention provides an alternative, more suitable method for mRNA  
CC purification from prokaryotes. The method of the invention comprises the  
CC incubation of a sample with a bridging oligonucleotide (containing a  
CC targeting region) and subsequently incubating with a capture  
CC oligonucleotide allowing the isolation of the target from the sample. The  
CC method is useful for depleting or isolating targeted nucleic acid, for  
CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S  
CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may  
CC comprise any one of 64 fully defined sequences as given in the  
CC specification. The present sequence is that of a DNA sequence which  
CC represents the sequence of 16S rRNA of Mycobacterium tuberculosis related  
CC to the invention.  
XX  
XX Sequence 1536 BP; 333 A; 366 C; 523 G; 314 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 1536;  
Best Local Similarity 91.3%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAAGGCCTTT 23  
|||||  
Db 59 GCAAGTCGAACGGAAAGGCTCT 81

## RESULT 100

ADB61682  
ID ADB61682 standard; DNA; 1536 BP.  
XX  
XX  
AC ADB61682;  
XX  
XX 04-DEC-2003 (first entry)  
XX  
DE 16S rRNA of Escherichia coli DNA sequence.  
XX  
KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;  
KW poly-A tail; mRNA purification; oligo-dT capture;  
KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;  
KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;  
KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;  
KW 28S eukaryotic rRNA bridging oligonucleotide; ds.  
XX  
OS Escherichia coli.  
XX  
XX WO2003054162-A2.  
XX  
XX 03-JUL-2003.  
XX  
FF 19-DEC-2002; 2002WO-US041014.  
XX  
XX 20-DEC-2001; 2001US-00029397.  
XX  
XX (AMBI-) AMBION INC.  
XX  
XX Murphy GL, Whitley JP;  
XX  
XX WPI; 2003-663255/62.  
XX

PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a  
PT bridging oligonucleotide comprising bridging region and a targeting  
PT region complementary to a targeted nucleic acid, and a capture  
XX oligonucleotide.

PS Claim 4; Page 169; 208pp; English.

XX This invention relates to a novel method for isolating, depleting or  
XX separating a targeted nucleic acid, such as rRNA, from a sample  
XX comprising targeted and non-targeted nucleic acids. It effects a way of  
XX enriching for non-targeted nucleic acids such as mRNAs. Isolating  
XX sufficient quantities of high quality bacterial mRNA is a demanding  
XX process which impedes analysis of bacterial gene expression in the  
XX presence of host cells. A small percentage of bacterial mRNAs may be poly  
XX -A tailed, but these are targeted for degradation and tend to be  
XX unstable. As a result, the commonly employed method for mRNA purification  
XX with eukaryotic cells, oligo-dT capture, is ineffective. The present  
XX invention provides an alternative, more suitable method for mRNA  
XX purification from prokaryotes. The method of the invention comprises the  
XX incubation of a sample with a bridging oligonucleotide (containing a  
XX targeting region) and subsequently incubating with a capture  
XX oligonucleotide allowing the isolation of the target from the sample. The  
XX method is useful for depleting or isolating targeted nucleic acid, for  
XX example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S  
XX or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may  
XX comprise any one of 64 fully defined sequences as given in the  
XX specification. The present sequence is that of a DNA sequence which  
XX represents the sequence of 16S rRNA of Escherichia coli related to the  
XX invention.

SQ Sequence 1536 BP; 333 A; 366 C; 523 G; 314 T; 0 U; 0 Other;

Query Match 79.2%; Score 19.8; DB 10; Length 1536;  
Best Local Similarity 91.3%; Pred. No. 26;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAAGGCCTTT 23  
|||||  
Db 59 GCAAGTCGAACGGAAAGGCTCT 81

Search completed: May 19, 2006, 04:18:54  
Job time : 304.729 secs



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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1671.99 Seconds  
(without alignments)  
836.120 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacggaaggcttcg 25

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_hnc:\*

7: gb\_est2:\*

8: gb\_est7:\*

9: gb\_est8:\*

10: gb\_est9:\*

11: gb\_gss1:\*

12: gb\_gss2:\*

13: gb\_gss3:\*

14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.8	87.2	657	8	CN208729 Tor9226 G
2	20.8	83.2	356	4	CD122074 ME1-0071G
3	20.2	80.8	312	7	BB241896 BB241896
4	20.2	80.8	683	14	DUB18647 OG_ABA009
5	20.0	80.0	650	8	CN204419 Tor7810 G
6	20.0	80.0	874	8	CN365133 RTK1_23 G
7	20.0	80.0	885	8	CN201712 Tor1780 G
8	19.2	76.8	452	11	AQ627316 CITBI-E1-
9	19.2	76.8	540	11	AQ549361 RPCI-11-3
10	18.8	75.2	903	12	CC453191 ZMMBC034
11	18.8	75.2	910	9	DN561788 92178421
12	18.6	74.4	399	3	BQ104075 991205.e
13	18.6	74.4	513	4	CA282280 SCAGSD204
14	18.6	74.4	526	2	BM131991 TGEStzyb0
15	18.6	74.4	806	2	BI157204 602923403
16	18.4	73.6	591	8	CN207299 Tor7720 G
17	18.4	73.6	735	5	CF882404 trico86xm
18	18.4	73.6	788	4	CB908942 trico86xm
19	18.4	73.6	817	8	CN207539 Tor7952 G

18.4	73.6	907	10	DR421359	CHHS5E05
18.2	72.8	327	10	DY091901	010128BEM
18.2	72.8	421	4	BY457153	BY457153
18.2	72.8	475	9	DN526979	1271790 M
18.2	72.8	609	4	CA934753	MTUSTS.P2
18.2	72.8	630	4	CB378019	rq08a11.y
18.2	72.8	719	5	CK950118	4075090 B
18.2	72.8	835	9	DN283722	1183944 M
18.2	72.8	835	14	CR077081	Reverse s
18.2	72.8	843	9	DN282351	1182408 M
18.2	72.8	906	14	DY746898	ASNC3551.
18.2	72.8	929	14	CNS06FX8	ALJ39578 T3 end of
18.2	72.8	943	10	DM640758	CLJ372-G0
18.2	72.8	994	14	CNS06CEP	ALJ392423 T3 end of
18.2	72.8	1043	14	DY760208	ASNG3054.
18.2	72.8	1052	6	DQ213078	Taeniopyg
18.2	72.8	1242	13	CL645653	CH213-99C
18.2	72.0	938	7	BF537535	602053182
18.2	72.0	994	4	BX342644	BX342644
17.8	71.2	223	10	W10183	W10183 ma43f03.r1
17.8	71.2	273	1	AA815626	AA815626 vt03c06.r
17.8	71.2	337	2	BG147420	mac03g07.
17.8	71.2	347	4	CB705072	AMGNNUC.S
17.8	71.2	357	10	W65078	me01d06.r1
17.8	71.2	384	5	CF425395	lad5e03.
17.8	71.2	400	1	ALJ36386	ALJ36386
17.8	71.2	419	1	AI050353	UB29F09.r
17.8	71.2	420	1	AI713707	UI-R-AGI-
17.8	71.2	424	1	AA818546	UI-R-A0-a
17.8	71.2	444	3	BU743860	mai49f01.
17.8	71.2	446	10	W47680	mc89h02.r1
17.8	71.2	473	1	AI593186	vt03c06.y
17.8	71.2	492	8	CN692701	E0326F01-
17.8	71.2	500	1	AA014214	mh18g10.r
17.8	71.2	502	1	AA509546	vh50C08.r
17.8	71.2	502	12	CG036380	PULV37TD
17.8	71.2	527	7	BE863637	UI-N-BHO-
17.8	71.2	532	3	BQ569727	gill35c11.
17.8	71.2	542	7	BF022607	uy51d11.y
17.8	71.2	543	1	AI603423	UI-R-ACI-
17.8	71.2	566	11	AZ024985	RPCI-23-3
17.8	71.2	571	8	CN692527	E0324C02-
17.8	71.2	577	9	BE288370	601094841
17.8	71.2	600	9	DN215604	MEST971.D
17.8	71.2	602	10	DR968997	ZM_BFB009
17.8	71.2	613	7	AW914801	EST346105
17.8	71.2	622	2	BI648126	603278444
17.8	71.2	635	9	CA734384	jbo1e11.y
17.8	71.2	641	2	BI331633	602983168
17.8	71.2	641	5	CF897511	A0226B05-
17.8	71.2	643	10	DV169729	ZM_BFB016
17.8	71.2	647	7	BF237353	602025026
17.8	71.2	651	5	CF898433	A0239B05-
17.8	71.2	651	5	CF898433	ZM_BFB014
17.8	71.2	680	10	DV023955	ZM_BFB012
17.8	71.2	682	8	CN525338	UI-N-HKO-
17.8	71.2	685	10	DT945027	ZM_BFB013
17.8	71.2	695	8	CO429338	UI-N-HWO-
17.8	71.2	700	2	BI649774	603279966
17.8	71.2	710	10	DV541234	ZM_BFB023
17.8	71.2	711	10	DT654257	ZM_BFB012
17.8	71.2	714	10	DT945215	ZM_BFB013
17.8	71.2	716	7	BF099995	601752156
17.8	71.2	729	3	BQ445033	UI-N-ERO-
17.8	71.2	738	8	CO383984	AGENCOURT
17.8	71.2	739	2	BI414831	602990771
17.8	71.2	740	4	EX855983	EX855983
17.8	71.2	745	4	BY732037	BY732037
17.8	71.2	746	10	DV942547	1000137-E
17.8	71.2	752	10	DR794419	ZM_BFB001
17.8	71.2	753	10	DV164476	ZM_BFB016
17.8	71.2	777	10	DR786717	ZM_BFB000
17.8	71.2	777	10	DR954333	ZM_BFB004
17.8	71.2	780	10	DV164117	ZM_BFB016

93	17.8	71.2	808	4	CB953248	CB953248	AGENCYCOURT	166	17.6	70.4	410	2	BI275046	BI275046	UI-R-CX0-
94	17.8	71.2	816	10	DR794420	DR794420	ZM_BFB001	167	17.6	70.4	410	4	BY435007	BY435007	BY435007
95	17.8	71.2	820	10	DV164477	DV164477	ZM_BFB016	168	17.6	70.4	410	5	CJ210358	CJ210358	CJ210358
96	17.8	71.2	824	10	DY361640	DY361640	ZO_EG000	169	17.6	70.4	414	4	BY458657	BY458657	BY458657
97	17.8	71.2	827	10	DR786718	DR786718	ZM_BFB000	170	17.6	70.4	416	3	BQ748621	BQ748621	UI-M-FA0-
98	17.8	71.2	848	10	DR966931	DR966931	ZM_BFB008	171	17.6	70.4	417	5	CJ210067	CJ210067	CJ210067
99	17.8	71.2	851	10	DT876921	DT876921	AGENCYCOURT	172	17.6	70.4	421	1	AA655960	AA655960	VS49F08.r
100	17.8	71.2	856	2	BI664538	BI664538	603290164	173	17.6	70.4	422	1	AI043633	AI043633	UI-R-CO-j
101	17.8	71.2	862	5	CF551692	CF551692	AGENCYCOURT	174	17.6	70.4	425	5	CJ317470	CJ317470	CJ317470
102	17.8	71.2	874	3	BU522312	BU522312	AGENCYCOURT	175	17.6	70.4	426	1	AV011735	AV011735	AV011735
103	17.8	71.2	891	10	DT942318	DT942318	ZM_BFB012	176	17.6	70.4	434	5	CJ228806	CJ228806	CJ228806
104	17.8	71.2	894	7	BE367787	BE367787	601217408	177	17.6	70.4	435	3	BU961211	BU961211	AGENCYCOURT
105	17.8	71.2	906	3	BO944677	BO944677	AGENCYCOURT	178	17.6	70.4	443	4	BY452887	BY452887	BY452887
106	17.8	71.2	912	10	DR815819	DR815819	ZM_BFB004	179	17.6	70.4	444	4	BY432547	BY432547	BY432547
107	17.8	71.2	918	2	BG247267	BG247267	602360162	180	17.6	70.4	447	4	CA563760	CA563760	K0317F10-
108	17.8	71.2	945	10	DV062398	DV062398	NEONATAL	181	17.6	70.4	452	8	CR470938	CR470938	CR470938
109	17.8	71.2	995	12	CL029182	CL029182	CH216-28J	182	17.6	70.4	462	4	BY559571	BY559571	BY559571
C	110	17.8	71.2	1199	9	DR045951	FP-11_G06	183	17.6	70.4	465	1	AI235898	AI235898	EST232460
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113	17.6	70.4	233	3	BQ322138	BQ322138	PM3-CT081	186	17.6	70.4	473	7	BB283360	BB283360	BB283360
114	17.6	70.4	239	1	AV366949	AV366949	AV366949	187	17.6	70.4	476	9	DN856279	DN856279	4153009 B
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119	17.6	70.4	257	1	AV140604	AV140604	AV140604	192	17.6	70.4	490	4	CB438188	CB438188	686678 MA
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122	17.6	70.4	277	1	AV105856	AV105856	AV105856	195	17.6	70.4	496	4	BY448707	BY448707	BY448707
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126	17.6	70.4	291	1	AV066368	AV066368	AV066368	199	17.6	70.4	504	9	DN363141	DN363141	LI183628-0
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130	17.6	70.4	295	7	BB511052	BB511052	BB511052	203	17.6	70.4	517	4	BX283328	BX283328	BX283328
131	17.6	70.4	297	7	BB031763	BB031763	BB031763	204	17.6	70.4	517	5	CK840680	CK840680	UI-R-CO-j
132	17.6	70.4	300	1	AV147017	AV147017	AV147017	205	17.6	70.4	521	11	B61927	B61927	T19K19F1A
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138	17.6	70.4	312	1	BB361078	BB361078	BB361078	211	17.6	70.4	569	1	AA542056	AA542056	vm43d12.r
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145	17.6	70.4	353	10	DR409871	DR409871	EST000056	218	17.6	70.4	601	3	BM735102	BM735102	MONO1_16-
146	17.6	70.4	359	4	BY445959	BY445959	BY445959	219	17.6	70.4	620	4	CB373903	CB373903	laa30H09.
147	17.6	70.4	361	7	BB991892	BB991892	UI-M-B21-	220	17.6	70.4	656	14	DE193783	DE193783	Branchios
148	17.6	70.4	362	4	BY426276	BY426276	BY426276	221	17.6	70.4	674	9	DN116917	DN116917	ME_Mba000
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151	17.6	70.4	377	1	BB791326	BB791326	BB791326	224	17.6	70.4	675	4	CD058105	CD058105	HO05011S
152	17.6	70.4	380	7	BB803041	BB803041	BB803041	225	17.6	70.4	675	5	CJ746041	CJ746041	BJ746041
153	17.6	70.4	390	2	BG146385	BG146385	mab91b09.	226	17.6	70.4	676	4	BY755829	BY755829	BY755829
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	155	17.6	392	4	BY625882	BY625882	BY625882	228	17.6	70.4	681	7	AW967239	AW967239	EST379313
156	17.6	70.4	394	4	CA976745	CA976745	AGENCYCOURT	229	17.6	70.4	684	9	DR027116	DR027116	bda010011
157	17.6	70.4	395	4	BY626963	BY626963	BY626963	230	17.6	70.4	694	2	B1184236	B1184236	UNL-P-PN-
158	17.6	70.4	398	4	BY434099	BY434099	BY434099	231	17.6	70.4	697	2	EG477861	EG477861	603522512
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162	17.6	70.4	405	8	CO059683	CO059683	esc_k_bre	235	17.6	70.4	725	14	CR921765	CR921765	Sus_sgrof
163	17.6	70.4	409	5	CJ199163	CJ199163	CJ199163	236	17.6	70.4	744	1	CK605206	CK605206	CT02040B2
164	17.6	70.4	409	7	BE173992	BE173992	QV1-HT057	237	17.6	70.4	755	4	BX667075	BX667075	BX667075
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c 239	17.6	70.4	770	1	AU167594	AU167594	AU167594
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c 247	17.6	70.4	801	14	AY410663	Mus muscu	
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c 271	17.6	70.4	953	12	CL065269	CH216-104	
272	17.6	70.4	953	6	AK166410	Mus muscu	
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274	17.6	70.4	957	3	AK011011	Mus muscu	
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c 277	17.6	70.4	1003	14	CNS04EXR	AL287640 Tetraodon	
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280	17.6	70.4	1085	3	BM803090	AGENCOURT	
281	17.6	70.4	1535	6	CR596731	full-leng	
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297	17.6	70.4	1802	6	CR859228	Pongo pyg	
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300	17.6	70.4	1986	6	CR605577	full-leng	

## ALIGNMENTS

RESULT 1  
CN208729  
LOCUS Tor9226 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA  
DEFINITION  
ACCESSION

657 bp  
linear  
EST 30-APR-2004

VERSION CN208729.1 GI:46905460  
KEYWORDS EST.  
SOURCE Tortula ruralis  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Dicranidae; Pottiaceae; Tortula.  
REFERENCE 1 (Bases 1 to 657)  
AUTHORS Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.  
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte Tortula ruralis: transcript classification and analysis  
JOURNAL BMC Genomics 5 (1), 89 (2004)  
PUBMED 15546486  
COMMENT Contact: Oliver Melvin J  
Plant Stress Lab  
USDA-ARS  
3810 4th St, Lubbock, TX 79415, USA  
Tel: 806-749-5560  
Fax: 806-723-5272  
Email: moliver@lbrk.ars.usda.gov  
PCR Primers  
FORWARD: GTTTTCCAGTCAGCAG  
BACKWARD: CAGGAACAGCTATGAC  
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ORIGIN  
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Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGAACGGAAAGCCCTTCG 25  
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Db 239 GCAAGTCGAGCGAAAGGCCCTTCG 263  
RESULT 2  
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LOCUS  
DEFINITION ME1-0071G-Al60-E04-1.B ME1-0071 Schistosoma mansoni cDNA clone  
ACCESSION CD122074  
VERSION CD122074.1 GI:34660126  
KEYWORDS EST.  
SOURCE Schistosoma mansoni  
ORGANISM Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigidae; Schistosomatidae; Schistosomidae.  
REFERENCE 1 (Bases 1 to 356)  
AUTHORS Verjovsky-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M., Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr., Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F., Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L., Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A., Nascimento, A.L.T.O., Ohnweiler, F.P., Reis, E.M., Ribeiro, M.A., Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T., Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M., Seubal, J.C., Leite, L.C.C. and Dias-Neto, E.  
TITLE Transcriptome analysis of the acoelomate human parasite Schistosoma mansoni  
JOURNAL Nat. Genet. 35 (2), 148-157 (2003)  
PUBMED 12973350  
COMMENT Other ESTs: ME1-0071G-Al60-E04-2.B  
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This sequence was derived from the FAPESP Schistosoma mansoni EST Genome Project. All sequences in the project were assembled and annotated. This entry and all the assembled sequences can be seen in the following URL <http://bioinfo.iq.usp.br/schisto/>  
 Plate: ME1-0071G-A160 row: 4 column: E.

#### FEATURES

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#### ORIGIN

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 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAAGCCCTTC 24

Db 295 GCAAAGTCGACGGAAAGCCCTGC 272

#### RESULT 3

BB241896/c

LOCUS BB241896 RIKEN full-length enriched, 3 days neonate thymus Mus  
 DEFINITION musculus cDNA clone A630089H08 3', mRNA sequence.

ACCESSION BB241896

VERSION BB241896.1 GI:8934642

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.

#### REFERENCE

AUTHORS

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Harozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kuakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

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Email: genome-res@sc.riken.jp, URL:<http://genome.gsc.riken.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,

Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length

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Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

#### FEATURES

Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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/note="Site\_1: SalI; Site\_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'-GAGAGAGAAGATCCAAAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-GAGAGAGATCTCGATTAAATTAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

#### ORIGIN

Query Match 80.8%; Score 20.2; DB 7; Length 312;  
 Best Local Similarity 88.0%; Pred. No. 1.3e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGACGGAAAGCCCTTCG 25

Db 75 GTAAGTCTAACGGAAAGCCCTTACG 51

#### RESULT 4

DU818647

LOCUS DU818647 683 bp DNA linear GSS 13-DEC-2005  
 DEFINITION OG\_Aba0092L10.r OG\_Aba Oryza granulata genomic clone OG\_Aba0092L10  
 3', genomic survey sequence.

ACCESSION DU818647

VERSION DU818647.1 GI:83614306

KEYWORDS GSS.

SOURCE Oryza granulata

ORGANISM Oryza granulata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 683)

SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D.,

Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,

Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.

OMAP (Oryza Map Alignment Project) - Purdue University

Unpublished (2004)

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 7654963621

Fax: 7654967255

Email: [sjackson@purdue.edu](mailto:sjackson@purdue.edu)  
 Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lcy version 1.198. Bases 111-793 of the raw sequence (length 1048) were retained after clipping.

Plate: 0092    row: L    column: 10  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.

**FEATURES**

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ORIGIN
/note=vector; pageback; size_1: hhhhhh; size_2: hhhhhh

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Qy 1 GCAAGTCGAACGGAAGGCTTTCG 25  
237 GCAAGTCGAGCGGTAAAGGCCCTTCG 26

RESULT 5
CN204419
LOCUS
CN204419       650 bp       mRNA            linear     EST 30-APR-2004
DEFINITION
Tor4810 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA sequence.

REFERENCE  
 AUTHORS Oliver, M.J., Dowd, S.E., Zaragosa, J., Maugat, S.A. and Payton, P.R.  
 TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte  
 Tortula ruralis: transcript classification and analysis  
 JOURNAL BMC Genomics 5 (1), 89 (2004)  
 PUBMED 15546486  
 COMMENT Contact: Oliver Melvin J

```

FEATURES
source
1. .650
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte reh
/notes="Organ: Green Gametop
Sal: Site 2: NotI"

```

	Sarr,	Site_2:	NOCI
<hr/>			
ORIGIN			
Query Match	80.0%	Score 20;	DB 8; Length 650;
Best Local Similarity	100.0%;	Pred. No.	1.9e+02;
Matches 20;	Conservative	0;	Mismatches 0;
		Indels	0;
Gaps			0;

Qy 1 GCAAGTCGAACGGAAAGGCC 20

Db 33 GCAAGTCGAACGGAAAGGCC 52

RESULT 6  
C0365133

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
1 (bases 1 to 874)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

TITLE	An EST database from potassium-deficient loblolly pine (Pinus taeda) roots
JOURNAL	Unpublished (2004)
COMMENT	Other ESTs: RTK1_23 G09.bi A029

Email: mmprat@uga.edu  
 RNA prepared and library constructed by W. Walter Lorenz (School of  
 Forest Resources, University of Georgia); plant material prepared  
 by Craig Zimmermann (School of Forest Resources, University of  
 Georgia) using rooted cuttings provided by the Forest Biology  
 Research Cooperative (FBRC) and the COLONES project at the  
 University of Florida; sequencing done in the Laboratory for  
 Genomics and Bioinformatics, University of Georgia. Sequence ends  
 have been trimmed to exclude vector and regions below phred quality  
 16. Three-prime sequences are presented as their reverse complement  
 and have been trimmed to exclude polyA.  
 Seq primer: JENREV (CAGGAACAGCTATCACT)

## ORIGIN

Query Match	80.0%	Score 20;	DB 8;	Length 874;
Best Local Similarity	100.0%	Pred. No. 1.9e+02;		
Matches 20:	Conservative	0: Mismatches	0: Indels	

Qy 1 GCAAGTCGAACGGAAAGGCC 20

Db 23 GCAAGTCGAACGGAAGGCC 42

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RESULT 7
CN201712
LOCUS      CN201712
DEFINITION Tort1780 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
sequence.
ACCESSION CN201712
VERSION   CN201712.1
KEYWORDS  GI:46898443
SOURCE    Tortula ruralis
ORGANISM  Tortula ruralis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 885)
AUTHORS   Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE     The rehydration transcriptome of the desiccation-tolerant bryophyte
            Tortula ruralis: transcript classification and analysis
JOURNAL   BMC Genomics 5 (1), 89 (2004)
PUBMED    15546486
COMMENT    Contact: Oliver Melvin J
            Plant Stress Lab
            USDA-ARS
            3810 4th St, Lubbock, TX 79415, USA
            Tel: 806-749-5560
            Fax: 806-723-5272
            Email: moliver@lbk.ars.usda.gov
PCR PRIMERS
FORWARD: GTTTCCCGAGTCACGAC
BACKWARD: CAGAAACAGCTATGAC.
FEATURES             source
            1..885
            /organism="Tortula ruralis"
            /mol_type="mRNA"
            /db_xref="taxon:38588"
            /clone_lib="Gametophyte rehydration Library"
            /note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
            Salt; Site_2: NoI"

ORIGIN
Query Match      80.0%; Score 20; DB 8; Length 885;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GCAAGTCGACGGAAGGCC 20
        |||||||
Db       53  GCAAGTCGACGGAAGGCC 72

RESULT 8
AQ627316
LOCUS      AQ627316
DEFINITION CITBI-EI-2650I13.TR CITBI-EI Homo sapiens genomic clone 2650I13,
genomic survey sequence.
ACCESSION  AQ627316
VERSION    AQ627316.1
KEYWORDS   GI:5089708
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 452)
AUTHORS    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
TITLE      Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
JOURNAL    Unpublished (1997)
COMMENT    Other GSs: CITBI-EI-2650I13.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850

REFERENCE  1 (bases 1 to 452)
AUTHORS    Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
TITLE      Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
JOURNAL    Unpublished (1997)
COMMENT    Other GSs: CITBI-EI-2650I13.TF
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850

```

```

Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
            Location/Qualifiers
            1..452
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /clone="2650I13"
            /sex="male"
            /cell_type="sperm"
            /clone_lib="CITBI-EI"
            /notes="Vector: pBelOBAC11; Site_1: EcoRI; Site_2: EcoRI;
            CalTech Human BAC Library D"

ORIGIN
Query Match      76.8%; Score 19.2; DB 11; Length 452;
Best Local Similarity 87.5%; Pred. No. 4.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GCAAGTCGACGGAAGGCCCTTTC 24
        |||||||
Db       191  GCAAGTGGACCTGAAAGGCCCTTTC 214

RESULT 9
AQ549361
LOCUS      AQ549361
DEFINITION RPCI-11-371H1.TV RPCI-11 Homo sapiens genomic clone RPCI-11-371H1,
genomic survey sequence.
ACCESSION  AQ549361
VERSION    AQ549361.1
KEYWORDS   GI:4908538
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 540)
AUTHORS    Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
            Venter,J.C.
TITLE      Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
JOURNAL    Unpublished (1997)
COMMENT    Other GSs: RPCI-11-371H1.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieterdejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
            Location/Qualifiers
            1..540
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="GDB:7642248"
            /db_xref="taxon:9606"
            /clone="RPCI-11-371H1"
            /sex="Male"

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```

/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

ORIGIN
Query Match      76.8%; Score 19.2; DB 11; Length 540;
Best Local Similarity 87.5%; Pred. No. 4.2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 171 GCAAGTGACCTGGAAGGCGCTTTC 194

RESULT 10
CC453191/c
LOCUS      CC453191          903 bp      DNA      linear      GSS 22-MAY-2003
DEFINITION ZMMBBc0347A07f ZMMBBc Zea mays genomic clone ZMMBBc0347A07 5',
genomic survey sequence.
ACCESSION  CC453191
VERSION     CC453191.1  GI:31000754
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 903)
AUTHORS     Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Rouzaud,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE       Sequencing of the maize genome at PGIR (2003b)
JOURNAL     Unpublished (2003)
COMMENT     Contact: Bharti.A.K.
Dr Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: 77
Class: BAC ends
High quality sequence start: 398.
FEATURES             source
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     1..903
     /organism="Zea mays"
     /mol_type="genomic DNA"
     /cultivar="B73"
     /db_xref="taxon:4577"
     /clone="ZMMBBc0347A07"
     /lab_host="E. coli DH10B"
     /clone_lib="ZMMBBc"
     /note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"

ORIGIN
Query Match      75.2%; Score 18.8; DB 12; Length 903;
Best Local Similarity 90.9%; Pred. No. 6.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTT 23
||||| ||||| ||||| ||||| |||||
Db 75 CAAGTTGATCGGAAGGCGCTTT 54

RESULT 11
DN561788
LOCUS      DN561788          910 bp      mRNA      linear      EST 14-MAR-2005
DEFINITION 92178421 Sea Urchin primary mesenchyme cell cDNA library
Strongylocentrotus purpuratus cDNA clone PMCSPr2-102A16 5', mRNA
sequence.
ACCESSION  DN561788
VERSION     DN561788.1  GI:61120827

/cell_type="Strongylocentrotus purpuratus"
/clone_lib="RPCI-11"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
RPC11 Human Male BAC Library"

ORIGIN
Query Match      75.2%; Score 18.8; DB 9; Length 910;
Best Local Similarity 90.9%; Pred. No. 6.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCGCTTTCG 25
||||| ||||| ||||| ||||| |||||
Db 790 AGGCGAACGGAAGGCGCTTTCG 811

RESULT 12
BQ104075
LOCUS      BQ104075          399 bp      mRNA      linear      EST 16-APR-2002
DEFINITION gg1205.e Rose Petals (Golden Gate) Lambda Zap Express Library Rosa
hybrid cultivar cDNA clone gg1205.e 5', mRNA sequence.
ACCESSION  BQ104075
VERSION     BQ104075.1  GI:20153737
KEYWORDS    EST.
SOURCE      Rosa hybrid cultivar
ORGANISM    Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE   1 (bases 1 to 399)
AUTHORS     Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,
Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
Adam,Z., Pichersky,E., Lewinson,E., Zamir,D., Vainstein,A. and
Weiss D.
Rose Scent: Genomics Approach to Discovering Novel Floral
Fragrance-Related Genes
Plant Cell 14 (10), 2325-2338 (2002)
COMMENT     Contact: Naama Menda
Petat Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel

KEYWORDS      Strongylocentrotus purpuratus
SOURCE        Strongylocentrotus purpuratus
ORGANISM      Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE     1 (bases 1 to 910)
AUTHORS      Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
Ettensohn,C.A.
TITLE        A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
JOURNAL      Development 128 (13), 2615-2627 (2001)
PUBMED       11493577
COMMENT      Contact: Erica Sodergren
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-7676
Fax: 713-798-6977
Email: ericas@bcm.tmc.edu
NCBI Trace Archive: 486682679
Insert Length: 1750 Std Error: 0.25
Plate: 102 row: A column: 16.
FEATURES             location/Qualifiers
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     /db_xref="taxon:7668"
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     /tissue_type="embryo"
     /cell_type="primary mesenchyme cells"
     /lab_host="E.coli"
     /clone_lib="Sea Urchin primary mesenchyme cell cDNA
library"
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dt priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match      75.2%; Score 18.8; DB 9; Length 910;
Best Local Similarity 90.9%; Pred. No. 6.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCGCTTTCG 25
||||| ||||| ||||| ||||| |||||
Db 790 AGGCGAACGGAAGGCGCTTTCG 811

RESULT 12
BQ104075
LOCUS      BQ104075          399 bp      mRNA      linear      EST 16-APR-2002
DEFINITION gg1205.e Rose Petals (Golden Gate) Lambda Zap Express Library Rosa
hybrid cultivar cDNA clone gg1205.e 5', mRNA sequence.
ACCESSION  BQ104075
VERSION     BQ104075.1  GI:20153737
KEYWORDS    EST.
SOURCE      Rosa hybrid cultivar
ORGANISM    Rosa hybrid cultivar
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Rosales; Rosaceae; Rosoideae; Rosa.
REFERENCE   1 (bases 1 to 399)
AUTHORS     Guterman,I., Shalit,M., Menda,N., Piestun,D., Dafny-Yelin,M.,
Shalev,G., Bar,E., Davydov,O., Ovadis,M., Emanuel,M., Wang,J.,
Adam,Z., Pichersky,E., Lewinson,E., Zamir,D., Vainstein,A. and
Weiss D.
Rose Scent: Genomics Approach to Discovering Novel Floral
Fragrance-Related Genes
Plant Cell 14 (10), 2325-2338 (2002)
COMMENT     Contact: Naama Menda
Petat Genomics
Faculty of Agricultural, Food and Environmental Quality Sciences,
The Hebrew University of Jerusalem
P.O. Box 12, Rehovot, 76100, Israel

```

Tel: 972 8 9489 683  
 Fax: 972 8 9468 265  
 Email: shaham@agri.huji.ac.il  
 Seq primer: T3 forward.

## FEATURES

source

1. .399  
 /organism="Rosa hybrid cultivar"  
 /mol\_type="mRNA"  
 /strain="Golden Gate"  
 /db\_xref="taxon:128735"  
 /clone="gg1205.e"  
 /tissue\_type="Petals"  
 /dev\_stage="Young open flower at stage four"  
 /clone\_lib="Rose Petals (Golden Gate) Lambda Zap Express Library"  
 /note="Vector: pBKMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 74.4%; Score 18.6; DB 3; Length 399;  
 Best Local Similarity 84.0%; Pred. No. 7.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 5' mRNA sequence.  
 1 GCAAGTCGAACGGAAGGCCTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 262 GCAAGTTGACCGGAATGCGCTTCG 286

## RESULT 13

CA282280

## LOCUS

CA282280 513 bp mRNA linear EST 26-SEP-2003  
 SCAGSD2042H09.g SD2 Saccharum officinarum cDNA clone SCAGSD2042H09

## ACCESSION

CA282280

## VERSION

CA282280.1

## KEYWORDS

EST.

## SOURCE

Saccharum officinarum

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

## REFERENCE

1 (bases 1 to 513)

Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 042 row: H column: 09

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1. .513

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCAGSD2042H09"

/lab\_host="DH10B"

/clone\_lib="SD2"

/note="Organ: Developing seeds (small insert library);

Vector: pSport1; Site 1: SalI; Site 2: NotI; An

unidirectional cDNA library generated from [Developing

seeds (small insert library)]. cDNA was prepared from

polyA+ mRNA using SuperScript Plasmid System kit

(Invitrogen). The double-strand cDNAs were fractionated

in a sapharose CL-2B 40cm-columns and fragments sizing

between 0.8 and 1.5 Kb were directionally cloned into the

vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>

## ORIGIN

Query Match 74.4%; Score 18.6; DB 4; Length 513;  
 Best Local Similarity 84.0%; Pred. No. 8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 1 GCAAGTCGAACGGAAGGCCTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 27 GCAAGTCGAACGGTGAAGCCCTTCG 51

## RESULT 14

BM131991/c

## LOCUS

BM131991 526 bp mRNA linear EST 27-NOV-2001  
 TgESTzyb05b12.y1 TgRH Tachyzoite Subtracted cDNA Library Toxoplasma gondii cDNA clone TgESTzyb05b12.y1 5' similar to TR:O15793 O15793 STRAIN DD2 HEAT SHOCK PROTEIN 86 ;, mRNA sequence.

## ACCESSION

BM131991

## VERSION

BM131991.1

## KEYWORDS

EST.

## SOURCE

Toxoplasma gondii

## ORGANISM

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.

1 (bases 1 to 526)

Tang,K., Cole,R., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.

Toxoplasma EST Project

Unpublished (2001)

Contact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: toxo@watson.wustl.edu

Contact David Sibley (toxost@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 421.

Location/Qualifiers

1. .526

/organism="Toxoplasma gondii"

/mol\_type="mRNA"

/strain="RH (Type I)"

/db\_xref="taxon:5811"

/clone="TgESTzyb05b12.y1"

/dev\_stage="Tachyzoite"

/lab\_host="DH10B (GeneHog, Invitrogen, Inc.)"

/clone\_lib="TgRH Tachyzoite Subtracted cDNA Library"

/note="Vector: pBluscript SK-; Site 1: EcoRI; Site 2:

XhoI; Toxoplasma RH strain tachyzoites were grown in human

foreskin fibroblast cultures in vitro. The library was

originally constructed by K.L.Wan, Cambridge University.

cDNAs were synthesized from polyA RNAs by oligo d(T)

priming and directionally cloned into the EcoRI to XhoI

sites of the Lambda ZapII vector using the ZAP-cDNA

synthesis kit (Stratagene). The primary cDNA library was

mass excised as phagemid using EXassist helper phage

(Stratagene). Phagemid DNA was extracted by

phenol-chloroform method, and hybridized against a pool of

over-represented ESTs (N&gt;=12, from 5596 previous reads).

The subtracted library was electroporated into DH10B

(GeneHog, Invitrogen, Inc). WARNING: the library contains

a small percentage of cDNAs derived from the human host

cells. Library Source: David Sibley, Washington

University."



## ORIGIN

Query Match 74.4%; Score 18.6; DB 2; Length 526;  
 Best Local Similarity 84.0%; Pred. No. 8e+02; Mismatches 0; Gaps 0;  
 Matches 21; Conservative 0; Indels 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGCCCTTTTCG 25  
 ||||| || || ||||| |||||  
 Db 478 GCAAGACGCACAGAAAGTCCTTTTCG 454

## RESULT 15

BI157204  
 LOCUS 602923403F1 NCI\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5063424 5',  
 DEFINITION mRNA sequence.

ACCESSION BI157204

VERSION BI157204.1 GI:14617205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: L2AM1171 row: f column: 01

High quality sequence stop: 667.

## FEATURES

source

1..806  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="129,C57BL/6J,FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5063424"  
 /tissue\_type="tumor, gross tissue"  
 /dev\_stage="10 months"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP Mam3"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Library constructed by Life Technologies Investigators.  
 Providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH  
 Reference for transgenic model: Xu et al., Nature Genetics  
 22, 37-43 (1999)."

## ORIGIN

Query Match 74.4%; Score 18.6; DB 2; Length 306;  
 Best Local Similarity 84.0%; Pred. No. 8.5e+02; Mismatches 0; Gaps 0;  
 Matches 21; Conservative 0; Indels 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGCCCTTTTCG 25  
 ||||| || || ||||| |||||

Db 601 GCAAGACGCACAGAAAGCCCTTTTCG 625  
 ||||| || || ||||| |||||

## RESULT 16

CN207299  
 LOCUS Tor7720 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA  
 DEFINITION sequence.

ACCESSION CN207299

591 bp mRNA linear EST 30-APR-2004

## VERSION

KEYWORDS CN207299.1 GI:46904030

SOURCE EST.

## ORGANISM

Tortula ruralis  
 Tortula ruralis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.

## REFERENCE

AUTHORS 1 (bases 1 to 591)

TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte

Tortula ruralis: transcript classification and analysis

JOURNAL BMC Genomics 5 (1), 89 (2004)

PUBMED 15546486

COMMENT Contact: Oliver Melvin J

Plant Stress Lab

USDA-ARS

3810 4th St, Lubbock, TX 79415, USA

Tel: 806-749-5560

Fax: 806-723-5272

Email: [moliver@lbk.ars.usda.gov](mailto:moliver@lbk.ars.usda.gov)

PCR Primers

FORWARD: GTTTCCTCAGTCACGAC

BACKWARD: CAGGAACAGCTATGAC.

## FEATURES

source

Location/Qualifiers

1..591

/organism="Tortula ruralis"

/mol\_type="mRNA"

/db\_xref="taxon:38588"

/clone\_lib="Gametophyte rehydration Library"

/note="Organ: Green Gametophyte; Vector: pSport1; Site\_1:

SalI; Site\_2: NotI"

## ORIGIN

Query Match 73.6%; Score 18.4; DB 8; Length 591;  
 Best Local Similarity 95.0%; Pred. No. 1e+03; Mismatches 0; Gaps 0;  
 Matches 19; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGCC 20  
 ||||| ||||| |||||

Db 274 GCAAGTCGAACGCTAAGGCC 293  
 ||||| ||||| |||||

## RESULT 17

CF882404

LOCUS

DEFINITION

tric086xm16.b1 T.reesei mycelial culture, Version 6 October 2003

Hypocrea jecorina cDNA clone tric086xm16, mRNA sequence.

CF882404

ACCESSION CF882404.1 GI:38137086

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Hypocrea jecorina (anamorph: Trichoderma reesei)

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

REFERENCE 1 (bases 1 to 735)

AUTHORS Diener, S.E., Dunn-Coleman, N., Foreman, P., Houfek, T.D.,  
 Teunissen, P.J.M., van Solingen, P., Dankmeyer, L., Mitchell, T.K.,  
 Ward, M. and Dean, R.A.

TITLE Characterization of the protein processing and secretion pathways

in a comprehensive set of expressed sequence tags from Trichoderma

reesei

JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)

PUBMED 14757250

COMMENT Contact: Ralph A. Dean

Fungal Genomics Laboratory

North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA

Tel: 919-513-0020

Fax: 919-513-0024

Email: [ralph.dean@ncsu.edu](mailto:ralph.dean@ncsu.edu)

Seq primer: LT-Fl primer.

Location/Qualifiers

1..735

/organism="Hypocrea jecorina"

/mol\_type="mRNA"  
/strain="QM6a"  
/db\_xref="taxon:51453"  
/clone="tric086xm16"  
/dev\_stage="mycelia"  
/clone\_lib="T.reesei mycelial culture, Version 6 October 2003"  
/notes="vector: pREP3Y; Site\_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."  
73.6%; Score 18.4; DB 5; Length 735;  
Best Local Similarity 95.0%; Pred. No. 1e+03; Mismatches 0; Gaps 0;  
Matches 19; Conservative 0; Indels 1; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGCGCTTTC 24  
|||||  
Db 58 GTCGAACGGAACGCTTTC 77

RESULT 18  
CB908942  
LOCUS  
DEFINITION  
tric086xm16 T.reesei mycelial culture, Version 3 april Hypocrea  
jecorina cDNA clone tric086xm16, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Hypocrea jecorina (anamorph: Trichoderma reesei)  
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.  
REFERENCE  
AUTHORS  
Foreman,P.K., Brown,D.B., Dankmeyer,L., Dean,R., Diener,S.,  
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,  
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,  
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.  
Transcriptional regulation of biomass-degrading enzymes in the  
filamentous fungus Trichoderma reesei  
J. Biol. Chem. 278 (34), 31988-31997 (2003)  
J788920  
COMMENT  
Contact: Pamela K. Foreman  
Genencor Intl.  
925 Page Mill Road, Palo Alto, CA 94304, USA  
Tel: (650) 846-7635  
Fax: (650) 621-7817  
Email: Pforeman@genencor.com  
Seq primer: LT-F1 primer.  
Location/Qualifiers  
1..788  
/organism="Hypocrea jecorina"  
/mol\_type="mRNA"  
/strain="QM6a"  
/db\_xref="taxon:51453"  
/clone="tric086xm16"  
/dev\_stage="mycelia"  
/clone\_lib="T.reesei mycelial culture, Version 3 april"  
/notes="vector: pREP3Y; Site\_1: Not I/Sal I; Mycelial culture grown from 24 hrs to 6 days with varying Carbon and Nitrogen sources and concentrations."

Qy 5 GTCGAACGGAAGCGCTTTC 24  
|||||  
Db 111 GTCGAACGGAACGCTTTC 130

RESULT 19

CN207539  
LOCUS  
DEFINITION  
Tor7952 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA  
sequence.  
ACCESSION  
VERSION  
CN207539.1 GI:46904270  
SOURCE  
Tortula ruralis  
ORGANISM  
Tortula ruralis  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.  
REFERENCE  
AUTHORS  
Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.  
The rehydration transcriptome of the desiccation-tolerant bryophyte  
Tortula ruralis: transcript classification and analysis  
BMC Genomics 5 (1), 89 (2004)  
15546486  
COMMENT  
Contact: Oliver Melvin J  
Plant Stress Lab  
USDA-ARS  
3810 4th St, Lubbock, TX 79415, USA  
Tel: 806-749-5560  
Fax: 806-723-5272  
Email: moliver@lbrk.ars.usda.gov  
PCR Primers  
FORWARD: GTTTTCCCACTCAGCAGC  
BACKWARD: CAGGAACAGCTATGAC.  
Location/Qualifiers  
1..817  
/organism="Tortula ruralis"  
/mol\_type="mRNA"  
/db\_xref="taxon:38588"  
/clone\_lib="Gametophyte rehydration Library"  
/notes="Organ: Green Gametophyte; Vector: pSport1; Site\_1:  
SalI; Site\_2: NotI"

ORIGIN  
Query Match 73.6%; Score 18.4; DB 8; Length 817;  
Best Local Similarity 95.0%; Pred. No. 1.1e+03;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20  
|||||  
Db 50 GCAAGTCGAACGCTAAGGCC 69

RESULT 20  
DR421359  
LOCUS  
DEFINITION  
DR421359 Coprinus cinereus heat-shocked mycelia cDNAs Coprinopsis  
cinerea cDNA, mRNA sequence.  
ACCESSION  
VERSION  
DR421359.1 GI:68323375  
KEYWORDS  
SOURCE  
ORGANISM  
Coprinopsis cinerea (Coprinus cinereus)  
Coprinopsis cinerea  
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
Agaricales; Psathyrellaceae; Coprinopsis.  
REFERENCE  
AUTHORS  
1 (bases 1 to 907)  
Carlson,M.D., Barr,C., Murphy,B., Wilke,S.K., Gathman,A.C.,  
Lilly,W.W. and Pukkila,P.J.  
Expressed sequence tags from Coprinus cinereus (Coprinopsis  
cinerea) cDNAs, spring 2005  
Unpublished (2005)  
COMMENT  
Contact: Gathman AC  
Biology Department  
Southeast Missouri State University  
1 University Plaza, Cape Girardeau, MO 63701, USA  
Tel: 5736512361  
Fax: 573 651 2382  
Email: agathman@semo.edu.  
Location/Qualifiers  
1..907



```

further details.
FEATURES
  source
    1..421
      Location/Qualifiers
        /organism="Mus musculus"
        /mol_type="mRNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="K630096B19"
        /sex="female"
        /tissue_type="amnion"
        /dev_stage="15 days pregnant adult"
        /clone_lib="RIKEN full-length enriched, 15 days pregnant
        adult female amnion"

ORIGIN
  Query Match      72.8%; Score 18.2; DB 4; Length 421;
  Best Local Similarity 87.0%; Pred. No. 1.2e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCCTTC 24
      ||||| ||||| ||||| |||||
Db  272 CAAGTCGAGCAGAAGTCCITTC 294

RESULT 23
LOCUS      DN526979              475 bp      mRNA      linear      EST 11-MAR-2005
DEFINITION 1271790 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  DN526979
VERSION     DN526979.1 GI:60972211
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 475)
AUTHORS   Smith,T.P.L., Roberts,J.W., Echterkamp,S.E., Chitko-McKown,C.G.,
          Wray,J.E. and Keele,J.W.
TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL   Unpublished (2003)
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called with phred v0.020425.c and
          trimmed with the aid of the trim_alt option. Vector identified with
          cross_match v0.990329.
          Plate: RUK8046 row: I column: 10
          Seq primer: GTAATACGACTCACTATAGG.

FEATURES
  source
    1..475
      Location/Qualifiers
        /organism="Bos taurus"
        /mol_type="mRNA"
        /db_xref="taxon:9913"
        /tissue_type="pooled"
        /lab_host="DH10B"
        /clone_lib="MARC 7BOV"
        /note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
        Library made with RNA pooled from multiple tissues
        including ovary, hindbrain, uterus, and day-30 whole
        embryos."

ORIGIN
  Query Match      72.8%; Score 18.2; DB 9; Length 475;
  Best Local Similarity 87.0%; Pred. No. 1.2e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAGGCCTTC 24
      ||||| ||||| ||||| |||||
Db  163 CAAGTCGAACTGAAGGAGCTGC 185

```

```

RESULT 24
LOCUS      CA934753/c              609 bp      mRNA      linear      EST 30-DEC-2002
DEFINITION MTU5TS.P23.C06 Aspen stem cDNA Library Populus tremuloides cDNA,
          mRNA sequence.
ACCESSION  CA934753
VERSION     CA934753.1 GI:27423233
KEYWORDS   EST.
SOURCE     Populus tremuloides (quaking aspen)
ORGANISM   Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE  1 (bases 1 to 609)
AUTHORS   Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
          Tsai,C-J.
TITLE     Expressed sequence tags from Aspen
JOURNAL   Unpublished (2003)
COMMENT   Contact: Tsai C-J
          Plant Biotech Research Center
          Michigan Technological University, School of Forest Resources &
          Environmental Science
          1400 Townsend Drive, Houghton, MI 49931-1295, USA
          Tel: 906 487 2914
          Fax: 906 487 2915
          Email: chtsai@mtu.edu.

FEATURES
  source
    1..609
      Location/Qualifiers
        /organism="Populus tremuloides"
        /mol_type="mRNA"
        /db_xref="taxon:3693"
        /clone_lib="Aspen stem cDNA Library"
        /note="Organ: stem"

ORIGIN
  Query Match      72.8%; Score 18.2; DB 4; Length 609;
  Best Local Similarity 87.0%; Pred. No. 1.3e+03;
  Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1  GCAAGTCGAACGGAAGGCCTTT 23
      ||||| ||||| ||||| |||||
Db  276 GAAAGTCGTTCCGGAAGGCCTTT 254

RESULT 25
LOCUS      CB378019              630 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION rg06a11.y1 Heterodera glycines J3 Heterodera glycines cDNA 5',
          similar to WP:CE23823 H24K24.4 RNA-binding protein,, mRNA
          sequence.
ACCESSION  CB378019
VERSION     CB378019.1 GI:29127315
KEYWORDS   EST.
SOURCE     Heterodera glycines
ORGANISM   Heterodera glycines
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
REFERENCE  1 (bases 1 to 630)
AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
          Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
          Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
          Tsagarishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
          Underwood,K., Sceptoe,M., Allen,M., Person,B., Swaller,T.,
          Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
          McCann,R., Waterston,R. and Wilson,R.
          The Washington Univ. Nematode EST Project, 1999
          Unpublished (1999)
          Contact: McCarter JP
          The Washington Univ. Nematode EST Project, 1999
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

```

Tel: 314 286 1800  
Fax: 314 286 1810

Email: est@watson.wustl.edu

This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised (now in pBluescript SK(+)) and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jmcderm@iastate.edu).

Seq primer: T3 from Gibco.

#### FEATURES

Location/Qualifiers  
1..630  
/organism="Heterodera glycines"  
/mol\_type="mRNA"  
/db\_xref="taxon:51029"  
/sex="mixed"  
/tissue\_type="whole organism"  
/dev\_stage="3rd stage juvenile"  
/lab\_host="DH10B"  
/clone\_lib="Heterodera glycines J3"  
/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI; Site 2: EcoRI; This library was generated by cloning cDNAs directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI are at the 3'-end). The library was excised (now in pBluescript SK(+)) and normalized (Bonaldo et al 1996 Genome Research 6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa State University, Plant Pathology Department and Jeff McDermott (jmcderm@iastate.edu)."

#### ORIGIN

Query Match 72.8%; Score 18.2; DB 4; Length 630;  
Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCTTTTCG 25

|||||

Db 509 AATTCGAACGGAAGGCTTTTGG 531

#### RESULT 26

CK950118 719 bp mRNA linear EST 15-MAR-2004  
LOCUS 4075090 BARC 10BOV Bos taurus cDNA clone 10BOV2\_B11 3', mRNA  
DEFINITION

CK950118

CK950118.1 GI:45464498

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cattle)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (Bases 1 to 719)

Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M., and Gasbarre, L.C.

Production of EST from cDNA libraries derived from immunologically

activated bovine gut

Unpublished (2004)

Contact: Tad S. Sonstegard

Bovine Functional Genomics Laboratory

Animal and Natural Resources Institute

Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA

Tel: 3015048416

Fax: 3015048414

Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt -trim fasta. Vector identified

by cross\_match using options -minmatch 12 -minscore 18

Plate: 2 row: B column: 11

Seq primer: ACGGATACCAATTTCACACAGG

High quality sequence stop: 719.

#### FEATURES

Location/Qualifiers  
1..719  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/strain="Holstein"  
/db\_xref="taxon:9913"  
/clones="10BOV2\_B11"  
/sex="Male"  
/tissue\_type="pooled"  
/dev\_stage="Multiple"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="BARC 10BOV"  
/note="Organ: Small Intestine; Vector: pagen-1; Site 1: EcoRV; Site 2: NotI; Equimolar amounts of mRNA extracted from proximal jejunums of 18 and 21 wk old steers, and distal ileums of 14 day old calves, proximal jejunum exposed to C. oncophora for 3 and 6 weeks, and distal ileum exposed to C. parvum for 7 days"

#### ORIGIN

Query Match 72.8%; Score 18.2; DB 5; Length 719;  
Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAATCGAACGGAAGGCTTTTC 24

|||||

Db 129 CAATCGAACGGAAGGACTGTC 151

#### RESULT 27

DN283722 835 bp mRNA linear EST 02-MAR-2005  
LOCUS 1183944 MARC 7BOV Bos taurus cDNA 5', mRNA sequence.  
DEFINITION

DN283722

DN283722.1 GI:60452332

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cattle)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (Bases 1 to 835)

Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,

Wray, J.E., and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries

Unpublished (2003)

Contact: Smith, TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425 c and

trimmed with the aid of the trim\_alt option. Vector identified with

cross\_match v0.990329.

Plate: RLK8014 row: J column: 12

Seq primer: GTAATACGACTACTATAGG.

Location/Qualifiers

1..835

/organism="Bos taurus"

/mol\_type="mRNA"

/db\_xref="taxon:9913"

/tissue\_type="pooled"

/lab\_host="DH10B"

/clone\_lib="MARC 7BOV"

/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;

Library made with RNA pooled from multiple tissues

including ovary, hindbrain, uterus, and day-30 whole

embryos."

#### ORIGIN

Query Match 72.8%; Score 18.2; DB 9; Length 835;  
Best Local Similarity 87.0%; Pred. No. 1.3e+03;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 24  
|||||  
Db 552 CAAGTCGAACGGAAGGACTGTC 574

RESULT 28  
LOCUS CR077081 835 bp DNA linear GSS 05-JUL-2004  
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP284c21, genomic survey sequence.  
ACCESSION CR077081.1 GI:49810669  
VERSION GSS; genome survey sequence; MICR.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 835)  
AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.  
TITLE Direct Submission  
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>  
FEATURES  
source Location/Qualifiers  
1 .835  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="MHP284c21"  
/clone\_lib="MHP"

ORIGIN  
Query Match 72.8%; Score 18.2; DB 14; Length 835;  
Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCGCTTCG 25  
|||||  
Db 519 AATTAGAAAGGAAGGCGCTTCG 541

RESULT 29  
DN282351/c  
LOCUS DN282351 843 bp mRNA linear EST 02-MAR-2005  
DEFINITION 1182408 MARC 7BOV Bos taurus CDNA 3', mRNA sequence.  
ACCESSION DN282351  
VERSION DN282351.1 GI:60450961  
KEYWORDS EST.  
SOURCE Bos taurus (cattle)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 843)  
AUTHORS Smith,T.P.L., Roberts,A.J., Ehternkamp,S.E., Chitko-McKown,C.G., Wray,J.E. and Keefe,J.W.  
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries  
JOURNAL Unpublished (2003)  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross\_match v0.990329.  
Plate: RLK8014 row: J column: 12  
Seq primer: TAGAAGGCACAGTCGAGG.

FEATURES  
source Location/Qualifiers  
1 .843  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH108"  
/clone\_lib="MARC 7BOV"  
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI; Library made with RNA pooled from multiple tissues including ovary, hindbrain, uterus, and day-30 whole embryos."

ORIGIN  
Query Match 72.8%; Score 18.2; DB 9; Length 843;  
Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 24  
|||||  
Db 284 CAAGTCGAACGGAAGGACTGTC 262

RESULT 30  
LOCUS DU746898/c  
DEFINITION DU746898 906 bp DNA linear GSS 27-JAN-2006  
ASNC3551.b2 HF10 10-07-02 uncultured marine microorganism HF10\_10-07-02 genomic clone HF0010\_049G12, genomic survey sequence.  
ACCESSION DU746898  
VERSION DU746898.1 GI:85756734  
KEYWORDS GSS.  
SOURCE uncultured marine microorganism HF10\_10-07-02  
ORGANISM uncultured marine microorganism HF10\_10-07-02  
unclassified sequences; environmental samples.  
REFERENCE 1 (bases 1 to 906)  
AUTHORS DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J., Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W. and Karl,D.M.  
TITLE Comparative genomics reveals ecological trends in stratified microbial communities in the ocean's interior  
JOURNAL Science (2006) In press  
COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus, Kerrie Barry, Tijana Glavinadelio, David Bruce, Paul Richardson and Edward DeLong  
US DOE Joint Genome Institute  
US DOE Joint Genome Institute  
2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA  
Tel: 617-253-5271  
Fax: 617-253-2679  
Email: [PMRichardson@lbl.gov](mailto:PMRichardson@lbl.gov); [delong@mit.edu](mailto:delong@mit.edu)  
North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Sample Date: 10/7/2002  
Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C  
Salinity 35.08 psu Oxygen: 204.6 umol/kg  
Class: fosmid ends.  
FEATURES  
source Location/Qualifiers  
1 .906  
/organism="uncultured marine microorganism HF10\_10-07-02"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:361145"  
/clone="HF0010\_049G12"  
/cell\_type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"  
/clone\_lib="HF10\_10-07-02"  
/note="Vector: pCC1FOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 10 m depth on 10/7/2002, Coordinates: 22.45 N, 158 W. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6 umol/kg"

## ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 906;  
 Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCTTCG 25  
 |||||  
 Db 421 AAGTCGAACGCGAGGCTTCG 399  
 |||||

## RESULT 31

CNS06FX8 929 bp DNA linear GSS 17-JUN-2001  
 LOCUS T3 end of clone XAR0AA001H08 of library XAR0AA from strain CBS 732  
 DEFINITION of Zygosaccharomyces rouxii, genomic survey sequence.

ACCESSION AL396978  
 VERSION AL396978.1 GI:12149467

## KEYWORDS

SOURCE GSS.

## ORGANISM

Zygosaccharomyces rouxii  
 Zygosaccharomyces rouxii  
 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomycetales; Saccharomycetaceae; Zygosaccharomycetes.

1 (bases 1 to 929)

Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,

Boiotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,

de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,

Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,

Saurin,W., Tekaiia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,

Winker,P. and Weissenbach,J.

Genomic exploration of the hemiascomycetous yeasts: 1. A set of

yeast species for molecular evolution studies

FEMS Lett. 487 (1), 3-12 (2000)

11152876

2 (bases 1 to 929)

de Montigny,J., Straub,M., Potier,S., Tekaiia,F., Dujon,B.,

Winker,P., Artiguenave,F. and Souciet,J.

Genomic exploration of the hemiascomycetous yeasts: 8.

Zygosaccharomyces rouxii

FEMS Lett. 487 (1), 52-55 (2000)

11152883

3 (bases 1 to 929)

Genoscope.

Direct Submission

Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :

secref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.

Location/Qualifiers

1..929

/organism="Zygosaccharomyces rouxii"

/mol\_type="genomic DNA"

/strain="CBS 732"

/db\_xref="taxon:4956"

/clone="XAR0AA001H08"

/clone\_lib="XAR0AA"

/note="end : 73"

complement(<1..>927)

/inferences="non-experimental evidence, no additional

details recorded"

/note="similar to Saccharomyces cerevisiae ORF YLR399C [

BDF1 ; sporulation protein ]

1 putative frameshift(s)"

complement(<16..>927)

misc\_feature

source

/inference="non-experimental evidence, no additional  
 details recorded"

/note="similar to Saccharomyces cerevisiae ORF YDL070w [

BDF2 ; similarity to bromodomain protein Bdf1p ]

1 putative frameshift(s)"

## ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 929;  
 Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTTT 23  
 |||||  
 Db 902 GCAAGTTGACGTAATGCTTTT 880  
 |||||

## RESULT 32

DW640758/c

LOCUS

DEFINITION

DW640758

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gasterosteus aculeatus (three spined stickleback)

Gasterosteus aculeatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;

Gasterosteidae; Gasterosteus.

1 (bases 1 to 943)

Kingsley,D.M., Peichel,C., Knecht,A., Balabhadra,S., Grimwood,J.,

Dickson,M., Schmutz,J. and Myers,R.M.

Expressed sequence tags from Gasterosteus aculeatus (2004)

Unpublished (2004)

Contact: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@hgc.stanford.edu

Plate: 372

High quality sequence stop: 751.

Location/Qualifiers

1..943

/organism="Gasterosteus aculeatus"

/mol\_type="mrna"

/strain="Bittufjordur marine sticklebacks, Iceland"

/db\_xref="taxon:69293"

/clones="CLJ372-G02"

/sex="mixed male and female"

/tissue\_types="whole larva"

/dev\_stages="21 day old larvae collected at Swarup Stage 30

(J. Embryol. Exp. Morphol 6: 373-383 1958)"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="SHGC-CLJ2"

/note="Vector: Express 1: Total and poly A+ RNA was

isolated from the indicated stickleback tissue, and a cDNA

library was constructed in the Express 1 plasmid vector by

Open Biosystems. First strand cDNA synthesis was primed

with an 54 bp linker primer containing an oligodT sequence

preceded by a synthetic NotI site (first strand primer:

5'-GACTAGTCTAGATCGGCGGCC(T)25-3'). Following

second strand synthesis, cDNAs were made blunt at the end

corresponding to the original 5 prime end of mRNA, and

cloned directionally into the NotI and EcoRV sites of

Express 1. Note that the EcoRV site is typically destroyed

in the blunt end cloning, leaving a junction of the form

'xxxATC' (where is ATC is the second half of the EcoRV

site, and xxx is derived from the cDNA sequence). A map of

the Express 1 vector is available at:

http://www.openbiosystems.com/cdna\_library\_construction\_fa

q.php#8 The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria."

```

ORIGIN
Query Match          72.8%; Score 18.2; DB 10; Length 943;
Best Local Similarity 87.0%; Pred. No. 1.3e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    ||||| ||||| ||||| ||||| |||||
Db 893 GCAAATTGAACGGAAGGCCTTT 871

RESULT 33
CNS06CEP/c          994 bp DNA linear GSS 14-JUN-2001
LOCUS               T3 end of clone AR0AA004E02 of library AR0AA from strain CBS 732 of
DEFINITION          Zygosaccharomyces rouxii, genomic survey sequence.
ACCESSION           AL392423.1 GI:12141725
VERSION             AL392423
KEYWORDS            Zygosaccharomyces rouxii
SOURCE              Zygosaccharomyces rouxii
ORGANISM            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
REFERENCE           1 (bases 1 to 994)
AUTHORS             Souci t,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
                    Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
                    de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Illorente,B.,
                    Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
                    Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
                    Winkler,P. and Weissenbach,J.
TITLE               Genomic exploration of the hemiascomycetous yeasts: 1. A set of
                    yeast species for molecular evolution studies
JOURNAL             FEBS Lett. 487 (1), 3-12 (2000)
PUBMED              11152876
REFERENCE           2 (bases 1 to 994)
AUTHORS             de Montigny,J., Straub,M., Potier,S., Tekala,F., Dujon,B.,
                    Winkler,P., Artiguenave,F. and Souci t,J.
TITLE               Genomic exploration of the hemiascomycetous yeasts: 8.
                    Zygosaccharomyces rouxii
JOURNAL             FEBS Lett. 487 (1), 52-55 (2000)
PUBMED              11152883
REFERENCE           3 (bases 1 to 994)
AUTHORS             Genoscope.
TITLE               Direct Submission
COMMENT             Submitted (06-SEP-2000) Genoscope - Centre National de Sequencage,
                    2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
                    seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                    This GSS is part of a random genomic sequencing program of thirteen
                    yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
                    exiguus, Saccharomyces servazii, Zygosaccharomyces rouxii,
                    Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
                    lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
                    angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
                    Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
                    5 kb were prepared and both extremities were sequenced. See
                    keywords for description of this sequence and for the sequence of
                    the other extremity of this insert.
FEATURES
    source
        1..994
            /organism="Zygosaccharomyces rouxii"
            /mol_type="genomic DNA"
            /strain="CBS 732"
            /db_xref="taxon:4956"
            /clone="AR0AA004E02"
            /clone_lib="AR0AA"
            /note="end : T3"
            complement(<2..>964)
            /inference="non-experimental evidence, no additional
            details recorded"
            /note="similar to Saccharomyces cerevisiae ORF YLR399c [
            BDF1 ; sporulation protein ]"

misc_feature
    complement(<2..>964)
            /inference="non-experimental evidence, no additional
            details recorded"
            /note="similar to Saccharomyces cerevisiae ORF YLR399c [
            BDF1 ; sporulation protein ]"

```

## ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 994;  
 Best Local Similarity 87.0%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
 ||||| ||||| ||||| ||||| |||||  
 Db 921 GCAAGTTGAACGTAAATGCCTTT 899

## RESULT 34

DU760208 1043 bp DNA linear GSS 27-JAN-2006  
 LOCUS ASNG3054.b2 HF200\_10-06-02 uncultured marine microorganism  
 DEFINITION HF200\_10-06-02 genomic clone HF0200\_090F10, genomic survey  
 sequence.  
 ACCESSION DU760208  
 VERSION DU760208.1 GI:857770044  
 KEYWORDS GSS.  
 SOURCE uncultured marine microorganism HF200\_10-06-02  
 ORGANISM uncultured marine microorganism HF200\_10-06-02  
 unclassified sequences; environmental samples.  
 REFERENCE 1 (bases 1 to 1043)  
 AUTHORS DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,  
 Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.  
 and Karl,D.M.  
 TITLE Comparative genomics reveals ecological trends in stratified  
 microbial communities in the ocean's interior  
 JOURNAL Science (2006) In press  
 COMMENT Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,  
 Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson  
 and Edward DeLong  
 US DOE Joint Genome Institute  
 2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA  
 Tel: 617-253-5271  
 Fax: 617-253-2679  
 Email: PMRichardson@lbl.gov; delong@mit.edu  
 North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid  
 DNA library prepared from marine picoplankton in the less than 1.6  
 um, greater than 0.22 um fraction. Sample Date: 10/6/2002  
 Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C  
 Salinity: 35.04 psu Oxygen: 198.8 umol/kg  
 Class: fosmid ends.

## FEATURES

source  
 1..1043  
 /organism="uncultured marine microorganism HF200\_10-06-02"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:361147"  
 /clone="HF200\_090F10"  
 /cell\_type="marine picoplankton, less than 1.8 um, greater  
 than 0.22 um fraction"  
 /clone\_lib="HF200\_10-06-02"  
 /notes="Vector: pCifOS; North Pacific Subtropical Gyre  
 (Hawaii) picoplankton genomic fosmid DNA library prepared  
 from marine picoplankton in the less than 1.6 um, greater  
 than 0.22 um fraction. Picoplankton collected at 200 m  
 depth on 10/6/2002, Coordinates: 22.45 N, 158 W. Sample  
 Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m  
 Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8  
 umol/kg"

## ORIGIN

Query Match 72.8%; Score 18.2; DB 14; Length 1043;  
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;  
 Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTCG 25  
 ||||| ||||| ||||| ||||| |||||  
 Db 79 GCCAGNCNCGCCGAAGGCCTTTG 103



[illegible]

/lab host="DH10B (T1 phage-resistant)"	
/clone.lib="NCI_CGAP_SG2"	
/note="Organ: salivary gland; vector: pCMV-SPORT6; Site: 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."	
ORIGIN	
Query Match	72.0%; Score 18; DB 7; Length 938;
Best Local Similarity	100.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 GCAAGTCGAACGGAAGG 18 
Db	648 GCAAGTCGAACGGAAGG 665 
RESULT 38	
BX342644	994 bp mRNA linear EST 07-APR-2004
LOCUS	
DEFINITION	BX342644 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
ACCESSION	Homo sapiens cDNA clone CS0DL004YB13 5-PRIME, mRNA sequence.
VERSION	BX342644
KEYWORDS	BX342644.2 GI:46275066
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
JOURNAL	Hominidae; Homo.
COMMENT	1 (bases 1 to 994) Full-length cDNA libraries and normalization Unpublished (2001) On May 2, 2003 this sequence version replaced gi:30342105. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6269.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QP1&c=6269.f.
FEATURES	
source	1..994 Location/Qualifiers /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DL004YB13" /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /cell_line="RAMOS CELL LINE" /clone.lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN	
Query Match	72.0%; Score 18; DB 4; Length 994;
Best Local Similarity	75.0%; Pred. No. 1.7e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Qy	2 CAAGTCGAACGGAAGGCTTTCG 25 
Db	928 CAATCGAATTKAAGGCTCTCG 951 
RESULT 39	
BX342644	273 bp mRNA linear EST 13-FEB-1998
LOCUS	
DEFINITION	vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
ACCESSION	IMAGS:1161994 5', mRNA sequence.
VERSION	AA815626
KEYWORDS	AA815626.1 GI:2885222
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)
REFERENCE	The WashU-HMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAG Consortium (info@image.llnl.gov) for further information. MGI: 204085 Seq primer: mob.REGA+ET High quality sequence stop: 213. Location/Qualifiers 1..223 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGS:313469" /dev_stage="19.5 dpc total fetus" /lab_host="DH10B (ampicillin resistant)" /clone.lib="Soares mouse p3NMF19.5" /note="Vector: pT73D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACATCTGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Wayne State University)."
ORIGIN	
Query Match	71.2%; Score 17.8; DB 10; Length 223;
Best Local Similarity	90.5%; Pred. No. 1.7e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	2 CAAGTCGAACGGAAGGCTTT 22 
Db	42 CAAGTCGAACGGAAGGACTT 62 
RESULT 40	
AA815626	273 bp mRNA linear EST 13-FEB-1998
LOCUS	
DEFINITION	vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
ACCESSION	IMAGS:1161994 5', mRNA sequence.
VERSION	AA815626
KEYWORDS	AA815626.1 GI:2885222
SOURCE	EST.
ORGANISM	Mus musculus (house mouse)



fraction &gt; 1 kb"

## ORIGIN

Query Match 71.2%; Score 17.8; DB 4; Length 347;  
 Best Local Similarity 90.5%; Pred. No. 1.8e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
 |||||  
 Db 95 CAAGTCGAACGGAAGGCCTT 115  
 |||||

## RESULT 43

W65078 357 bp mRNA linear EST 10-JUN-1996  
 LOCUS me01d06.r1 Soares mouse embryo NBME13.5 14.5 Mus musculus cDNA  
 clone IMAGE:386219 5', mRNA sequence.

W65078  
 W65078.1 GI:1372728  
 EST.  
 Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 357)  
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
 Schellenberg,K., Streptoe,M., Tan,F., Underwood,K., Moore,B.,  
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
 Waterston,R.

TITLE The WashU-HMI Mouse EST Project  
 JOURNAL Unpublished (1996)  
 COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:238051

Seq primer: mob.REGA+ET

High quality sequence stop: 327.

## FEATURES

source

1..357  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone\_image="386219"

/sex="unknown"

/tissue\_type="embryo"

/dev\_stage="13.5-14.5dpc total fetus"

/lab\_host="DH10B"

/clone\_lib="Soares mouse embryo NBME13.5 14.5"

/note="Vector: pT7T3D-Paci; Site\_1: Not I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5,

TGTTACCAACTGAGTGGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT  
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
 State Univ., from 2]; double-stranded cDNA was ligated to  
 Eco RI adaptors (Pharmacia), digested with Not I and  
 cloned into the Not I and Eco RI sites of the modified  
 pT7T3 vector. Library went through one round of  
 normalization, and was constructed by Bento Soares and  
 M. Fatima Bonaldo."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 357;  
 Best Local Similarity 90.5%; Pred. No. 1.8e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
 |||||  
 Db 183 CAAGTCGAACGGAAGGCCTT 203  
 |||||

RESULT 44  
 CF425395/c  
 LOCUS

DEFINITION CF425395 384 bp mRNA linear EST 03-SEP-2003  
 lad53e02.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5',  
 similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A.;, mRNA  
 sequence.

CF425395

CF425395.1 GI:34438096

EST.

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (bases 1 to 384)  
 Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,  
 Ronko,I., Tsagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,  
 Waterston,R. and Wilson,R.  
 WashU Stem cell EST Project  
 Unpublished (2002)  
 COMMENT Contact: Jeff Gordon and Mike Lovett

## JOURNAL

## COMMENT

Washington University School of Medicine  
 1st strand of cDNA was synthesized with reverse transcriptase and  
 oligo(dT) beads, then cDNA was amplified by PCR using modified  
 SMART primers. The final cDNA was cloned in pAMP1 vector in  
 annealing reaction with Uracil DNA Glycosylase (UDG). Library  
 constructed by Y.Korshunova and M. Lovett. Library materials  
 provided by Mills JC & Gordon JI.

Putative full length read

vector to vector length is

Possible reversed clone: similarity on wrong strand

Seq primer: -4ORP from Gibco.

## FEATURES

source

1..384

/organism="Mus musculus"

/mol\_type="mRNA"

/db\_xref="taxon:10090"

/tissue\_type="Gastric Epithelial Progenitor"

/dev\_stage="adult"

/lab\_host="DH5alpha"

/clone\_lib="Gastric Epithelial Progenitor"

/note="Vector: pAMP1; This library was created from  
 laser-captured isthmal cells from tox176 transgenic mice.

1st strand of cDNA was synthesized with reverse  
 transcriptase and oligo(dT) beads, then cDNA was amplified  
 by PCR using modified SMART primers. The final cDNA was

cloned in pAMP1 vector in annealing reaction with Uracil  
 DNA Glycosylase (UDG). Library constructed by Y.Korshunova  
 and M. Lovett. Library materials provided by Mills JC &  
 Gordon JI."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 5; Length 384;

Best Local Similarity 90.5%; Pred. No. 1.9e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

|||||

Db 90 CAAGTCGAACGGAAGGCCTT 70

|||||

## RESULT 45

## LOCUS

AL363886 400 bp mRNA linear EST 04-AUG-2000

This clone is available royalty-free through LNL; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
 MG1:901645  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 418.  
 Location/Qualifiers  
 1. .419  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:137917"  
 /sex="male"  
 /tissue\_type="Thymus"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares thymus 2NBMT"  
 /note="Vector: pT73D-PacI; Site\_1: Not I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Not I - oligo(dT) primer  
 [5',  
 TGTTCACCAATCGAAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. RNA  
 provided by Dr. Bertrand Jordan. Library went through two  
 rounds of normalization, and was constructed by Bento  
 Soares and M.Fatima Bonaído."

ORIGIN

Query Match 71.2%; Score 17.8; DB 1; Length 419;  
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
 ||||| ||||| ||||| ||||| |||||  
 Db 367 CAAGTCGAACGGAAGGACTT 387

RESULT 47  
 A1713707

LOCUS  
 A1713707 420 bp mRNA linear EST 08-JUN-1999

DEFINITION  
 UI-R-AG1-aao-b-08-0-UI.s1 UI-R-AG1 Rattus norvegicus cDNA clone

ACCESSION  
 A1713707

VERSION  
 A1713707.1 GI:5017507

KEYWORDS  
 EST.

SOURCE  
 Rattus norvegicus (Norway rat)

ORGANISM  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE  
 1 (bases 1 to 420)  
 Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 Normalization and subtraction: two approaches to facilitate gene  
 discovery  
 Genome Res. 6 (9), 791-806 (1996)

AUTHORS  
 Title

JOURNAL  
 PUBMED  
 COMMENT

Contact: Soares, MB  
 Coordinated Laboratory for Computational Genomics  
 University of Iowa  
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: bento-soares@uiowa.edu

Oligo-dT track not found, Not I site shown in beginning of sequence  
 is likely internal to the message. cDNA Library Preparation: M.B.  
 Soares Lab Clone distribution: clones will be available through  
 Research Genetics ([www.resgen.com](http://www.resgen.com))  
 Seq primer: M13 Forward  
 POLA=No. Location/Qualifiers  
 1. .420  
 /organism="Rattus norvegicus"

FEATURES  
 source

```

/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-AGI-aao-b-08-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-AGI"
/notes="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
The UI-R-AGI library is a normalized library constructed
from 13 dpc rat ventricle. The tag is a string of 6
nucleotides present between the Not I site and the
oligo-dt track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Jim Lin, Department of
Biology, University of Iowa.
TAG_TISSUE=atrium at 16.5 dpc
TAG_LIB=UI-R-AGI
TAG_SEQ=GATTC"

```

## ORIGIN

```

Query Match      71.2%; Score 17.8; DB 1; Length 420;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CAAGTCGAACGGAAGGCCTT 22
|||||  |||||  |||||  |||||  |||||
Db      143 CAAGTCGAACGGAAGGCCTT 163

```

```

RESULT 48
AA818546
LOCUS

```

```

DEFINITION UI-R-A0-aw-f-05-0-UI.s1 UI-R-A0 Rattus norvegicus cDNA clone
UI-R-A0-aw-f-05-0-UI 3' similar to gb|L02529|RA1PRZ2H Rattus
norvegicus Drosophila polarity gene (frizzled) homologue mRNA,
complete cds, mRNA sequence.

```

```

ACCESSION AA818546
VERSION AA818546.1 GI:4228339
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)

```

```

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

```

```

1 (bases 1 to 424)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery

```

```

JOURNAL Genome Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT On Feb 17, 1998 this sequence version replaced gi:2889285.
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu

```

```

Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatima Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
ID=1776549
Seq primer: M13 Forward
POLYA=No.

```

```

FEATURES
source

```

```

1. .424
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clones="UI-R-A0-aw-f-05-0-UI"

```

```

/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-A0"
/notes="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
This library consists of a mixture of individually tagged
normalized libraries constructed from rat placenta, adult
lung, brain, liver, kidney, heart, spleen, ovary, and
muscle. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dt track which allows
identification of the library of origin of a clone within
the mixture."

```

## ORIGIN

```

Query Match      71.2%; Score 17.8; DB 1; Length 424;
Best Local Similarity 90.5%; Pred. No. 1.9e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 CAAGTCGAACGGAAGGCCTT 22
|||||  |||||  |||||  |||||  |||||
Db      143 CAAGTCGAACGGAAGGCCTT 163

```

```

RESULT 49
BU743860
LOCUS

```

```

DEFINITION BU743860 444 bp mRNA linear EST 21-APR-2003
mai49f01.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone
IMAGE:6449520 5', mRNA sequence.

```

```

ACCESSION BU743860
VERSION BU743860.1 GI:23691980
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

```

```

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

```

```

1 (bases 1 to 444)
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,
Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,
Ritter, E., Tsagaris, R., Ronko, I., Maguire, L., Kennedy, S.,
Bennett, J., Waterston, R. and Wilson, R.

```

```

NIEHS Mouse
Unpublished (2002)
Contact: McCarrey/Eddy NIEHS Mouse

```

```

NIEHS Mouse
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

```

```

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:2093832
Seq primer: -40RP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
1. .444
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="CD-1"
/clone_xref="taxon:10090"
/clones="IMAGE:6449520"
/sex="male"
/tissue_type="round spermatids, pooled from multiple mice"

```

```

/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/notes="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-BATTGCGACGAG-3'
and 5'-CTCGTCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UnizAP-XR) and resulting

```

```

FEATURES
source

```

```

1. .444
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="CD-1"
/clones="IMAGE:6449520"
/sex="male"
/tissue_type="round spermatids, pooled from multiple mice"

```

```

/dev_stage="60 day"
/lab_host="DH10B (phage-resistant)"
/clone_lib="McCarrey Eddy round spermatid"
/notes="Organ: testis; Vector: pBluescript SK+
(Stratagene); Site 1: XhoII; Site 2: EcoRI; cDNA oligo
dt-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTTT-3'] and
directionally cloned using 5' linkers 5'-BATTGCGACGAG-3'
and 5'-CTCGTCCG-3'. Size selection of >400bp material
gives average insert size ranging from 1-2 kb. Library was
mass excised (from lambda-UnizAP-XR) and resulting

```

single-stranded phagemids were prepped and transformed into DH10B. Library contains 98.5% recombinants.  
References: J. Androl. 20:635-639 and Gene 25:263-269.  
Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics); excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Institute of Environmental Health Sciences). Original lambda-based library is available through ATCC, catalog #63423."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 444;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTT 22  
|||||  
Db 12 CAAGTCGAACGGAAGGACTT 32

## RESULT 50

W47680 446 bp mRNA linear EST 12-SEP-1996  
LOCUS mc89h02.ri Soares mouse embryo NM013.5 14.5 Mus musculus cDNA  
DEFINITION clone IMAGE:355731 5', mRNA sequence.

ACCESSION W47680

VERSION W47680.1

KEYWORDS GI:1537643

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 446)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)

## TITLE

## JOURNAL

## COMMENT

On Sep 12, 1996 this sequence version replaced gi:1332776.  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:227531

Seq primer: -28M13 rev2 from Amersham

High quality sequence stop: 400.

## FEATURES

## source

1..446  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:355731"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse embryo NM013.5 14.5"  
/note="Vector: pTT73D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to

Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 446;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTT 22  
|||||  
Db 80 CAAGTCGAACGGAAGGACTT 100

## RESULT 51

## LOCUS

## DEFINITION

AI593186 473 bp mRNA linear EST 21-APR-1999  
IMAGE:1161994 5', mRNA sequence.

ACCESSION AI593186

VERSION AI593186.1

KEYWORDS GI:4602234

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
1 (bases 1 to 473)  
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)

## REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:627906

This read is a RESEQUENCE of a previously sequenced mouse clone  
This read has been verified (found to hit its original self in the correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 466.

## FEATURES

## source

1..473  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C3H"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1161994"  
/cell\_line="C2C12"  
/lab\_host="DH10B"  
/clone\_lib="Barstead mouse myotubes MPLRB5"  
/note="Vector: pTT73D-PacI; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTCGGAGCGCGCGCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AAATCGAGCTTGG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT73 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 1; Length 473;  
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
 |||||  
 Db 293 CAAGTCGAACGGAAGGCATT 313

RESULT 52  
 CN692701  
 LOCUS  
 DEFINITION E0326F01-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus  
 musculus cDNA clone NTA:E0326F01 IMAGE:30861468 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,  
 VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C.,  
 Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L.,  
 Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,  
 Nagaraja, R., Boheler, K.R., Taub, D., Hodess, R.J., Longo, D.L.,  
 Schlesinger, D., Keller, J., Klotz, E., Kelsce, G., Umezawa, A.,  
 Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,  
 D'Urso, M., Kelsce, J., Hide, W. and Ko, M.S.

TITLE  
 JOURNAL  
 COMMENT  
 Transcription analysis of mouse stem cells and early embryos  
 PLoS Biol. 1 (3), 410-419 (2003)  
 Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: cdna@lgsun.grc.nia.nih.gov  
 Plate: E0326 row: F column: 01  
 Seq primer: M13 Reverse  
 High quality sequence stop: 492  
 POLYA=No.

FEATURES  
 source  
 1..492  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="niaEST:E0326F01-5"  
 /clone="NIA:E0326F01 IMAGE:30861468"  
 /tissue\_type="whole embryo including extraembryonic  
 tissues at 10.5-days postcoitum"  
 /dev\_stage="E10.5"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse E10.5 whole embryo cDNA library  
 (Long)"  
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;  
 Site 2: NotI; Mouse cDNA project by the Laboratory of  
 Genetics, National Institute on Aging (NIA), Intramural  
 Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).  
 This is a long-transcript enriched cDNA library (Ref.  
 Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total  
 RNAs were extracted from a pool of 8 embryos at 10.5-days  
 postcoitum. Double-stranded cDNAs were synthesized with an  
 oligo(dT) primer [Invitrogen]:  
 5'-pGACTGATCTAGTCGAGCGCGCCCTTTT-3' from  
 2ug of total RNA, treated with T4 DNA polymerase, and  
 purified by ethanol-precipitation. The cDNAs were ligated  
 to Lona-linker Li-Sal4, purified by phenol/chloroform, and  
 separated from free linkers by Centricon 100. Then, the  
 cDNAs were amplified by long-range high fidelity PCR using  
 Ex Taq polymerase (Takara) with a primer Sal4-S. The

products were purified by phenol/chloroform and Centricon  
 100. The cDNAs were digested with SalI and NotI enzymes  
 and cloned into SalI/NotI site of pCMV-SPORT6 plasmid  
 vector. The DH10B E. coli host was transformed with the  
 ligation mixture by the standard chemical method. The  
 average insert size is about 3.4Kb. The library was  
 constructed by Yulan Piao."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 492;  
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
 |||||  
 Db 107 CAAGTCGAACGGAAGGCATT 127

RESULT 53  
 AA014214/c

LOCUS  
 DEFINITION  
 AA014214  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 500)  
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

TITLE  
 JOURNAL  
 COMMENT  
 The WashU-HHMI Mouse EST Project  
 Unpublished (1996)  
 Contact: Marra M/Mouse EST Project  
 WashU-HHMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:268250

Seq primer: mob.REGA+ET  
 High quality sequence stop: 477.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:442914"  
 /sex="unknown"  
 /tissue\_type="placenta"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse placenta 4NbMP13.5 14.5"  
 /note="Organ: placenta; Vector: pT73D-PacI; Site 1: Not  
 I; Site 2: EcoRI; 1st strand cDNA was primed with a Not I  
 - oligo(dT) primer [5',  
 TGTACCAATCTGAAGTGGGCGCGCGGAATAATTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M.Fatima Bonaldo."

FEATURES  
source

1..500  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:442914"  
 /sex="unknown"  
 /tissue\_type="placenta"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse placenta 4NbMP13.5 14.5"  
 /note="Organ: placenta; Vector: pT73D-PacI; Site 1: Not  
 I; Site 2: EcoRI; 1st strand cDNA was primed with a Not I  
 - oligo(dT) primer [5',  
 TGTACCAATCTGAAGTGGGCGCGCGGAATAATTTTTTTTTTTTTTTTTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified pT73 vector. Library  
 went through one round of normalization, and was  
 constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN



DB	RESULT 55 CG036380/c	CG036380	502 bp	DNA	linear	GSS 19-AUG-2003
	LOCUS	PULY377D	ZM 0.6_1.0 KB	Zea mays	genomic clone ZMMBTA0612H02,	
	DEFINITION		recombinant survey sequence			
		58 CAAGTCGAACCTGAAGGACTT 78				

VERSION	KEYWORDS	SOURCE	ORGANISM
CG036380.1	GI:33908536		
GSS.			
	Zea mays		
	Zea mays		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
REFERENCE	1 (bases 1 to 502)		
whitehouse	Quakerbush	Y	Var. Mays C. Waterhouse

TITLE	JOURNAL	COMMENT
Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUILV37TB Contact: Cathy Whitelaw TIGR		
7712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org		

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ORIGIN
FEATURES             source
    Location/Qualifiers
        1..502
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBtra0612H02"
            /clone_lib="ZM_0.6_1.0 kb"
            /notes="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                    Cot selected genomic DNA library"
Seq primer: TF
Class: sheared ends.
anna1: whiteflower91.01g
```

Query Match	71.2%	Score 17.8	DB 12	Length 502
Best Local Similarity	90.5%	Pred. No. 1.9e+03		
Matches	19	Conservative 0	Mismatches 2	Indels 0
Gaps	0			
QY	2	CAAGTCGAACGGAAAGCCCTT	22	
Db	431	CAAGTCGAACGAAAGGCCCTT	411	
LOCUS	BE863637			
DEFINITION	UI-M-BHO-ake-d-02-0-UI.r1 NIH BMAP M S1 Mus musculus cDNA clone			
ACCESSION	BE863637			
VERSION	BE863637.1			
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus			
	527 bp mRNA linear EST 29-SEP-2000			

REFERENCE	Sciurognathini; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 527)
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE	Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL	Genome Res. 6 (9), 791-806 (1996)
PUBMED	8889548
COMMENT	Contact: Chin, H National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890

Email: mst@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It  
should be noted that Bento Soares is generating a small number of  
additional specialized non-redundant arrays of BMAP cDNAs whose  
availability will be considered under appropriate and limited  
collaborative arrangements

Seq primer: M13 Reverse.

## FEATURES

source

Location/Qualifiers

1..527  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clones="UI-M-BH0-ake-d-02-0-UI"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH-BMAP\_M\_S1"  
/notes="Vector: pRT3D-PacI; Site\_1: Not I; Site\_2: Eco RI;  
The NIH BMAP\_M\_S1 library is a subtracted library derived  
from a mixture of normalized libraries from ten regions of  
the mouse brain (cerebellum, brain stems, olfactory bulbs,  
hypothalamus, cortex, amygdala, basal ganglia, pineal  
gland, striatum, hippocampus). The driver used for  
subtraction consisted of a pool of 20,000 cDNA clones  
obtained from non-normalized and normalized libraries of  
these ten regions of the mouse brain."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 527;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22

DB 83 CAAGTCGAACGGAAGGACTT 103

## RESULT 57

BQ569727

LOCUS

DEFINITION BQ569727 532 bp mRNA linear EST 19-JUN-2002  
clone gi135c11.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA

clone gi135c11.5', mRNA sequence.

ACCESSION BQ569727

VERSION BQ569727.1 GI:21473044

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 532)

Kachar,B

EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing

Unpublished (2002)

Contact: Kachar,B

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 135 row: C column: 11

Seq primer: M13Rpl reverse primer (ABI).

## FEATURES

source

Location/Qualifiers

1..532

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"  
/db\_xref="taxon:10090"  
/clone="gi135c11"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pbluescript"  
/notes="Organ: Organ of Corti; Vector: pbluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the Micro Fasttrack kit  
(catalog # KI593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 ug mRNA was  
reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
primed with the linker-primer and transcribed using  
Mooney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with Pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
with Xho I. The cDNA was sequentially size fractionated  
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)  
columns to enrich for cDNAs greater than 400bp and 1000  
bp, respectively. The cDNA was then directionally ligated  
to the Uni-Zap XR vector, which had been predigested with  
EcoR I and Xho I. The phagemid was packaged with Gigapack  
III Gold and, upon titration on Xli Blue MRF' cells, the  
yield of the phage library was estimated to be 11,100,000  
recombinants. Stratagene's ExAssist Interference  
resistance helper phage (catalogue # 211203) was adopted  
to rescue plasmid DNA from the phages. Upon plating of the  
rescued library, individual cDNA clones were selected and  
grown in 96-well, 2 ml growth plate. Plasmid DNA was  
purified from 200 ul of saturated culture with the  
Concert96(TM) plasmid purification kit (Invitrogen,  
Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the  
universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25x  
strength BigDye terminator sequencing chemistry (Applied  
Biosystems, Foster City, CA). Sequencing reactions were  
performed on MJ Tetrad thermal cyclers (MJ Research,  
Waltham, MA), and analyzed on 3700 automated capillary  
sequencers using POP5 polymer (Applied Biosystems, Foster  
City, CA). The frequency distribution of the library is  
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
genes are present in GenBank and have know function; 23%  
have hits in GenBank, but do not have assigned function;  
12% are uncharacterized ESTs and 20% are unidentified."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 532;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22

DB 334 CAAGTCGAACGGAAGGACTT 354

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RESULT 58
BF022607/c
LOCUS
DEFINITION
  BF022607 542 bp mRNA linear EST 29-DEC-2000
  uy51dl1.y1 NCI CGAP Lu30 Mus musculus cDNA clone IMAGE:3663093 5',
  similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA
  sequence.
ACCESSION
VERSION
  BF022607.1 GI:10753940
KEYWORDS
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 542)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
CONTACT: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Gilbert Smith, Ph.D.
  CNA Library Preparation: Life Technologies, Inc.
  CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  image.llnl.gov/image/html/iresources.shtml
MG1:1423861
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 461.
FEATURES
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    location/Qualifiers
      1..542
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        /mol_type="mRNA"
        /strain="Czech II"
        /db_xref="taxon:10090"
        /clone="IMAGE:3663093"
        /tissue_type="tumor, metastatic to mammary"
        /lab_host="DH10B"
        /clone_lib="NCI CGAP Lu30"
        /note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
        Site 2: SalI; transgenic model WNT-1, expression driven by
        MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
        dT. Library constructed by Life Technologies.
        Investigator providing samples: Gilbert Smith, NIH"
ORIGIN
  Query Match 71.2%; Score 17.8; DB 7; Length 542;
  Best Local Similarity 90.5%; Pred. No. 1.9e+03;
  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
  |||||
Db 135 CAAGTCGAACGGAAGGACTT 115

RESULT 59
AI603423
LOCUS
DEFINITION
  AI603423 543 bp mRNA linear EST 21-APR-1999
  UI-R-AC1-xu-b-09-0-UI.s1 UI-R-AC1 Rattus norvegicus cDNA clone
  UI-R-AC1-xu-b-09-0-UI 3', mRNA sequence.
ACCESSION
VERSION
  AI603423.1 GI:4612584
KEYWORDS
SOURCE
  Rattus norvegicus (Norway rat)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
  1 (bases 1 to 543)
REFERENCE
  1 (bases 1 to 543)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
JOURNAL
CONTACT: Robert Strausberg, Ph.D.
  Email: cgapbs-remail.nih.gov
  Tissue Procurement: Gilbert Smith, Ph.D.
  CNA Library Preparation: Life Technologies, Inc.
  CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  image.llnl.gov/image/html/iresources.shtml
MG1:1423861
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 461.
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        /strain="Sprague-Dawley"
        /db_xref="taxon:10116"
        /clone="UI-R-AC1-xu-b-09-0-UI"
        /dev_stage="adult"
        /lab_host="DH10B (Life Technologies)"
        /clone_lib="UI-R-AC1"
        /note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;
        The UI-R-AC1 library is a normalized library constructed
        from 16.5 dpc rat atrioventricular (AV) canal. The tag
        is a string of 5 nucleotides present between the Not I
        site and the oligo-dT track. The library was constructed
        as described by Bonaldo, Lennon and Soares, Genome
        Research 6: 791-806, 1996. Tissue provided by Jim Lin,
        Department of Biology, University of Iowa."
ORIGIN
  Query Match 71.2%; Score 17.8; DB 1; Length 543;
  Best Local Similarity 90.5%; Pred. No. 1.9e+03;
  Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22
  |||||
Db 143 CAAGTCGAACGGAAGGACTT 163

RESULT 60
AZ024985/c
LOCUS
DEFINITION
  AZ024985 566 bp DNA linear GSS 25-FEB-2000
  RPCI-23-386J13.TJ RPCI-23 Mus musculus genomic clone
  RPCI-23-386J13, genomic survey sequence.
ACCESSION
VERSION
  AZ024985.1 GI:7100369
KEYWORDS
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 566)
  Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
  Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de
  Jong,P. and Fraser,C.M.
  Mouse BAC End Sequences from Library RPCI-23
  Unpublished (1999)
  Other GSSs: RPCI-23-386J13.TV
  Contact: Shaying Zhao
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850, USA
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: szhao@tigr.org

```

AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

Bonaldo,M.F., Lennon,G. and Soares,M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
889548  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9585  
Email: [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Oligo-dT track not found, Not I site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: Clones will be available through  
Research Genetics ([www.resgen.com](http://www.resgen.com))  
Seq primer: M13 Forward.  
Location/Qualifiers  
1..543  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="UI-R-AC1-xu-b-09-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-AC1"  
/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;  
The UI-R-AC1 library is a normalized library constructed  
from 16.5 dpc rat atrioventricular (AV) canal. The tag  
is a string of 5 nucleotides present between the Not I  
site and the oligo-dT track. The library was constructed  
as described by Bonaldo, Lennon and Soares, Genome  
Research 6: 791-806, 1996. Tissue provided by Jim Lin,  
Department of Biology, University of Iowa."

FEATURES  
source

Location/Qualifiers  
1..543  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
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/clone="UI-R-AC1-xu-b-09-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-AC1"  
/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI;  
The UI-R-AC1 library is a normalized library constructed  
from 16.5 dpc rat atrioventricular (AV) canal. The tag  
is a string of 5 nucleotides present between the Not I  
site and the oligo-dT track. The library was constructed  
as described by Bonaldo, Lennon and Soares, Genome  
Research 6: 791-806, 1996. Tissue provided by Jim Lin,  
Department of Biology, University of Iowa."

ORIGIN

Query Match 71.2%; Score 17.8; DB 1; Length 543;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CAAGTCGAACGGAAGGCCTT 22  
|||||  
Db 143 CAAGTCGAACGGAAGGACTT 163  
RESULT 60  
AZ024985/c  
LOCUS  
DEFINITION  
AZ024985 566 bp DNA linear GSS 25-FEB-2000  
RPCI-23-386J13.TJ RPCI-23 Mus musculus genomic clone  
RPCI-23-386J13, genomic survey sequence.  
ACCESSION  
VERSION  
AZ024985.1 GI:7100369  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 566)  
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,  
Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de  
Jong,P. and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-386J13.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [szhao@tigr.org](mailto:szhao@tigr.org)

RESULT 60  
AZ024985/c

LOCUS  
DEFINITION  
AZ024985 566 bp DNA linear GSS 25-FEB-2000  
RPCI-23-386J13.TJ RPCI-23 Mus musculus genomic clone  
RPCI-23-386J13, genomic survey sequence.  
ACCESSION  
VERSION  
AZ024985.1 GI:7100369  
KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 566)  
Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,  
Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de  
Jong,P. and Fraser,C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-386J13.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: [szhao@tigr.org](mailto:szhao@tigr.org)

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

AI603423  
UI-R-AC1-xu-b-09-0-UI.s1 UI-R-AC1 Rattus norvegicus cDNA clone  
UI-R-AC1-xu-b-09-0-UI 3', mRNA sequence.  
AI603423  
AI603423.1 GI:4612584  
KEYWORDS  
SOURCE  
Rattus norvegicus (Norway rat)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
1 (bases 1 to 543)  
REFERENCE  
1 (bases 1 to 543)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL  
CONTACT: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Gilbert Smith, Ph.D.  
CNA Library Preparation: Life Technologies, Inc.  
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
MG1:1423861  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco  
High quality sequence stop: 461.  
FEATURES  
source  
location/Qualifiers  
1..542  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3663093"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu30"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; transgenic model WNT-1, expression driven by  
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([info@resgen.com](http://info@resgen.com)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 386 row: J column: 13  
 Seq primer: SP6  
 Class: BAC ends.

# FEATURES

Location/Qualifiers  
 1. .566  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-386J13"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

# ORIGIN

Query Match 71.2%; Score 17.8; DB 11; Length 566;  
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
 Db 417 CAAGTCGAACGGAAGGCCTT 397

RESULT 61  
 CN692527  
 LOCUS E0324C02-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus  
 DEFINITION musculus cDNA clone NIA:E0324C02 IMAGE:30861241 5', mRNA sequence.  
 CN692527  
 ACCESSION CN692527.1 GI:47461275  
 VERSION EST.  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Sharov,A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Faico,G., Martin,P.R., Stagg,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodes,R.J., Longo,D.L., Schlesinger,D., Keller,J., Klotz,E., Kelsoe,G., Umezawa,A., Vecovici,A.L., Rossant,J., Kunath,F., Hogan,B.L., Curcio,A., D'Urso,M., Kelsoe,J., Hide,W. and Ko,M.S.  
 TITLE Transcriptional analysis of mouse stem cells and early embryos  
 JOURNAL PLoS Biol. 1 (3), 410-419 (2003)  
 COMMENT Contact: Dawood B. Dudekula  
 Laboratory of Genetics  
 National Institute on Aging/National Institutes of Health  
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
 Email: [cdna@lgsun.grc.nia.nih.gov](mailto:cdna@lgsun.grc.nia.nih.gov)  
 Plate: E0324 row: C column: 02  
 Seq primer: M13 Reverse  
 High quality sequence stop: 571  
 POLYA-No.

# FEATURES

Location/Qualifiers  
 1. .571  
 /organism="Mus musculus"

/mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="niaEST:E0324C02-5"  
 /db\_xref="taxon:10090"  
 /clone="NIA:E0324C02 IMAGE:30861241"  
 /tissue\_type="whole embryo including extraembryonic tissues at 10.5-days postcoitum"  
 /dev\_stage="E10.5"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse E10.5 whole embryo cDNA library (Long)"  
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 8 embryos at 10.5-days postcoitum. Double-stranded cDNAs were synthesized with an oligo(dT) primer [Invitrogen: 5'-PGACTAGTCTTAGTCGAGCGGCCCTTTTCTTTT-3'] from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loner-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4Kb. The library was constructed by Yulan Piao."

# ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 571;  
 Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
 Db 107 CAAGTCGAACGGAAGGCCTT 127

RESULT 62  
 BE288370/c  
 LOCUS BE288370  
 DEFINITION 601094841F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3489299 5', mRNA sequence.  
 ACCESSION BE288370.1 GI:9168018  
 VERSION EST.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue procurement: Lothar Hennighausen Ph.D., Robin Humphreys  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: LLAM8530 row: a column: 12  
 High quality sequence stop: 577.

FEATURES  
source

Location/Qualifiers  
1. 577  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="mix FVB/N, C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3489299"  
/tissue\_type="tumor, gross tissue"  
/dev\_stages="7 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI CCAP Mam5"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

## ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 577;  
Best Local Similarity 90.5%; Pred. No. 1.9e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22

Db 202 CAAGTCGAACGGAAGGACTT 182

## RESULT 63

DN215604/c  
LOCUS DN215604 600 bp mRNA linear EST 28-FEB-2005  
DEFINITION MEST971.D01.77-1 UGA-ZmSAM-X22 Zea mays cDNA, mRNA sequence.  
ACCESSION DN215604  
VERSION DN215604.1 GI:60348631

## KEYWORDS

EST.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 600)  
Chen, H.D., Zhang, X., Zhou, R.L., Arias, L.A.C., Shendelman, J.M., Zazubovits, N., Borsuk, L.A., Emrich, S.J., Ashlock, D.A., Scanlon, M.J. and Schnable, P.S.

Expressed Sequence Tags from B73 Maize Shoot Apical Meristems

Unpublished (2004)

Contact: Patrick S. Schnable

Schnable Laboratory

Iowa State University

2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA

Tel: 515-294-0975

Fax: 515-294-5256

Email: schnable@iastate.edu.

Location/Qualifiers

1. 600

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="inbred B73"

/db\_xref="taxon:4577"

/tissue\_type="vegetative Shoot Apical Meristem (SAM) and

leaf primordia staged P1-P4"

/lab\_host="XLI-Blue"

/clone\_lib="UGA-ZmSAM-X22"

/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1:

EcoRI; Site 2: XhoI; This library was constructed by

Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and

leaf primordia staged P1-P4 from 14-17 day-after

germination seedlings were quickly dissected into dry ice

under a light microscope. Total RNA was isolated using

Trizol and mRNA was purified with Dynal Oligo-DT25.

ds-cDNA molecules were generated as follows. First-strand

cDNA was prepared from oligo-dT selected mRNA by priming

with an XhoI oligo-dT primer

(5'-GAGAGAGAGAGAGAGACTAGTCTCGAGTGTGTTTTTTTTTTTTTTT).

The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector.

The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XLI-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates.

Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria:

(-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle

contamination. After processing ~30% of the sequences contained a minimum of 10 Ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 9; Length 600;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22

Db 550 CAAGTCGAACGGAAGGCCTT 530

## RESULT 64

DR968997/c  
LOCUS DR968997 602 bp mRNA linear EST 03-AUG-2005  
DEFINITION ZM\_BFB090I18.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DR968997  
VERSION DR968997.1 GI:71771060

## KEYWORDS

EST.

## SOURCE

Zea mays

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 602)

Klm, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,

Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0090 row: I column: 18.

Location/Qualifiers

1. 602

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stages="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFB"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 602;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

|||||

Db 583 CAAGTCGAACGGAAGGCCTT 563

## RESULT 65

AW914801 613 bp mRNA linear EST 25-MAY-2000  
LOCUS EST346105 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone  
DEFINITION RGI8H48 5' end, mRNA sequence.

ACCESSION AW914801

VERSION AW914801.1

KEYWORDS GI:8080481

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 613)

Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.

Rat Genome Project: Generation of a Rat EST (RESt) Catalog & Rat Gene Index

Unpublished (1998)

Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0208

Email: nhlee@igrr.org

This clone is available through the ATCC, contact the ATCC

tel#703-365-2700 for further information

Seq primer: M13 Reverse.

## FEATURES

source

1. .613

Location/Qualifiers

/organism="Rattus sp."

/mol\_type="mRNA"

/db\_xref="taxon:10118"

/clone="RGI8H48"

/note="Organ: ovary; Vector: pT73pac; Site\_1: EcoRI;

Site\_2: NotI"

## ORIGIN

Query Match 71.2%; Score 17.8; DB 7; Length 613;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22

|||||

Db 61 CAAGTCGAACGGAAGGCCTT 81

## RESULT 66

BI648126

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 622)

AUTHORS NIH-MGC

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-x@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM1808

row: g

column: 11

High quality sequence stop: 605.

Location/Qualifiers

1. .622

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="129,C57BL/6J,FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:5318818"

/tissue\_type="tumor, gross tissue"

/dev\_stage="10 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP\_Mam3"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;

Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH

Reference for transgenic model: Xu et al., Nature Genetics

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

22, 37-43 (1999)."

Mammalia; Euthera; Euarchoptoglyres; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 635)  
AUTHORS Wistow G. and Tonarev, S.  
TITLE Expressed sequence tag analysis of mouse whole eye  
JOURNAL Unpublished (2004)  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov

Plate: 01 row: e column: 11  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. 635

## FEATURES

source

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL6J"  
/db\_xref="taxon:10090"  
/clone="jb01e11"  
/tissue\_type="whole eye"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/note="Organ: Eye; Vector: pSPORT1; Approximately 1mg total RNA was extracted from 100 adult mouse whole eyes. A directionally cloned cDNA library in the pSPORT1 vector (Invitrogen) was constructed at Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (http://www.lifetech.com/). First strand synthesis was carried out using a Not I primer-adaptor [5'-pGATCTAGTTCGACGCGCCGCTT]15-3'. cDNA was cloned in Not I/Sal I sites. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 9; Length 635;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
|||||  
Db 403 CAAGTCGAACGGAAGGCCTT 383

RESULT 68  
BI331633  
LOCUS BI331633  
DEFINITION 602983168F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5136040 5', mRNA sequence.

ACCESSION BI331633  
VERSION BI331633.1 GI:15016290  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Euarchoptoglyres; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 641)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM11334 row: g column: 17  
High quality sequence stop: 640.  
Location/Qualifiers  
1. 641

## FEATURES

source

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5136040"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP\_L19"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 641;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
|||||  
Db 206 CAAGTCGAACGGAAGGCCTT 226

## RESULT 69

CF897511

LOCUS

DEFINITION CF897511 641 bp mRNA linear EST 04-NOV-2003  
A0226805-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long,  
subtracted) Mus musculus cDNA clone NIA:A0226805 IMAGE:30730864 5',  
mRNA sequence.

ACCESSION

CF897511

VERSION

CF897511.1

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Euarchoptoglyres; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 641)

AUTHORS

Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.

TITLE

Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method

JOURNAL

Genome Res. 11 (9), 1553-1558 (2001)

PUBMED

11544199

COMMENT

Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: A0226 row: B column: 05  
Seq primer: M13 Reverse  
High quality sequence stop: 641  
POLYA-No.

Location/Qualifiers

1. 641

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL6"

/db\_xref="taxon:10090"

/clone="NIA:A0226805 IMAGE:30730864"

/sex="male"

/dev\_stage="embryonic day 8"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse Embryonic Germ Cell cDNA Library  
(Long, subtracted)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site\_1: SalI;

Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lqson.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. EG cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark C. Carter (NIH/NIA-IRP). EG cells were cultured at 37° C, 5% CO<sub>2</sub> in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10<sup>-7</sup> units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-TGACTAGTCTAGATCGAGCGCGCCCTTTTTTTTTT-3'] from 2.5 µg of total RNA, treated with T<sub>4</sub> DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Long-linker L-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at AISIS Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCMV-SPORTs plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo.

## ORIGIN

```

Query Match      71.2%; Score 17.8; DB 5; Length 641;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  CAAGTCGAACGGAAAGGCCTT  22
      |||||
Db  468 CAAGTCGAACCTGAAAGGACTT  488
      |||||

```

RESULT	70
DV169729/c	
LOCUS	DV169729
DEFINITION	ZM_BP00168P08.f_ZM_Bfb Zea mays cDNA 3', mRNA linear EST 04-OCT-2005
ACCESSION	DV169729
VERSION	DV169729.1 GI:76923942
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 643) Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE	Maize Full-length cDNA Project
COMMENT	Unpublished (2005) Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0168 row: P column: 08.

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FEATURES
source
    Location/Qualifiers
      1..643
        /organism="Zea mays"
        /mol_type="mRNA"
        /cultivar="B73"
        /db_xref="taxon:4577"
        /tissue type="mixed silks, husks, ears pollen, shoot

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## ORIGIN

Query Match	71.2%	Score 17.8;	DB 10;	Length 643;
Best Local Similarity	90.5%;	Pred. No. 2e+03;		
Matches 19; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2	CAAGTCGAACGGAAAGGCCTT	22	
Db	535	CAAGTGGAACGAAAAGGCCTT	515	

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RESULT 71
BF237353
LOCUS
DEFINITION
60205026F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4160215 5',
mRNA sequence.
647 bp mRNA linear EST 14-NOV-2000

ACCESSION
BF237353
VERSION
BF237353.1
KEYWORDS
GI:11151271
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 647)
REFERENCE
NTH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNAW9439 row: d column: 08
High quality sequence stop: 647.
Location/Qualifiers
1. 647
/organism="Mus musculus"
/mol type="mRNA"
FEATURES
source

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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4160215"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP_Lig"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match 71.2%; Score 17.8; DB 7; Length 647;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22
Db 530 CAAGTCGAACGGAAGGCCTT 550

RESULT 72
CF898433
LOCUS CF898433 651 bp mRNA linear EST 04-NOV-2003
DEFINITION A0239B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (Long, substracted) Mus musculus cDNA clone NIA:A0239B05 IMAGE:30732112 5', mRNA sequence.
ACCESSION CF898433
VERSION CF898433.1 GI:38165482
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 651)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
Genome Res. 11 (9), 1553-1558 (2001)
1154199
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: A0239 row: B column: 05
Seq primer: M13 Reverse
High quality sequence stop: 651
POLYA=No.

FEATURES
source
1..651
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL6"
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/db_xref="taxon:10090"
/clone="NIA:A0239B05 IMAGE:30732112"
/sex="male"
/dev_stages="embryonic day 8"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library (Long, substracted)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). EG cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37. C, 5% CO2 in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7 units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dt) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTT-3'] from 2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at AIGIN Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

 acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7 units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dt) primer [Invitrogen: 5'-pGACTAGTTCTAGATCGGAGCGCGCCCTTTT-3'] from 2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lona-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at AIGIN Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

ORIGIN
Query Match 71.2%; Score 17.8; DB 5; Length 651;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22
Db 468 CAAGTCGAACGGAAGGCCTT 488

RESULT 73
DV023955/c
LOCUS DV023955 680 bp mRNA linear EST 26-SEP-2005
DEFINITION ZM_BF0143008.f ZM_BFb Zea mays cDNA 3', mRNA sequence.
ACCESSION DV023955
VERSION DV023955.1 GI:76284387
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 680)
Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0143 row: O column: 08.
Location/Qualifiers
1..680
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_types="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stages="varies by tissue"
/clone_lib="DH10B T1 phage resistant"
/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, 15% ES cell-qualified FBS, 0.1mM non-essential amino

```

permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 680;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||  
Db 513 CAAGTGGACGAAAGGCCTT 493

## RESULT 74

CN525338  
LOCUS UI-M-HK0-cmw-p-08-0-UI.r1 NIH BMAP\_HK0 Mus musculus cDNA clone  
DEFINITION IMAGE:30623887 5', mRNA sequence. 682 bp mRNA linear EST 29-APR-2004

ACCESSION CN525338  
VERSION CN525338.1 GI:46852991  
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 682)

REFERENCE NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

COMMENT Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Jim Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

Location/Qualifiers

## FEATURES

source  
1. .682  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
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/tissue\_type="Upper Head"  
/dev\_stage="9.5 and 10.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_HK0"  
/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTCGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 682;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||  
Db 148 CAAGTCGAAGGAGGACTT 168

## RESULT 75

DT945027/c  
LOCUS ZM\_BFB0132B03.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
DEFINITION ZM\_BFB0132B03.f 685 bp mRNA linear EST 21-SEP-2005

ACCESSION DT945027  
VERSION DT945027.1 GI:76017857  
KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 685)

AUTHORS Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

TITLE Maize Full-length cDNA Project

JOURNAL Unpublished (2005)

COMMENT Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9385

Fax: 520 621 1259

Email: [yeisoo@genome.arizona.edu](mailto:yeisoo@genome.arizona.edu)

Plate: 0132 row: B column: 03.

Location/Qualifiers

## FEATURES

source

1. .685  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(<http://www.genome.arizona.edu/orders/>).

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 685;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||

Db 506 CAACTGGAACGGAAGGCCTT 486

## RESULT 76

CO429338  
LOCUS  
DEFINITION UI-M-HWO-crq-b-13-0-UI\_r1 NIH BMAP\_HWO Mus musculus cDNA clone  
IMAGE:30681540 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CO429338.1 GI:49675632  
EST.  
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 695)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

## FEATURES

## source

1. 695  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30681540"  
/tissue\_type="whole eye"  
/dev\_stage="newborn (1, 5, 15 days)"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP\_HWO"  
/note="Organ: Eye; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag between the Not I site and the polyA tail is AATAATTACG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 695;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||

Db 355 CAACTCGAACTGAAAGGACTT 375

## RESULT 77

BI649774  
LOCUS  
DEFINITION 603279966F1 NCI\_CGAP\_Mam3 Mus musculus cDNA clone IMAGE:5319904 5',  
mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BI649774  
BI649774.1 GI:15564010  
EST.  
Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 700)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>  
Plate: LLAM1811 Row: d Column: 17  
High quality sequence start: 62  
High quality sequence stop: 684.

## FEATURES

## source

1. 700  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="129,C57BL/6J,FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5319904"  
/tissue\_type="tumor, gross tissue"  
/dev\_stage="10 months"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Mam3"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 700;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAACTCGAACGGAAGGCCTT 22  
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Db 363 CAACTCGAACTGAAAGGACTT 383

## RESULT 78

DV541234/c

LOCUS DV541234 710 bp mRNA linear EST 25-OCT-2005  
 DEFINITION ZM\_BFb0235018.f ZM\_BFb Zea mays cDNA 3', mRNA sequence.  
 ACCESSION DV541234  
 VERSION DV541234.1 GI:78122850  
 KEYWORDS EST.  
 SOURCE Zea mays

## ORGANISM

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 710)  
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
 Zea Full-length cDNA Project

## TITLE

Maize Full-length cDNA Project

## JOURNAL

Unpublished (2005)

## COMMENT

Contact: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: yeisoo@genome.arizona.edu

Plate: 0235 row: O column: 18.  
 Location/Qualifiers

## FEATURES

source  
 1..710

/organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
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 tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM\_BFb"  
 /note="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site 2:  
 NotI; Zea Full length cDNA library (3530 library)  
 created by Invitrogen from multiple tissues; Organ: silks,  
 husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector.  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A)+ mRNA was  
 prepared by Invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Zea Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona  
 (http://www.genome.arizona.edu/orders/)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 710;  
 Best Local Similarity 90.5%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGACGAAAGGCCTT 22

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Db 565 CAAGTCGACGAAAGGCCTT 545

## RESULT 79

DT654257/c

## LOCUS

DT654257 711 bp mRNA linear EST 07-SEP-2005  
 DEFINITION ZM\_BFb0127110.f ZM\_BFb Zea mays cDNA 3', mRNA sequence.  
 ACCESSION DT654257  
 VERSION DT654257.1 GI:74246343  
 KEYWORDS EST.  
 SOURCE Zea mays

## ORGANISM

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

1 (bases 1 to 711)  
 Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
 Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
 Zea Full-length cDNA Project

## TITLE

Maize Full-length cDNA Project

## JOURNAL

Unpublished (2005)

## COMMENT

Contact: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259  
 Email: yeisoo@genome.arizona.edu

Plate: 0127 row: I column: 10.  
 Location/Qualifiers

## FEATURES

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 1..711

/organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
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 tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM\_BFb"  
 /note="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site 2:  
 NotI; Zea Full length cDNA library (3530 library)  
 created by Invitrogen from multiple tissues; Organ: silks,  
 husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector.  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A)+ mRNA was  
 prepared by Invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Zea Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona  
 (http://www.genome.arizona.edu/orders/)."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 711;  
 Best Local Similarity 90.5%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CAAGTCGACGAAAGGCCTT 22

|||||

Db 510 CAAGTCGACGAAAGGCCTT 490

## RESULT 80

DT945215/c

LOCUS DT945215 714 bp mRNA linear EST 21-SEP-2005  
 DEFINITION ZM\_BF0132F09.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
 ACCESSION DT945215  
 VERSION DT945215.1 GI:76018045  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 714)  
 Kim, H., Collura, K., Wisotzki, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.  
 Maize Full-length cDNA Project  
 Unpublished (2005)  
 Contact: Yeisoo Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259  
 Email: yeisoo@genome.arizona.edu  
 Plate: 0132 row: F column: 09.  
 Location/Qualifiers  
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 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
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 /tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="ZM BPb"  
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
 (http://www.genome.arizona.edu/orders/)."

ORIGIN  
 Query Match 71.2%; Score 17.8; DB 10; Length 714;  
 Best Local Similarity 90.5%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 CAAGTCGAACGGAAGGCCTT 22  
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 Db 513 CAAGTGAACGGAAGGCCTT 493

RESULT 81  
 BF099995

LOCUS BF099995 716 bp mRNA linear EST 19-OCT-2000  
 DEFINITION 601752156P1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:3980005 5', mRNA sequence.  
 ACCESSION BF099995  
 VERSION BF099995.1 GI:10882521  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 716)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: csapbs@mail.nih.gov  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: LLAM9174 row: o column: 14  
 High quality sequence stop: 670.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:3980005"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, virgin"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI\_CGAP Mam1"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN  
 Query Match 71.2%; Score 17.8; DB 7; Length 716;  
 Best Local Similarity 90.5%; Pred. No. 2e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 2 CAAGTCGAACGGAAGGCCTT 22  
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 Db 513 CAAGTCGAACGGAAGGCCTT 533

RESULT 82  
 BQ445033  
 LOCUS UI-M-ER0-bxp-o-13-0-UI.r1 NIH\_BMAP\_ER0 Mus musculus cDNA clone IMAGE:5711460 5', mRNA sequence.  
 ACCESSION BQ445033  
 VERSION BQ445033.1 GI:21248145  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 729)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: csapbs@mail.nih.gov  
 Tissue Procurement: Dr. James Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

#### FEATURES source

Seq primer: pYX-5.  
Location/Qualifiers  
1. .729  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:5711460"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 15.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH\_BMAP\_ER0"  
/note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;  
Site 2: Not I; The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured mRNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was size selected according to mRNA size fraction,  
ligated with EcoR I adaptor, digested with Not I, and then  
cloned directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA  
tail, is GTGCGTGGAA. This library was created for the  
University of Iowa Mouse Brain Molecular Anatomy Project  
(BMAP): 'Gene Discovery in the Developing Mouse Nervous  
System', supported by National Institutes of Mental Health  
(NIMH), Hemin Chin, Ph.D., program coordinator."

#### ORIGIN

Query Match 71.2%; Score 17.8; DB 3; Length 729;  
Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| |||||

Db 142 CAAGTCGAACGGAAGGCCTT 162  
||||| ||||| ||||| |||||

#### RESULT 83

CO383984  
LOCUS  
DEFINITION AGENCOURT 26623469 NIH MGC 253 Rattus norvegicus cDNA clone  
IMAGE:7304949 5', mRNA sequence.

CO383984

CO383984.1 GI:49489807

EST.

SOURCE Rattus norvegicus (Norway rat)

#### ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 738)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical

College of Wisconsin

CDNA Library Preparation: Express Genomics

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM15342 row: f column: 19

High quality sequence stop: 612.

#### FEATURES

##### source

Location/Qualifiers  
1. .738  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7304949"  
/tissue\_type="Ovary - Brown Norway Line 3 Age 8 weeks.  
Tissues were snap-frozen and transferred in -70C. RNase  
free the entire procedure."  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH\_MGC\_253"  
/note="Organ: ovary; Vector: pExpress-1; Site 1: EcoRV;  
Site 2: NotI; RNA obtained from female animals at 8 wk  
old. Tissues were snap-frozen and kept at -80C for two  
days before RNA extraction and purification (Tri-reagent  
method). cDNA was primed using oligo-dT primer:  
5'-pGACTAGTTTGTAGTCGAGCGCCGCC(T)25-3' and cloned into  
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25Kb  
resulted in an average insert size of 1.5 kb. This primary  
library is normalized (non-normalized primary library is  
NIH MGC 252) and was constructed by Express Genomics  
(Frederick, MD). Note: this is a NIH\_MGC library."

#### ORIGIN

Query Match 71.2%; Score 17.8; DB 8; Length 738;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| |||||

Db 202 CAAGTCGAACGGAAGGCCTT 222  
||||| ||||| ||||| |||||

#### RESULT 84

##### LOCUS

DEFINITION B1414831 739 bp mRNA linear EST 14-AUG-2001

mRNA sequence.

B1414831

VERSION B1414831.1 GI:15175754

EST.

SOURCE Mus musculus (house mouse)

#### ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 739)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM1362 row: m column: 17

High quality sequence start: 23

High quality sequence stop: 739.

Location/Qualifiers

#### FEATURES

##### source

1. .739

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="Czech II"

/db\_xref="taxon:10090"

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QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
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BY732037			
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Conservative			
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Mismatches			
2;			
Indels			
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Gaps			
0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
RESULT 86			
BY732037			
LOCUS			
DEFINITION			
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Matches 19;			
Conservative			
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Mismatches			
2;			
Indels			
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Gaps			
0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
RESULT 86			
BY732037			
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DEFINITION			
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Conservative			
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Mismatches			
2;			
Indels			
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Db 552 CACGTCGAACGGAAGGCCTT 532			
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Mismatches			
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QY 2 CAAGTCGAACGGAAGGCCTT 22			
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Mismatches			
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QY 2 CAAGTCGAACGGAAGGCCTT 22			
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2;			
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BY732037			
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Mismatches			
2;			
Indels			
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Db 552 CACGTCGAACGGAAGGCCTT 532			
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BY732037			
LOCUS			
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Mismatches			
2;			
Indels			
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Gaps			
0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
RESULT 86			
BY732037			
LOCUS			
DEFINITION			
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Best Local			
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Conservative			
0;			
Mismatches			
2;			
Indels			
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0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
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BY732037			
LOCUS			
DEFINITION			
Query Match			
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Conservative			
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Mismatches			
2;			
Indels			
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0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
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BY732037			
LOCUS			
DEFINITION			
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Matches 19;			
Conservative			
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Mismatches			
2;			
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QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
RESULT 86			
BY732037			
LOCUS			
DEFINITION			
Query Match			
Best Local			
Matches 19;			
Conservative			
0;			
Mismatches			
2;			
Indels			
0;			
Gaps			
0;			
QY 2 CAAGTCGAACGGAAGGCCTT 22			
Db 552 CACGTCGAACGGAAGGCCTT 532			
RESULT 86			
BY732037			
LOCUS			
DEFINITION			
Query Match			
Best Local			
Matches 19;			
Conservative			
0;			
Mismatches			
2;			
Indels			

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

# FEATURES

source  
 1. 745  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="E860117P18"  
 /cell\_type="8 cells"  
 /dev\_stage="8 cells embryo"  
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## ORIGIN

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 Best Local Similarity 90.5%; Pred. No. 2e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
 |||||  
 Db 368 CAAGTCGAACGGAAGGACTT 388

# RESULT 87

DV942547/c  
 LOCUS 1000137-E05.T7-1 UGI-Reseq Zea mays cDNA, mRNA sequence. EST 05-DEC-2005  
 DEFINITION 746 bp  
 ACCESSION DV942547  
 VERSION DV942547.1 GI:83278539  
 KEYWORDS EST.  
 SOURCE Zea mays

## ORGANISM

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 746)  
 Zhou,R.L., Shendelman,J.M., Borsuk,L.A., Chen,H.D., Chen,Y.R. and Schnable,P.S.

# REFERENCE

AUTHORS Zhou,R.L., Shendelman,J.M., Borsuk,L.A., Chen,H.D., Chen,Y.R. and Schnable,P.S.  
 TITLE Resequencing Unigene I EST set  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Patrick S. Schnable  
 Schnable Laboratory  
 Iowa State University  
 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA  
 Tel: 515-294-0975  
 Fax: 515-294-5256  
 Email: [schnable@iastate.edu](mailto:schnable@iastate.edu)

# FEATURES

source  
 Location/Qualifiers  
 1. 746  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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## ORIGIN

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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
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 Db 613 CAAGTCGAACGGAAGGCCTT 593

# RESULT 88

DR794419/c  
 LOCUS 752 bp  
 DEFINITION ZM Bfb0015C05.f ZM\_Bfb Zea mays cDNA 3', mRNA sequence.  
 ACCESSION DR794419

VERSION DR794419.1 GI:71315610  
 KEYWORDS EST.  
 SOURCE Zea mays

# ORGANISM

Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogoneae; Zea.

# REFERENCE

AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.  
 TITLE Maize Full-length cDNA Project  
 JOURNAL Unpublished (2005)  
 COMMENT Contact: Yeisoo Yu

## Arizona Genomics Institute

The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259

Email: [Yeisoo@genome.arizona.edu](mailto:Yeisoo@genome.arizona.edu)  
 Plate: 0015 row: C column: 05.

## FEATURES

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 /mol\_type="mRNA"  
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 /clone\_lib="ZM Bfb"  
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

## ORIGIN

Query Match 71.2%; Score 17.0; DB 10; Length 752;



Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	2	CAAGTCGAACGGAAGGCCTT 22 	22
Db	583	CAAGTGGAAACGGAAGGCCTT 563 	563
RESULT 89			
DV164476/c			
LOCUS	DV164476	753 bp	mRNA linear EST 04-OCT-2005
DEFINITION	ZM_BFB0160P07.f ZM_BFB Zea mays cDNA 3', mRNA sequence.		
ACCESSION	DV164476		
VERSION	DV164476.1 GI:76911873		
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	1 (bases 1 to 753)		
AUTHORS	Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.		
TITLE	Maize Full-length cDNA Project		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0160 row: P column: 07.		
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/dev_stage="varies by tissue"			
/lab_host="DH10B T1 phage resistant"			
/clone_lib="ZM_BFB"			
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Zea Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona ( <a href="http://www.genome.arizona.edu/orders/">http://www.genome.arizona.edu/orders/</a> )."			
ORIGIN			
Query Match	71.2%;	Score 17.8;	DB 10; Length 753;

Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	2	CAAGTCGAACGGAAGGCCTT 22 	22
Db	510	CAAGTGGAAACGGAAGGCCTT 490 	490
RESULT 90			
DR786717/c			
LOCUS	DR786717	777 bp	mRNA linear EST 27-JUL-2005
DEFINITION	ZM_BFB0003M18.f ZM_BFB Zea mays cDNA 3', mRNA sequence.		
ACCESSION	DR786717		
VERSION	DR786717.1 GI:71301364		
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	1 (bases 1 to 777)		
AUTHORS	Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.		
TITLE	Maize Full-length cDNA Project		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0003 row: M column: 18.		
FEATURES	Location/Qualifiers		
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/organism="Zea mays"			
/mol_type="mRNA"			
/cultivar="B73"			
/db_xref="taxon:4577"			
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"			
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/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Zea Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona ( <a href="http://www.genome.arizona.edu/orders/">http://www.genome.arizona.edu/orders/</a> )."			
ORIGIN			
Query Match	71.2%;	Score 17.8;	DB10; Length 777;

Best Local Similarity 90.5%; Pred. No. 2e+03; Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
QY	2	CAAGTCGAACGAAAGGCCTT 22 	22
Db	510	CAAGTGGAAACGAAAGGCCTT 490 	490
RESULT 90			
DR786717/c			
LOCUS	DR786717	777 bp	mRNA linear EST 27-JUL-2005
DEFINITION	ZM_BFB003M18.f ZM_BFB Zea mays cDNA 3', mRNA sequence.		
ACCESSION	DR786717		
VERSION	DR786717.1 GI:71301364		
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.			
REFERENCE	1 (bases 1 to 777)		
AUTHORS	Kim,H., Collura,K., Wisotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.		
TITLE	Maize Full-length cDNA Project		
JOURNAL	Unpublished (2005)		
COMMENT	Contact: Yeisoo Yu Arizona Genomics Institute The University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9585 Fax: 520 621 1259 Email: yeisoo@genome.arizona.edu Plate: 0003 row: M column: 18.		
FEATURES	Location/Qualifiers		
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	/mol_type="mRNA"		
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	/dev_stage="varies by tissue"		
	/lab_host="DH10B T1 phage resistant"		
	/clone_lib="ZM BFB"		
	/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Zea Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona ( <a href="http://www.genome.arizona.edu/orders/">http://www.genome.arizona.edu/orders/</a> )."		
ORIGIN			
Query Match	71.2%;	Score 17.8;	DB 10; Length 777;

Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
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Db 535 CAAGTCGAACGGAAGGCCTT 515

RESULT 91  
DR954333/c  
LOCUS DR954333 777 bp mRNA linear EST 03-AUG-2005  
DEFINITION ZM BFB046F03.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DR954333  
VERSION DR954333.1 GI:71756396  
KEYWORDS EST.

SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 777)  
AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.  
TITLE Maize Full-length cDNA Project  
JOURNAL Unpublished (2005)  
COMMENT Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: Yeisoo@genome.arizona.edu  
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FEATURES  
source  
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/organism="Zea mays"  
/mol\_type="mRNA"  
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tips, leaf, root tips, whole seed, embryo)"  
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NotI; Maize Full length cDNA library (3530 library)  
created by Invitrogen from multiple tissues; Organ: silks,  
husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector,  
permitting clone movement to new vector backbones for  
expression in diverse host cells using recombination  
rather than restriction enzymes. poly(A)+ mRNA was  
prepared by Invitrogen, and equimolar amounts of RNA from  
each of the 12 tissue samples were mixed together for  
selection of mRNA with a 5' cap. After synthesis of cDNA,  
a normalization step was conducted against the mixture of  
RNA sources. Tissues prepared: 1. just emerging silks; 2.  
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
15 day old seedlings; all leaves with an expanded or  
partially expanded sheath were removed; 8. mature leaf  
tissue; 9. 0.5 cm long root tips from 15 day old  
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
embryo; 12. 17 dap endosperm and embryo. All of the  
sequenced clones in Maize Full-length cDNA Project will be  
archived at the University of Arizona. Clones, high  
density filters and amplified library can be ordered from  
the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 777;

Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| |||||  
Db 535 CAAGTCGAACGGAAGGCCTT 515

RESULT 92  
DV164117/c  
LOCUS DV164117 780 bp mRNA linear EST 04-OCT-2005  
DEFINITION ZM BFB0160H01.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DV164117  
VERSION DV164117.1 GI:76910962  
KEYWORDS EST.

SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 780)  
AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,  
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.  
TITLE Maize Full-length cDNA Project  
JOURNAL Unpublished (2005)  
COMMENT Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: Yeisoo@genome.arizona.edu  
Plate: 0160 row: H column: 01.

FEATURES  
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tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:  
NotI; Maize Full length cDNA library (3530 library)  
created by Invitrogen from multiple tissues; Organ: silks,  
husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector,  
permitting clone movement to new vector backbones for  
expression in diverse host cells using recombination  
rather than restriction enzymes. poly(A)+ mRNA was  
prepared by Invitrogen, and equimolar amounts of RNA from  
each of the 12 tissue samples were mixed together for  
selection of mRNA with a 5' cap. After synthesis of cDNA,  
a normalization step was conducted against the mixture of  
RNA sources. Tissues prepared: 1. just emerging silks; 2.  
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
15 day old seedlings; all leaves with an expanded or  
partially expanded sheath were removed; 8. mature leaf  
tissue; 9. 0.5 cm long root tips from 15 day old  
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
embryo; 12. 17 dap endosperm and embryo. All of the  
sequenced clones in Maize Full-length cDNA Project will be  
archived at the University of Arizona. Clones, high  
density filters and amplified library can be ordered from  
the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 780;

Best Local Similarity 90.5%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
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Db 510 CAAGTCGAACGGAAGGCCTT 490

## RESULT 93

CB953248

LOCUS

DEFINITION AGNCOURT\_13687210 NIH\_MGC\_176 Mus musculus cDNA clone

IMAGE:30304304 5', mRNA sequence.

ACCESSION CB953248

VERSION CB953248.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 808)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Michael Brownstein Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDCM76 row: d column: 09

High quality sequence stop: 477.

## FEATURES

source

Location/Qualifiers

1..808

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/clone="IMAGE:30304304"

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/clone\_lib="NIH MGC 176"

/note="Organ: kidney; Vector: pDNR-LIB; Site 1: SfII

(ggccattatggcc); Site 2: SfiI (ggcgctcgcc); cDNA made

by oligo-dT priming and directionally cloned. 5' and 3'

adaptors were used in cloning as follows:

5'-AAGCAGTGTATCAACGAGATGGCCATTACGCCGGG-3' and

5'-ATTCTAGAGCGGCGGCCCATG-dt(30)NN-3'. Full-length

enriched library was constructed using the Clontech

Creator SMART kit and size-selected to contain the 0.5 kb

size fraction. Library created in the laboratory of M.

Brownstein (NIH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 71.2%; Score 17.8; DB 4; Length 808;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||

Db 394 CAAGTCGAACGGAAGGCCTT 414  
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## RESULT 94

DR794420

LOCUS

DEFINITION ZM\_BF0015C05.r ZM\_BFb Zea mays cDNA 5', mRNA sequence.

ACCESSION DR794420

VERSION DR794420.1

KEYWORDS EST.

SOURCE Zea mays

## ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 816)

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,

Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu.Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Veisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: [veisoo@genome.arizona.edu](mailto:veisoo@genome.arizona.edu)

Plate: 0015 row: C column: 05.

## FEATURES

source

Location/Qualifiers

1..816

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="B73"

/db\_xref="taxon:4577"

/tissue\_type="mixed (silks, husks, ears, pollen, shoot

tips, leaf, root tips, whole seed, embryo)"

/dev\_stage="varies by tissue"

/lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFb"

/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:

NotI; Maize Full length cDNA library (3530 library)

created by Invitrogen from multiple tissues; Organ: silks,

husks, ears, pollen, shoot tips, leaf, root tips, whole

seed, embryo. This is a Gateway compatible vector,

permitting clone movement to new vector backbones for

expression in diverse host cells using recombination

rather than restriction enzymes. poly(A) + mRNA was

prepared by Invitrogen, and equimolar amounts of RNA from

each of the 12 tissue samples were mixed together for

selection of mRNA with a 5' cap. After synthesis of cDNA,

a normalization step was conducted against the mixture of

RNA sources. Tissues prepared: 1. just emerging silks; 2.

inner husks from ears of sample #1; 3. 20 dap aleurone; 4.

immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from

15 day old seedlings; all leaves with an expanded or

partially expanded sheath were removed; 8. mature leaf

tissue; 9. 0.5 cm long root tips from 15 day old

seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and

embryo; 12. 17 dap endosperm and embryo. All of the

sequenced clones in Maize Full-length cDNA Project will be

archived at the University of Arizona. Clones, high

density filters and amplified library can be ordered from

the University of Arizona

(http://www.genome.arizona.edu/orders/).

## ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 816;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||

Db 776 CAAGTCGAACGGAAGGCCTT 796  
||||| ||||| ||||| ||||| |||||

## RESULT 95

DV164477

LOCUS

DEFINITION ZM\_BF50160P07.r ZM\_BFb Zea mays cDNA 5', mRNA sequence.

ACCESSION DV164477

VERSION DV164477.1

KEYWORDS EST.

SOURCE Zea mays

```

ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 820)
AUTHORS        Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
               Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE          Maize Full-length cDNA Project
JOURNAL        Unpublished (2005)
COMMENT        Contact: Yeisoo Yu
               Arizona Genomics Institute
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 626 9585
               Fax: 520 621 1259
               Email: yeisoo@genome.arizona.edu
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                   /mol_type="mRNA"
                   /cultivar="B73"
                   /db_xref="taxon:4577"
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                   tips, leaf, root tips, whole seed, embryo)"
                   /dev_stage="varies by tissue"
                   /lab_host="DH10B T1 phage resistant"
                   /clone_lib="ZM_BFB"
                   /notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site 2:
                   NotI; Maize Full length cDNA library (3530 library)
                   created by Invitrogen from multiple tissues; Organ: silks,
                   husks, ears, pollen, shoot tips, leaf, root tips, whole
                   seed, embryo. This is a Gateway compatible vector,
                   permitting clone movement to new vector backbones for
                   expression in diverse host cells using recombination
                   rather than restriction enzymes. poly(A)+ mRNA was
                   prepared by Invitrogen, and equimolar amounts of RNA from
                   each of the 12 tissue samples were mixed together for
                   selection of mRNA with a 5' cap. After synthesis of cDNA,
                   a normalization step was conducted against the mixture of
                   RNA sources. Tissues prepared: 1. just emerging silks; 2.
                   inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
                   immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
                   2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
                   15 day old seedlings; all leaves with an expanded or
                   partially expanded sheath were removed; 8. mature leaf
                   tissue; 9. 0.5 cm long root tips from 15 day old
                   seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
                   embryo; 12. 17 dap endosperm and embryo. All of the
                   sequenced clones in Maize Full-length cDNA Project will be
                   archived at the University of Arizona. Clones, high
                   density filters and amplified library can be ordered from
                   the University of Arizona
                   (http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 820;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CAAGTCGAACGGAAGGCGCTT 22
        ||||| ||||| ||||| |||||
Db      776  CAAGTCGAACGGAAGGCGCTT 796

RESULT 96
DY361640
LOCUS      DY361640      824 bp      mRNA      linear      EST 09-FEB-2006
DEFINITION      ZO_Ed0007M16.r ZO__Ed Zingiber officinale cDNA clone ZO__Ed0007M16
               3'..mRNA sequence.
ACCESSION      DY361640
VERSION      DY361640.1 GI:87094856
KEYWORDS      EST.

ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 820)
AUTHORS        Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
               Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE          Maize Full-length cDNA Project
JOURNAL        Unpublished (2005)
COMMENT        Contact: Yeisoo Yu
               Arizona Genomics Institute
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 626 9585
               Fax: 520 621 1259
               Email: yeisoo@genome.arizona.edu
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ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  AGTCGAACGGAAGGCGCTTTC 24
        || ||||| ||||| ||||| |||||
Db      337  AGACGAACGGAAGGCGCTTTC 357

RESULT 97
DR786718
LOCUS      DR786718      827 bp      mRNA      linear      EST 27-JUL-2005
DEFINITION      ZM_BFB003M18.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION      DR786718
VERSION      DR786718.1 GI:71301367
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 827)
AUTHORS        Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
               Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE          Maize Full-length cDNA Project
JOURNAL        Unpublished (2005)
COMMENT        Contact: Yeisoo Yu
               Arizona Genomics Institute
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 626 9585
               Fax: 520 621 1259
               Email: yeisoo@genome.arizona.edu
               Plate: 0003 row: M column: 18.
               Location/Qualifiers
                 1..827
                   /organism="Zea mays"
                   /mol_type="mRNA"
                   /cultivar="B73"
                   /db_xref="taxon:4577"

FEATURES
source
1..824
/organism="Zingiber officinale"
/mol_type="mRNA"
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/db_xref="taxon:94328"
/clone="ZO__Ed0007M16"
/tissue_type="rhizome"
/lab_host="TJC 121"
/clone_lib="ZO__Ed"
/notes="Vector: pBluescriptII-SK-; Site_1: EcoRI; Site_2:
XhoI; Greenhouse, soil grown"

ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  AGTCGAACGGAAGGCGCTTTC 24
        || ||||| ||||| ||||| |||||
Db      337  AGACGAACGGAAGGCGCTTTC 357

RESULT 97
DR786718
LOCUS      DR786718      827 bp      mRNA      linear      EST 27-JUL-2005
DEFINITION      ZM_BFB003M18.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION      DR786718
VERSION      DR786718.1 GI:71301367
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 827)
AUTHORS        Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
               Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE          Maize Full-length cDNA Project
JOURNAL        Unpublished (2005)
COMMENT        Contact: Yeisoo Yu
               Arizona Genomics Institute
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 626 9585
               Fax: 520 621 1259
               Email: yeisoo@genome.arizona.edu
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FEATURES
source
1..827
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SOURCE      Zingiber officinale
ORGANISM      Zingiber officinale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
Zingiberaceae; Zingiber.
REFERENCE      1 (bases 1 to 824)
AUTHORS        Ma,X.Q., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
TITLE          Comparative Analysis of Expressed Sequence Tags from Different
               Organs of Ginger and Turmeric. Insights into Specialized Metabolism
               in Traditional Medicinal Plants
JOURNAL        Unpublished (2006)
COMMENT        Contact: David R. Gang
               Department of Plant Sciences
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 621 7154
               Fax: 520 621 7186
               Email: gang@ag.arizona.edu
               Plate: 0007 row: M column: 16.
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                   /notes="Vector: pBluescriptII-SK-; Site_1: EcoRI; Site_2:
                   XhoI; Greenhouse, soil grown"

ORIGIN
Query Match      71.2%; Score 17.8; DB 10; Length 824;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4  AGTCGAACGGAAGGCGCTTTC 24
        || ||||| ||||| ||||| |||||
Db      337  AGACGAACGGAAGGCGCTTTC 357

RESULT 97
DR786718
LOCUS      DR786718      827 bp      mRNA      linear      EST 27-JUL-2005
DEFINITION      ZM_BFB003M18.r ZM_BFB Zea mays cDNA 5', mRNA sequence.
ACCESSION      DR786718
VERSION      DR786718.1 GI:71301367
KEYWORDS      EST.
SOURCE      Zea mays
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 827)
AUTHORS        Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
               Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
TITLE          Maize Full-length cDNA Project
JOURNAL        Unpublished (2005)
COMMENT        Contact: Yeisoo Yu
               Arizona Genomics Institute
               The University of Arizona
               Forbes Building Room 303, Tucson, AZ 85721-0036, USA
               Tel: 520 626 9585
               Fax: 520 621 1259
               Email: yeisoo@genome.arizona.edu
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FEATURES
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1..827
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/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"

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tips, leaf, root tips, whole seed, embryo)"
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/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
/notes=vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/).

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## ORIGIN

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Query Match          71.2%; Score 17.8; DB 10; Length 827;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 774 CAAGTGGAAACGAAAGGCCTT 794

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RESULT 98
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LOCUS      ZM_BFB0087I16.r_ZM_BFB_Zea mays cDNA 5', mRNA linear EST 03-AUG-2005
DEFINITION
ACCESSION DR966931
VERSION    DR966931.1 GI:71768994
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 848)
Kim,H., Collura,K., Wissorski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
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Location/Qualifiers
1..848
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/cultivar="B73"
/db_xref="taxon:4579"

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## FEATURES

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tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
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/clone_lib="ZM_BFB"
/notes=vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector,
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A) + mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/).

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## ORIGIN

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Query Match          71.2%; Score 17.8; DB 10; Length 848;
Best Local Similarity 90.5%; Pred. No. 2e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 2 CAAGTCGAACGGAAGGCCTT 22
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Db 777 CAAGTGGAAACGAAAGGCCTT 797

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RESULT 99
DR876921
LOCUS      DT876921
DEFINITION DT876921 58666791 NIH_ZGC_9 Danio rerio cDNA clone IMAGE:8131516
5', mRNA sequence.
ACCESSION DT876921
VERSION    DT876921.1 GI:75846661
KEYWORDS   EST.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 851)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chi-Bin Chien
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM17503 row: c column: 02
High quality sequence stop: 701.

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FEATURES

source

Location/Qualifiers

1. 851

/organism="Danio rerio"

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/clones"IMAGE:8131516"

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/lab\_host="DH10B lona"

/clone\_lib="NIH\_ZGC\_9"

/note="Organ: eye; Vector: pME18S-FL3; Site 1: DraIII; Site 2: DraIII; 1st strand cDNA was primed with an oligo(dT) primer

[GGGCTGAAGAGCGCCTATGTGGCTTTTITTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [GGCCUACUG], digested and directionally cloned into distinct DraIII sites of the pME18S-FL3. Library was size selected for 1.0 kb, with a average insert size of ~1.2kb, and is not amplified. Library constructed by Yutaka Suzuki (University of Tokyo Institute of Medical Science). Custom primers recommended for sequencing: 5' end primer 5'-GGATGTCCTTTACTTCTA-3' and 3' end primer 5'-CGACTGCAGTCGACACA-3'. Note: This is a Zebrafish Gene Collection (ZGC) library"

ORIGIN

Query Match 71.2%; Score 17.8; DB 10; Length 851;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GCAAGTCGACGGAAGGCCT 21

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Db 688 GCAAGTCAGCGGAAGGCCT 708

RESULT 100

BI664538

LOCUS

DEFINITION 603290164F1 NCI\_CGAP Mam6 Mus musculus cDNA clone IMAGE:5324391 5', 856 bp mRNA linear EST 12-SEP-2001

BI664538

VERSION

KEYWORDS mRNA sequence.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLAM1822 row: 0 column: 16  
High quality sequence start: 2  
High quality sequence stop: 677.

FEATURES

source

Location/Qualifiers

1. 856

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/db\_xref="taxon:10090"

/clones"IMAGE:5324391"

/sex="female, virgin"

/tissue\_type="infiltrating ductal carcinoma"

ORIGIN

Query Match 71.2%; Score 17.8; DB 2; Length 856;

Best Local Similarity 90.5%; Pred. No. 2e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CAAGTCGAACGGAAGGCCTT 22

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Search completed: May 19, 2006, 07:05:41

Job time : 1696.99 secs

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OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 76.506 Seconds  
(without alignments)  
611.425 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacgaaaggcttctg 25

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

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Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents\_NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	25	100.0	25	US-09-738-274-21	Sequence 21, Appl
2	24	96.0	24	US-09-738-274-22	Sequence 22, Appl
3	21.8	87.2	1584	US-09-949-230A-1	Sequence 1, Appli
4	21.4	85.6	32	US-09-738-972-7	Sequence 7, Appli
5	21.4	85.6	32	US-09-738-972-14	Sequence 14, Appl
6	21	84.0	22	US-09-738-274-23	Sequence 23, Appl
7	21	84.0	1475	US-08-641-291A-92	Sequence 92, Appl
8	20.2	80.8	1437	US-10-085-871C-1	Sequence 1, Appli
9	20.2	80.8	1471	US-10-085-871C-2	Sequence 2, Appli
10	20.2	80.8	1488	US-10-756-683B-1	Sequence 1, Appli
11	20	80.0	1460	US-09-463-618A-1	Sequence 1, Appli
12	20	80.0	1460	US-10-062-777-1	Sequence 14, Appl
13	19.8	79.2	32	US-09-738-274-14	Sequence 14, Appl
14	19.8	79.2	1464	US-08-938-858-1	Sequence 1, Appli
15	19.8	79.2	1464	US-09-726-774-7	Sequence 7, Appli
16	19.8	79.2	36241	US-08-311-731A-134	Sequence 134, App
17	19.8	79.2	36470	US-08-311-731A-123	Sequence 123, App
18	19.8	79.2	4403765	US-09-103-840A-2	Sequence 2, Appli
19	19.8	79.2	4411529	US-09-103-840A-1	Sequence 1, Appli
20	19	76.0	23	US-09-738-274-27	Sequence 27, Appl
21	18	72.0	19	US-09-738-274-24	Sequence 24, Appl
22	18	72.0	23	US-07-915-922-1	Sequence 1, Appli
23	18	72.0	23	US-09-039-866-5	Sequence 5, Appli

24	17.2	68.8	1776	3	US-09-149-476-59	Sequence 59, Appl
25	17.2	68.8	1791	3	US-09-149-476-226	Sequence 226, App
c 26	17	68.0	417	3	US-09-252-991A-2715	Sequence 2715, Ap
27	17	68.0	2106	3	US-09-252-991A-6717	Sequence 6717, Ap
c 28	17	68.0	2427	3	US-09-252-991A-2899	Sequence 2899, Ap
29	17	68.0	2556	3	US-09-252-991A-3074	Sequence 3074, Ap
30	16.6	66.4	1569	2	US-08-632-470-47	Sequence 47, Appl
c 31	16.6	66.4	106418	3	US-09-949-016-13974	Sequence 13974, A
c 32	16.6	66.4	108341	3	US-09-949-016-16621	Sequence 16621, A
c 33	16.6	66.4	228851	3	US-09-949-016-13781	Sequence 13781, A
34	16.4	65.6	25	2	US-08-485-602-61	Sequence 61, Appl
35	16.4	65.6	25	2	US-08-757-180-60	Sequence 60, Appl
36	16.4	65.6	25	2	US-08-745-638-61	Sequence 61, Appl
37	16.4	65.6	1405	3	US-09-191-099-5	Sequence 5, Appli
38	16.4	65.6	1413	3	US-09-191-099-1	Sequence 1, Appli
39	16.4	65.6	1462	3	US-09-191-099-3	Sequence 3, Appli
40	16.4	65.6	1490	3	US-08-943-571-2	Sequence 2, Appli
41	16.4	65.6	1503	3	US-08-943-571-1	Sequence 1, Appli
42	16.2	64.8	601	3	US-09-949-016-69524	Sequence 69524, A
43	16.2	64.8	601	3	US-09-949-016-76807	Sequence 76807, A
44	16.2	64.8	637	3	US-09-533-559-7113	Sequence 7113, Ap
c 45	16.2	64.8	972	5	US-09-974-300-4677	Sequence 4677, Ap
c 46	16.2	64.8	1498	3	US-08-608-285A-45	Sequence 45, Appl
c 47	16.2	64.8	1498	3	US-09-557-800C-45	Sequence 45, Appl
c 48	16.2	64.8	1588	3	US-09-608-285A-53	Sequence 53, Appl
c 49	16.2	64.8	1588	3	US-09-557-800C-53	Sequence 53, Appl
c 50	16.2	64.8	2294	3	US-09-608-285A-49	Sequence 49, Appl
c 51	16.2	64.8	2294	3	US-09-557-800C-49	Sequence 49, Appl
52	16.2	64.8	2340	3	US-03-435-050A-215	Sequence 215, App
c 53	16.2	64.8	2371	3	US-09-608-285A-46	Sequence 46, Appl
c 54	16.2	64.8	2371	3	US-09-557-800C-46	Sequence 46, Appl
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c 56	16.2	64.8	2497	3	US-09-557-800C-51	Sequence 51, Appl
c 57	16.2	64.8	2693	3	US-09-608-285A-48	Sequence 48, Appl
c 58	16.2	64.8	2693	3	US-09-557-800C-48	Sequence 48, Appl
c 59	16.2	64.8	2762	3	US-09-608-285A-26	Sequence 26, Appl
c 60	16.2	64.8	2762	3	US-09-608-285A-52	Sequence 52, Appl
c 61	16.2	64.8	2762	3	US-09-240-639-1	Sequence 1, Appli
c 62	16.2	64.8	2762	3	US-09-370-265-26	Sequence 26, Appl
c 63	16.2	64.8	2762	3	US-09-557-800C-26	Sequence 26, Appl
c 64	16.2	64.8	2762	3	US-09-557-800C-52	Sequence 52, Appl
c 65	16.2	64.8	2762	3	US-09-370-625A-26	Sequence 26, Appl
c 66	16.2	64.8	2762	3	US-09-908-510A-1	Sequence 1, Appli
c 67	16.2	64.8	2762	3	US-09-905-744B-1	Sequence 1, Appli
c 68	16.2	64.8	2762	3	US-10-107-660-1	Sequence 1, Appli
c 69	16.2	64.8	2762	3	US-10-107-576-1	Sequence 1, Appli
c 70	16.2	64.8	2762	3	US-09-905-732B-1	Sequence 1, Appli
c 71	16.2	64.8	2762	3	US-09-905-743B-1	Sequence 1, Appli
c 72	16.2	64.8	2762	3	US-09-905-589-1	Sequence 1, Appli
c 73	16.2	64.8	2762	3	US-10-108-171A-1	Sequence 1, Appli
c 74	16.2	64.8	2805	3	US-09-608-285A-50	Sequence 50, Appl
c 75	16.2	64.8	2805	3	US-09-557-800C-50	Sequence 50, Appl
c 76	16.2	64.8	2882	3	US-09-608-285A-54	Sequence 54, Appl
c 77	16.2	64.8	2882	3	US-09-557-800C-54	Sequence 54, Appl
78	16	64.0	26	3	US-09-039-866-6	Sequence 6, Appli
79	16	64.0	26	3	US-09-738-274-28	Sequence 28, Appl
c 80	16	64.0	161	5	US-09-974-300-6612	Sequence 6612, Ap
c 81	16	64.0	248	3	US-09-621-976-17351	Sequence 17351, A
c 82	16	64.0	257	3	US-09-621-976-17350	Sequence 17350, A
83	16	64.0	455	3	US-09-640-211A-60	Sequence 60, Appl
84	16	64.0	455	3	US-09-640-211A-1958	Sequence 1958, Ap
85	16	64.0	460	3	US-09-252-991A-13661	Sequence 13661, A
86	16	64.0	470	3	US-09-270-767-13570	Sequence 13570, A
87	16	64.0	552	3	US-09-252-991A-6201	Sequence 6201, Ap
88	16	64.0	601	3	US-09-949-016-79652	Sequence 79652, A
c 89	16	64.0	601	3	US-09-949-016-201683	Sequence 201683,
90	16	64.0	834	3	US-09-134-001C-1552	Sequence 1552, Ap
c 91	16	64.0	855	3	US-09-252-991A-13763	Sequence 13763, A
c 92	16	64.0	990	3	US-09-252-991A-13865	Sequence 13865, A
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94	16	64.0	1430	3	US-09-927-904-6	Sequence 6, Appli
95	16	64.0	1430	3	US-10-401-337-6	Sequence 6, Appli
c 96	16	64.0	1532	3	US-09-118-324-1	Sequence 1, Appli

97	16	64.0	1698	3	US-09-252-991A-887	Sequence 887, App	170	15.6	62.4	12768	3	US-09-949-016-14316	Sequence 14316, A
98	16	64.0	1710	3	US-09-533-559-5520	Sequence 5520, App	c 171	15.6	62.4	35916	3	US-09-949-016-15957	Sequence 15957, A
99	16	64.0	2103	3	US-08-799-451-258	Sequence 258, App	c 172	15.6	62.4	38078	3	US-09-949-016-12429	Sequence 12429, A
100	16	64.0	9900	5	US-08-543-679A-2542	Sequence 2542, App	c 173	15.6	62.4	38084	3	US-09-949-016-16459	Sequence 16459, A
101	16	64.0	10514	5	US-08-543-679A-2543	Sequence 2543, App	174	15.6	62.4	105045	3	US-09-949-002-663	Sequence 663, App
102	16	64.0	12690	3	US-09-949-016-13799	Sequence 13799, A	175	15.6	62.4	107045	3	US-09-949-002-772	Sequence 772, App
c 103	16	64.0	36063	3	US-08-311-731A-140	Sequence 140, App	176	15.4	61.6	23	2	US-08-485-602-56	Sequence 56, Appl
104	16	64.0	119594	3	US-09-949-016-12080	Sequence 12080, A	177	15.4	61.6	23	2	US-08-757-180-55	Sequence 55, Appl
105	16	64.0	119601	3	US-08-949-016-15952	Sequence 15952, A	178	15.4	61.6	23	2	US-08-745-638-56	Sequence 56, Appl
c 106	16	64.0	139150	3	US-09-949-016-17398	Sequence 17398, A	179	15.4	61.6	27	2	US-08-485-602-53	Sequence 53, Appl
c 107	16	64.0	139577	3	US-09-949-016-12879	Sequence 12879, A	180	15.4	61.6	27	2	US-08-757-180-52	Sequence 52, Appl
108	16	64.0	784019	3	US-09-949-016-14033	Sequence 14033, A	181	15.4	61.6	27	2	US-08-745-638-53	Sequence 53, Appl
109	16	64.0	828152	3	US-09-949-016-12777	Sequence 12777, A	182	15.4	61.6	28	3	US-09-738-972-8	Sequence 8, Appl
110	15.8	63.2	375	3	US-09-489-039A-1391	Sequence 1391, App	c 183	15.4	61.6	28	3	US-09-738-972-15	Sequence 15, Appl
111	15.8	63.2	573	2	US-08-008-216-7	Sequence 7, Appl	184	15.4	61.6	108	3	US-09-270-767-6572	Sequence 6572, App
112	15.8	63.2	573	2	US-08-459-569-7	Sequence 7, Appl	185	15.4	61.6	108	3	US-09-270-767-22254	Sequence 22254, App
113	15.8	63.2	573	2	US-08-458-831-7	Sequence 7, Appl	186	15.4	61.6	289	3	US-09-513-999C-11630	Sequence 11630, A
114	15.8	63.2	585	3	US-09-902-540-3555	Sequence 3555, App	c 187	15.4	61.6	254	3	US-09-621-976-10015	Sequence 10015, A
115	15.8	63.2	601	3	US-09-949-016-82725	Sequence 82725, A	c 188	15.4	61.6	466	3	US-09-270-767-6474	Sequence 6474, App
116	15.8	63.2	601	3	US-09-949-016-82726	Sequence 82726, A	c 189	15.4	61.6	466	3	US-09-270-767-21756	Sequence 21756, A
117	15.8	63.2	601	3	US-09-949-016-82727	Sequence 82727, A	c 190	15.4	61.6	513	3	US-09-270-767-6571	Sequence 6571, App
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119	15.8	63.2	1074	2	US-08-459-569-6	Sequence 6, Appl	192	15.4	61.6	601	3	US-09-949-016-175492	Sequence 175492, A
120	15.8	63.2	1074	2	US-08-458-831-6	Sequence 6, Appl	193	15.4	61.6	601	3	US-09-949-016-175493	Sequence 175493, A
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122	15.8	63.2	1556	3	US-09-107-433-1056	Sequence 1056, App	c 195	15.4	61.6	825	3	US-09-976-594-437	Sequence 437, App
123	15.8	63.2	4029	3	US-08-270-767-163	Sequence 163, App	c 196	15.4	61.6	861	3	US-09-902-540-4420	Sequence 4420, App
124	15.8	63.2	4029	3	US-08-270-767-163	Sequence 163, App	c 197	15.4	61.6	1008	5	US-09-974-300-687	Sequence 687, App
125	15.8	63.2	4820	3	US-08-961-527-19	Sequence 19, App	198	15.4	61.6	1083	3	US-09-252-991A-8326	Sequence 8326, App
126	15.8	63.2	19019	3	US-09-902-540-1171	Sequence 1171, App	c 199	15.4	61.6	1179	3	US-09-252-991A-8523	Sequence 8523, App
127	15.8	63.2	21126	2	US-08-008-216-19	Sequence 19, App	c 200	15.4	61.6	1353	3	US-09-252-991A-8448	Sequence 8448, App
128	15.8	63.2	21126	2	US-08-459-569-19	Sequence 19, App	c 201	15.4	61.6	1366	3	US-09-149-476-49	Sequence 49, App
129	15.8	63.2	21126	2	US-08-458-831-19	Sequence 19, App	c 202	15.4	61.6	1377	3	US-09-927-504-5	Sequence 5, Appl
130	15.8	63.2	213456	3	US-09-820-007-3	Sequence 3, Appl	203	15.4	61.6	1377	3	US-10-401-337-5	Sequence 5, Appl
131	15.8	63.2	323820	3	US-09-949-016-14139	Sequence 14139, A	204	15.4	61.6	1414	3	US-09-191-099-6	Sequence 6, Appl
132	15.6	62.4	204	5	US-09-974-300-4209	Sequence 4209, App	205	15.4	61.6	1446	3	US-09-191-099-8	Sequence 8, Appl
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134	15.6	62.4	570	5	US-09-974-300-1034	Sequence 1034, App	207	15.4	61.6	1544	3	US-09-726-774-10	Sequence 10, Appl
135	15.6	62.4	601	3	US-09-949-016-79653	Sequence 79653, A	208	15.4	61.6	1551	3	US-09-023-655-697	Sequence 657, App
c 136	15.6	62.4	658	3	US-08-533-559-337	Sequence 337, App	209	15.4	61.6	2266	4	US-10-094-749-418	Sequence 418, App
137	15.6	62.4	768	3	US-09-270-767-1821	Sequence 1821, App	c 210	15.4	61.6	2894	3	US-09-949-016-1090	Sequence 1090, App
138	15.6	62.4	768	3	US-09-270-767-17103	Sequence 17103, A	c 211	15.4	61.6	2894	3	US-09-949-016-4962	Sequence 4962, App
139	15.6	62.4	897	3	US-09-328-352-1938	Sequence 1938, App	c 212	15.4	61.6	3152	3	US-09-221-1078-931	Sequence 931, App
c 140	15.6	62.4	900	3	US-09-252-991A-1168	Sequence 1168, App	c 213	15.4	61.6	4671	4	US-09-762-105A-26	Sequence 26, Appl
c 141	15.6	62.4	990	3	US-09-902-540-6736	Sequence 6736, App	c 214	15.4	61.6	5014	3	US-09-381-862-3	Sequence 3, Appl
c 142	15.6	62.4	1160	3	US-08-270-767-13705	Sequence 13705, A	c 215	15.4	61.6	5263	4	US-09-762-105A-27	Sequence 27, Appl
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144	15.6	62.4	1726	4	US-10-094-749-1510	Sequence 1510, App	c 217	15.4	61.6	30444	3	US-09-949-016-14937	Sequence 14937, A
145	15.6	62.4	1869	3	US-09-328-352-1510	Sequence 1510, App	c 218	15.4	61.6	37711	3	US-09-949-016-12832	Sequence 12832, A
c 146	15.6	62.4	2014	3	US-09-270-767-13561	Sequence 13561, A	c 219	15.4	61.6	37712	3	US-09-949-016-16704	Sequence 16704, A
c 147	15.6	62.4	2409	3	US-08-252-991A-1259	Sequence 1259, App	c 220	15.4	61.6	72455	3	US-09-949-016-13793	Sequence 13793, A
c 148	15.6	62.4	4009	3	US-08-902-540-941	Sequence 541, App	221	15.4	61.6	103792	3	US-09-949-016-13553	Sequence 13553, A
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151	15.6	62.4	12759	3	US-09-949-016-16301	Sequence 16301, A	224	15.4	61.6	111282	3	US-09-754-250-3	Sequence 3, Appl
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160	15.6	62.4	12768	3	US-08-949-016-14306	Sequence 14306, A	c 233	15.2	60.8	906	3	US-08-957-351-2	Sequence 2, Appl
161	15.6	62.4	12768	3	US-09-949-016-14307	Sequence 14307, A	c 234	15.2	60.8	906	3	US-08-957-351-6	Sequence 6, Appl
162	15.6	62.4	12768	3	US-09-949-016-14308	Sequence 14308, A	c 235	15.2	60.8	1017	3	US-08-957-351-5	Sequence 5, Appl
163	15.6	62.4	12768	3	US-09-949-016-14309	Sequence 14309, A	236	15.2	60.8	1023	3	US-09-543-681A-3911	Sequence 3911, App
164	15.6	62.4	12768	3	US-09-949-016-14310	Sequence 14310, A	237	15.2	60.8	1223	3	US-08-957-351-4	Sequence 4, Appl
165	15.6	62.4	12768	3	US-09-949-016-14311	Sequence 14311, A	c 238	15.2	60.8	1223	3	US-08-957-351-29	Sequence 29, Appl
166	15.6	62.4	12768	3	US-09-949-016-14312	Sequence 14312, A	c 239	15.2	60.8	1240	3	US-08-957-351-8	Sequence 8, Appl
167	15.6	62.4	12768	3	US-09-949-016-14313	Sequence 14313, A	c 240	15.2	60.8	1275	3	US-09-894-844-112	Sequence 112, App
168	15.6	62.4	12768	3	US-09-949-016-14314	Sequence 14314, A	c 241	15.2	60.8	1392	3	US-08-957-351-1	Sequence 1, Appl
169	15.6	62.4	12768	3	US-09-949-016-14315	Sequence 14315, A	242	15.2	60.8	1477	3	US-09-606-401B-1	Sequence 1, Appl



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243 15.2 60.8 1542 3 US-09-134-000C-2261 Sequence 2261, Ap
c 244 15.2 60.8 3405 4 US-10-154-419-35 Sequence 35, Appl
c 245 15.2 60.8 4064 3 US-10-209-792-1 Sequence 1, Appl
c 246 15.2 60.8 4614 3 US-09-364-707A-17 Sequence 17, Appl
c 247 15.2 60.8 4614 3 US-09-912-165-17 Sequence 17, Appl
c 248 15.2 60.8 4657 3 US-09-364-707A-18 Sequence 18, Appl
c 249 15.2 60.8 4657 3 US-09-912-165-18 Sequence 18, Appl
c 250 15.2 60.8 5916 3 US-09-826-630-9 Sequence 9, Appl
c 251 15.2 60.8 7507 4 US-08-975-763-1 Sequence 1, Appl
c 252 15.2 60.8 7745 4 US-10-154-419-33 Sequence 33, Appl
c 253 15.2 60.8 23951 3 US-09-902-540-1245 Sequence 1245, Ap
c 254 15.2 60.8 32155 3 US-08-311-731A-1 Sequence 1, Appl
c 255 15.2 60.8 35828 3 US-09-449-218D-17 Sequence 17, Appl
c 256 15.2 60.8 35828 3 US-09-668-529A-17 Sequence 17, Appl
c 257 15.2 60.8 35828 3 US-09-668-037A-17 Sequence 17, Appl
c 258 15.2 60.8 35828 3 US-09-668-021-17 Sequence 17, Appl
c 259 15.2 60.8 46819 3 US-09-453-702B-72 Sequence 72, Appl
c 260 15.2 60.8 46819 3 US-10-114-170-72 Sequence 72, Appl
c 261 15.2 60.8 47115 3 US-09-949-016-12278 Sequence 12278, A
c 262 15.2 60.8 47122 3 US-09-949-016-16520 Sequence 16520, A
c 263 15.2 60.8 50341 2 US-08-247-901C-1 Sequence 1, Appl
c 264 15.2 60.8 50341 2 US-09-075-904-1 Sequence 1, Appl
c 265 15.2 60.8 63860 3 US-09-949-016-15825 Sequence 15825, A
c 266 15.2 60.8 66933 3 US-09-544-378B-11 Sequence 11, Appl
c 267 15.2 60.8 66933 3 US-09-543-771B-11 Sequence 11, Appl
c 268 15.2 60.8 67088 4 US-09-531-120-186 Sequence 186, App
c 269 15.2 60.8 95223 4 US-09-531-120-188 Sequence 188, App
c 270 15.2 60.8 152132 3 US-09-949-016-13845 Sequence 13845, A
c 271 15.2 60.8 152145 3 US-09-949-016-12371 Sequence 12371, A
c 272 15.2 60.8 166698 3 US-09-949-016-16038 Sequence 16038, A
c 273 15.2 60.8 611587 4 US-09-531-120-209 Sequence 209, App
c 274 15 60.0 38 3 US-09-735-271-1390 Sequence 1390, App
c 275 15 60.0 208 3 US-09-513-999C-12870 Sequence 12870, A
c 276 15 60.0 335 3 US-09-270-767-9387 Sequence 9387, Ap
c 277 15 60.0 335 3 US-09-270-767-24669 Sequence 24669, A
c 278 15 60.0 564 3 US-09-533-559-1038 Sequence 1038, Ap
c 279 15 60.0 601 3 US-09-949-016-19418 Sequence 19418, A
c 280 15 60.0 601 3 US-09-949-016-19419 Sequence 19419, A
c 281 15 60.0 601 3 US-09-949-016-37443 Sequence 37443, A
c 282 15 60.0 601 3 US-09-949-016-49599 Sequence 49599, A
c 283 15 60.0 601 3 US-09-949-016-49600 Sequence 49600, A
c 284 15 60.0 601 3 US-09-949-016-145228 Sequence 145228,
c 285 15 60.0 601 3 US-09-949-016-163729 Sequence 163729,
c 286 15 60.0 601 3 US-09-949-016-167311 Sequence 167311,
c 287 15 60.0 601 3 US-09-949-016-195627 Sequence 195627,
c 288 15 60.0 601 3 US-09-949-016-200123 Sequence 200123,
c 289 15 60.0 678 3 US-08-998-416-1053 Sequence 1053, Ap
c 290 15 60.0 689 3 US-09-270-767-2314 Sequence 2314, Ap
c 291 15 60.0 689 3 US-09-270-767-17596 Sequence 17596, A
c 292 15 60.0 700 3 US-09-735-271-34 Sequence 34, Appl
c 293 15 60.0 700 3 US-09-735-271-35 Sequence 35, Appl
c 294 15 60.0 702 3 US-09-533-559-4619 Sequence 4619, Ap
c 295 15 60.0 762 4 US-09-297-648-5063 Sequence 5063, Ap
c 296 15 60.0 762 4 US-09-297-648-5065 Sequence 5065, Ap
c 297 15 60.0 765 3 US-09-620-312D-1089 Sequence 1089, Ap
c 298 15 60.0 770 3 US-09-303-518D-1385 Sequence 385, App
c 299 15 60.0 852 3 US-09-222-939-3 Sequence 3, Appl
c 300 15 60.0 921 3 US-09-902-540-6272 Sequence 6272, Ap

ALIGNMENTS

RESULT 1
US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc

RESULT 2
US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02, UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22
Query Match 100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTTTCG 25
| | | | | | | | | | | | | | | | | | | |
DB 1 GCAAGTCGAACGGAAGGCCTTTCG 25

RESULT 3
US-09-949-230A-1
; Sequence 1, Application US/09949230A
; Patent No. 6551591
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: New Antibiotics for Microbispora
; FILE REFERENCE: 262/095
; CURRENT APPLICATION NUMBER: US/09/949,230A

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02, UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22
Query Match 96.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTTTCG 25
| | | | | | | | | | | | | | | | | | | |
DB 1 CAAGTCGAACGGAAGGCCTTTCG 24

RESULT 3
US-09-949-230A-1
; Sequence 1, Application US/09949230A
; Patent No. 6551591
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: New Antibiotics for Microbispora
; FILE REFERENCE: 262/095
; CURRENT APPLICATION NUMBER: US/09/949,230A
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; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Microbispora corallina
; FEATURE:
; NAME/KEY: n
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
; NAME/KEY: misc feature
; LOCATION: (1350)..(1584)
; OTHER INFORMATION: Unsure
US-09-949-230A-1

Query Match      87.2%; Score 21.8; DB 3; Length 1584;
Best Local Similarity 92.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25
Db 124 GCAAGTCGACGGAAGGCCTTTCG 148

RESULT 4
US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match      85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 0.27;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 23
Db 1 GCAAGTCGAACGGAAGGCCTTTCG 23

RESULT 5
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match      85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 0.27;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 23
Db 32 GCAAGTCGAACGGAAGGCCTTTCG 10

RESULT 6
US-09-738-274-23
; Sequence 23, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      84.0%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTCG 25
Db 1 GTCGAACGGAAGGCCTTTCG 21

RESULT 7
US-08-641-291A-92
; Sequence 92, Application US/08641291A
; Patent No. 6037122
; GENERAL INFORMATION:
; APPLICANT: MABILAT Claude
; APPLICANT: RUINY Raymond
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERI
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
```

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release # 1.0, version # 1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/641,291A  
; FILING DATE: 30-APR-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bertrige, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 38273  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6400  
; TELEFAX: 703-836-2787  
; INFORMATION FOR SEQ ID NO: 92:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1475 base pairs  
; TYPE: nucleotide  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: rRNA  
US-08-641-291A-92

Query Match 84.0%; Score 21; DB 3; Length 1475;  
Best Local Similarity 90.5%; Pred. No. 1;  
Matches 19; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCT 21  
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Db 24 GCAAGUCGAACGGAAGGCCU 44

## RESULT 8

US-10-085-871C-1  
; Sequence 1, Application US/10085871C  
; Patent No. 6716615  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Chung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/085,871C  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1437  
; TYPE: DNA  
; ORGANISM: Saccharothrix 44442  
US-10-085-871C-1

Query Match 80.8%; Score 20.2; DB 3; Length 1437;  
Best Local Similarity 88.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
|||||  
Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

## RESULT 9

US-10-085-871C-2  
; Sequence 2, Application US/10085871C  
; Patent No. 6716615  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.

; APPLICANT: Chiu, Chung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/085,871C  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1471  
; TYPE: DNA  
; ORGANISM: Saccharothrix 45494  
US-10-085-871C-2

Query Match 80.8%; Score 20.2; DB 3; Length 1471;  
Best Local Similarity 88.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
|||||  
Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

## RESULT 10

US-10-756-683B-1  
; Sequence 1, Application US/10756683B  
; Patent No. 7022875  
; GENERAL INFORMATION:  
; APPLICANT: Hwang, Byung Kook  
; APPLICANT: Lee, Jung Yeop  
; TITLE OF INVENTION: THIOTRACIN AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR  
; FILE REFERENCE: 4228-102  
; CURRENT APPLICATION NUMBER: US/10/756,683B  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: KR 10-2003-0015628  
; PRIOR FILING DATE: 2003-03-13  
; PRIOR APPLICATION NUMBER: KR 10-2003-0015629  
; PRIOR FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1488  
; TYPE: DNA  
; ORGANISM: Lechevalieria aerocolonigenes  
US-10-756-683B-1

Query Match 80.8%; Score 20.2; DB 5; Length 1488;  
Best Local Similarity 88.0%; Pred. No. 2.5;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTCG 25  
|||||  
Db 42 GCAAGTCGAGCGGTAAGGCCCTTCG 66

## RESULT 11

US-09-463-618A-1  
; Sequence 1, Application US/09463618A  
; Patent No. 6368835  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION  
; FILE REFERENCE: 11142WO  
; CURRENT APPLICATION NUMBER: US/09/463,618A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: H10-166226  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1460  
; TYPE: DNA

US-09-463-618A-1  
; Sequence 1, Application US/09463618A  
; Patent No. 6368835  
; GENERAL INFORMATION:  
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD  
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION  
; FILE REFERENCE: 11142WO  
; CURRENT APPLICATION NUMBER: US/09/463,618A  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: H10-166226  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1460  
; TYPE: DNA

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; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t" or "t".
US-09-463-618A-1

Query Match      80.0%; Score 20; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 12
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match      80.0%; Score 20; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 3.2; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 13
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.U7
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; APPLICANT: Iversen, Patrick L.

; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match      79.2%; Score 19.8; DB 3; Length 32;
Best Local Similarity 91.3%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCCTTT 23
    |||||
Db 1 GCAAGTCGAACGGAAGGTCCT 23

RESULT 14
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; TITLE OF INVENTION: Specific Sequence of the Mycobacterium 16S rRNA Gene
; Patent No. 5985569
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; US-08-938-858-1

Query Match      79.2%; Score 19.8; DB 2; Length 1464;
Best Local Similarity 91.3%; Pred. No. 4; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGTCCT 42

RESULT 15
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
```

;; TITLE OF INVENTION: Antisense Antibacterial Method and  
;; FILE OF INVENTION: Composition  
;; FILE REFERENCE: 0450-0032.30  
;; CURRENT APPLICATION NUMBER: US/09/726,774  
;; PRIORITY FILING DATE: 2000-11-29  
;; PRIOR APPLICATION NUMBER: US 60/168,150  
;; PRIOR FILING DATE: 1999-11-29  
;; NUMBER OF SEQ ID NOS: 139  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 7  
;; LENGTH: 1464  
;; TYPE: DNA  
;; ORGANISM: Mycobacterium tuberculosis  
US-09-726-774-7

Query Match 79.2%; Score 19.8; DB 3; Length 1464;  
Best Local Similarity 91.3%; Pred. No. 4;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTT 23  
|||||  
Db 20 GCAAGTCGAACGAAAGGCTCT 42

## RESULT 16

US-08-311-731A-134/c  
; Sequence 134, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-I  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: C0044/7125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441  
; INFORMATION FOR SEQ ID NO: 134:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36241 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium leprae  
US-08-311-731A-134

Query Match 79.2%; Score 19.8; DB 3; Length 36241;  
Best Local Similarity 91.3%; Pred. No. 8.2;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGAACGAAAGGCCTTT 23  
|||||  
Db 3941 GCAAGTCGAACGAAAGGCTCT 3919

## RESULT 17

US-08-311-731A-123/c  
; Sequence 123, Application US/08311731A  
; Patent No. 6583266  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, DOUGLAS  
; APPLICANT: MAO, JEN-I  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES  
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 411  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.  
; STREET: 600 ATLANTIC AVENUE  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: USA  
; ZIP: 02210

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/311,731A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GATES, EDWARD R.  
; REGISTRATION NUMBER: 31,616  
; REFERENCE/DOCKET NUMBER: C0044/7125  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/720-3500  
; TELEFAX: 617/720-2441

; INFORMATION FOR SEQ ID NO: 123:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36470 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: MYCOBACTERIUM LEPRAE  
US-08-311-731A-123

Query Match 79.2%; Score 19.8; DB 3; Length 36470;  
Best Local Similarity 91.3%; Pred. No. 8.2;  
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGAAAGGCCTTT 23  
|||||  
Db 36188 GCAAGTCGAACGAAAGGCTCT 36166

## RESULT 18

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

```
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      79.2%; Score 19.8; DB 3; Length 4403765;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGACGGAAGGCCTTT 23
Db      1471427 GCAAGTCGACGGAAGGTCTCT 1471449

RESULT 19
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      79.2%; Score 19.8; DB 3; Length 4411529;
Best Local Similarity 91.3%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GCAAGTCGACGGAAGGCCTTT 23
Db      1471903 GCAAGTCGACGGAAGGTCTCT 1471925

RESULT 20
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 72.0%
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GAACGGAAGGCCTTTTCG 25
Db      1 GAACGGAAGGCCTTTTCG 18

RESULT 22
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
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; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match      76.0%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 CAAGTCGACGGAAGGCC 20
Db      1 CAAGTCGACGGAAGGCC 19

RESULT 21
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GAACGGAAGGCCTTTTCG 25
Db      1 GAACGGAAGGCCTTTTCG 18

RESULT 22
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
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COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/915,922  
FILING DATE: 19920717  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sias, Stacey R.  
REGISTRATION NUMBER: 32,630  
REFERENCE/DOCKET NUMBER: 8616  
TELEPHONE: (510) 814-2863  
TELEFAX: (510) 522-1285  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-915-922-1

Query Match 72.0%; Score 18; DB 2; Length 23;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGG 18  
|||||  
DB 6 GCAAGTCGAACGGAAGG 23

RESULT 23  
US-09-039-866-5  
Sequence 5, Application US/09039866  
Patent No. 6001611  
GENERAL INFORMATION:  
APPLICANT: Will, Stephen G.  
TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION  
TITLE OF INVENTION: PRIMERS  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Roche Molecular Systems  
STREET: 1080 U.S. Highway 202  
CITY: Branchburg  
STATE: New Jersey  
COUNTRY: United States  
ZIP: 08876  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/039,866  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Petry, Douglas A  
REGISTRATION NUMBER: 35,321  
REFERENCE/DOCKET NUMBER: 1023P  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-039-866-5

Query Match 72.0%; Score 18; DB 3; Length 23;

Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCAAGTCGAACGGAAGG 18  
|||||  
DB 6 GCAAGTCGAACGGAAGG 23  
RESULT 24  
US-09-149-476-59  
Sequence 59, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612





RESULT 25  
US-09-149-476-226  
Sequence 226 Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT APPLICATION NUMBER: US/09/149,476  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: PCT/US98/04493  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040,162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038,621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040,163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047,600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,584  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,500  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,587  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,492  
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EARLIER APPLICATION NUMBER: 60/047,598  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,613  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,582  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,596  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,612  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,632  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,601  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,580  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,568  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,314  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,569  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,311  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,671  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,674  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,669  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,312  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,313  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,672  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,315  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/056,886  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,877  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,889  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,893  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,630  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,878  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,662  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,872  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,882  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,637  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,903  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,888  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,879  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,880  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,894  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595



CLAS  
ATTOR

```
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16621
; LENGTH: 108341
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
US-09-949-016-16621

Query Match      66.4%; Score 16.6; DB 3; Length 108341;
Best Local Similarity 82.6%; Pred. No. 4.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCGCTTTC 24
        ||||| ||||| ||||| |||||
Db      94196 CAAGTCGAAGGAAGGCGATTTC 94174

RESULT 33
US-09-949-016-13781/c
; Sequence 13781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13781
; LENGTH: 228851
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(228851)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13781

Query Match      66.4%; Score 16.6; DB 3; Length 228851;
Best Local Similarity 82.6%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTTCG 25
        ||||| ||||| ||||| |||||
Db      132603 AAGTCCTACGGAAGGCGCTTTG 132581

RESULT 34
US-08-485-602-61
; Sequence 61, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; PROBES SPECIFIC FOR RIBOSOMAL RNA PRECURSORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; APPLICATION NUMBER: US 08/261,068
```

```
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
; ORGANISM: Mycobacterium habana
US-08-485-602-61

Query Match      65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      7 CGAACGGAAGGCGCTTTCG 25
        ||||| ||||| ||||| |||||
Db      1 CGAACGGAAGGCGCCUUCG 19

RESULT 35
US-08-757-180-60
; Sequence 60, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
```

```
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium simiae
;
US-08-757-180-60

Query Match 65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CGAACGGAAGCCCTTCG 25
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 36
US-08-745-638-61
; Sequence 61, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
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; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
;
US-08-745-638-61

Query Match 65.6%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 82;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 CGAACGGAAGCCCTTCG 25
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 37
US-09-191-099-5
; Sequence 5, Application US/09191099
; Patent No. 6096323
; GENERAL INFORMATION:
; APPLICANT: Walker, Richard L.
; APPLICANT: Read, Deryck H.
; APPLICANT: Hird, David W.
; APPLICANT: LeFebvre, Rance B.
; APPLICANT: Berry, Steven L.
; APPLICANT: Cullor, James S.
; APPLICANT: Lefler, Hank M.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)
; FILE REFERENCE: 023070-081110US
; CURRENT APPLICATION NUMBER: US/09/191,099
; CURRENT FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: US 08/943,571
; EARLIER FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Treponema sp.
; FEATURE:
; OTHER INFORMATION: 16S rRNA for spirochete 9-3143
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (42)
; OTHER INFORMATION: n = unknown
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (414)
; OTHER INFORMATION: n = unknown
;
US-09-191-099-5

Query Match 65.6%; Score 16.4; DB 3; Length 1405;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGG 18
Db 21 GCAAGTCGAACGGAAGG 38

RESULT 38
US-09-191-099-1
; Sequence 1, Application US/09191099
; Patent No. 6096323
; GENERAL INFORMATION:
; APPLICANT: Walker, Richard L.
; APPLICANT: Read, Deryck H.
; APPLICANT: Hird, David W.
; APPLICANT: LeFebvre, Rance B.
; APPLICANT: Berry, Steven L.
; APPLICANT: Cullor, James S.
; APPLICANT: Lefler, Hank M.
; APPLICANT: The Regents of the University of California
```

; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)  
; FILE REFERENCE: 023070-081110US  
; CURRENT APPLICATION NUMBER: US/09/191.099  
; CURRENT FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: US 08/943,571  
; EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1413  
; TYPE: DNA  
; ORGANISM: Treponema sp.  
; FEATURE:  
; OTHER INFORMATION: 16S rRNA for spirochete 2-1498  
; NAME/KEY: modified\_base  
; LOCATION: (43)  
; OTHER INFORMATION: n = unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (270)  
; OTHER INFORMATION: n = unknown  
; OTHER INFORMATION: n = unknown  
US-09-191-099-1

Query Match 65.6%; Score 16.4; DB 3; Length 1413;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGG 18  
|||||  
Db 25 GCAAGTCGAACGGAAGG 42

## RESULT 39

US-09-191-099-3  
; Sequence 3, Application US/09191099  
; Patent No. 6096323  
; GENERAL INFORMATION:  
; APPLICANT: Walker, Richard L.  
; APPLICANT: Read, Deryck H.  
; APPLICANT: Hird, David W.  
; APPLICANT: Lefebvre, Rance B.  
; APPLICANT: Berry, Steven L.  
; APPLICANT: Cullor, James S.  
; APPLICANT: Lefler, Hank M.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Vaccine Against Papillomatous Digital Dermatitis (PDD)  
; FILE REFERENCE: 023070-081110US  
; CURRENT APPLICATION NUMBER: US/09/191.099  
; CURRENT FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: US 08/943,571  
; EARLIER FILING DATE: 1997-10-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1462  
; TYPE: DNA  
; ORGANISM: Treponema sp.  
; FEATURE:  
; OTHER INFORMATION: 16S rRNA for spirochete 7-2009  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (274)  
; OTHER INFORMATION: n = unknown  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: (1115)  
; OTHER INFORMATION: n = unknown  
US-09-191-099-3

Query Match 65.6%; Score 16.4; DB 3; Length 1462;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGG 18  
|||||  
Db 29 GCAAGTCGAACGGAAGG 46

## RESULT 40

US-08-943-571-2  
; Sequence 2, Application US/08943571  
; Patent No. 6287575  
; GENERAL INFORMATION:  
; APPLICANT: Walker, Richard L.  
; APPLICANT: Read, Deryck H.  
; APPLICANT: Hird, David W.  
; APPLICANT: Lefebvre, Rance B.  
; APPLICANT: Berry, Steven L.  
; APPLICANT: Cullor, James S.  
; APPLICANT: Lefler, Hank M.  
; TITLE OF INVENTION: Vaccine Against Papillomatous Digital  
; TITLE OF INVENTION: Dermatitis (PDD)  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,571  
; FILING DATE: 03-OCT-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parent, Annette S.  
; REGISTRATION NUMBER: 42,058  
; REFERENCE/DOCKET NUMBER: 023070-081100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1490 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: rRNA  
; LOCATION: 1..1490  
; OTHER INFORMATION: /product= "16S rRNA"  
; OTHER INFORMATION: /note= "bovine Treponema spirochete  
; OTHER INFORMATION: strain 1-9185MED"  
US-08-943-571-2

Query Match 65.6%; Score 16.4; DB 3; Length 1490;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGG 18  
|||||  
Db 51 GCAAGTCGAACGGAAGG 68

## RESULT 41

US-08-943-571-1  
; Sequence 1, Application US/08943571  
; Patent No. 6287575  
; GENERAL INFORMATION:

APPLICANT: Walker, Richard L.  
APPLICANT: Read, Deryck H.  
APPLICANT: Hird, David W.  
APPLICANT: Lefebvre, Rance B.  
APPLICANT: Berry, Steven L.  
APPLICANT: Cullor, James S.  
APPLICANT: Lefler, Hank M.  
TITLE OF INVENTION: Vaccine Against Pappillomatous Digital  
TITLE OF INVENTION: Dermatitis (PDD)  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,571  
FILING DATE: 03-OCT-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Parent, Annette S.  
REGISTRATION NUMBER: 42,058  
REFERENCE/DOCKET NUMBER: 023070-081100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1503 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: rRNA  
LOCATION: 1..1503  
OTHER INFORMATION: /product= "16S rRNA"  
OTHER INFORMATION: /note= "bovine Treponema spirochete strain 2-1498"  
US-08-943-571-1  
Query Match 65.6%; Score 16.4; DB 3; Length 1503;  
Best Local Similarity 94.4%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GCAAGTCGACGGAAGG 18  
Db 51 GCAAGTCGACGGAAGG 68  
RESULT 42  
US-09-949-016-69524  
; Sequence 69524, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 1503  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7807  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-76807

PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 69524  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-69524  
Query Match 64.8%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 78.3%; Pred. No. 2.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 AAGTCGAACGGAAGGCTTTTCG 25  
Db 293 AAGTCCTAYGGAAGGCTTTTG 315  
RESULT 43  
US-09-949-016-76807  
; Sequence 76807, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 76807  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-76807  
Query Match 64.8%; Score 16.2; DB 3; Length 601;  
Best Local Similarity 78.3%; Pred. No. 2.1e+02;  
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 3 AAGTCGAACGGAAGGCTTTTCG 25  
Db 285 AAGTCCTACGGAAGGCTTTTG 307  
RESULT 44  
US-09-533-559-7113  
; Sequence 7113, Application US/09533559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjarke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7113





```
RESULT 48
US-09-608-285A-53/c
; Sequence 53, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-53

Query Match 64.8%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGTCCTGT 639

RESULT 49
US-09-557-800C-53/c
; Sequence 53, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447

Query Match 64.8%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 659 AAGTCGAACGGAATGTCCTGT 639

RESULT 50
US-09-608-285A-49/c
; Sequence 49, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-49

Query Match 64.8%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23
|||||
Db 191 AAGTCGAACGGAATGTCCTGT 171
```

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RESULT 51
US-09-557-800C-49/c
; Sequence 49, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1999-02-04
; PRIOR FILING DATE: 1999-02-04
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-49

Query Match      64.8%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      191 AAGTCGAACGGAATGCTCTGT 171

RESULT 52
US-09-495-050A-215
; Sequence 215, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED P
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR FILING DATE: 1998-11-18,318
; PRIOR FILING DATE: February 1, 1999
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: PERL Program
; SEQ ID NO 215
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6492505 2488060CT1
; NAME/KEY: unsure
; LOCATION: 2094
; OTHER INFORMATION: a, t, c, g, or other

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```

US-09-495-050A-215

Query Match      64.8%; Score 16.2; DB 3; Length 2340;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCCTT 21
Db      53 GCAAGTTGAAAGGAAGGCTT 73

RESULT 53
US-09-608-285A-46/c
; Sequence 46, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-46

Query Match      64.8%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 54
US-09-557-800C-46/c
; Sequence 46, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C

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; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 46  
; LENGTH: 2371  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-800C-46

Query Match 64.8%; Score 16.2; DB 3; Length 2371;  
Best Local Similarity 85.7%; Pred. No. 2.8e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 268 AAGTCGAACGGAATGCTCTGT 248

RESULT 55  
US-09-608-285A-51/c  
; Sequence 51, Application US/09608285A  
; Patent No. 6335013  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
; FILE REFERENCE: 28110/36570  
; CURRENT APPLICATION NUMBER: US/09/608,285A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 2497  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-608-285A-51

Query Match 64.8%; Score 16.2; DB 3; Length 2497;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 394 AAGTCGAACGGAATGCTCTGT 374

RESULT 56  
US-09-557-800C-51/c  
; Sequence 51, Application US/09557800C  
; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 51  
; LENGTH: 2497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-800C-51

Query Match 64.8%; Score 16.2; DB 3; Length 2497;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 394 AAGTCGAACGGAATGCTCTGT 374

RESULT 57  
US-09-608-285A-48/c  
; Sequence 48, Application US/09608285A  
; Patent No. 6335013  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
; FILE REFERENCE: 28110/36570  
; CURRENT APPLICATION NUMBER: US/09/608,285A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800

;; PRIOR FILING DATE: 2000-04-25  
;; PRIOR APPLICATION NUMBER: 09/481,238  
;; PRIOR FILING DATE: 2000-01-11  
;; PRIOR APPLICATION NUMBER: 09/370,265  
;; PRIOR FILING DATE: 1999-08-09  
;; PRIOR APPLICATION NUMBER: PCT/US99/16180  
;; PRIOR FILING DATE: 1999-07-16  
;; PRIOR APPLICATION NUMBER: 09/350,836  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: 09/273,447  
;; PRIOR FILING DATE: 1999-03-19  
;; PRIOR APPLICATION NUMBER: 09/244,444  
;; PRIOR FILING DATE: 1999-02-04  
;; PRIOR APPLICATION NUMBER: 09/122,449  
;; PRIOR FILING DATE: 1998-07-24  
;; PRIOR APPLICATION NUMBER: 09/118,205  
;; PRIOR FILING DATE: 1998-07-16  
;; NUMBER OF SEQ ID NOS: 60  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 48  
;; LENGTH: 2693  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-608-285A-48

Query Match 64.8%; Score 16.2; DB 3; Length 2693;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCTTT 23  
|||||  
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 58  
US-09-557-800C-48/c  
;; Sequence 48, Application US/09557800C  
;; Patent No. 6476211  
;; GENERAL INFORMATION:  
;; APPLICANT: Ford, John  
;; APPLICANT: Mulero, Julio  
;; APPLICANT: Yeung, George  
;; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
;; FILE REFERENCE: 28110/36457  
;; CURRENT APPLICATION NUMBER: US/09/557,800C  
;; CURRENT FILING DATE: 2000-04-25  
;; PRIOR APPLICATION NUMBER: 09/481,238  
;; PRIOR FILING DATE: 2000-01-11  
;; PRIOR APPLICATION NUMBER: 09/370,265  
;; PRIOR FILING DATE: 1999-08-09  
;; PRIOR APPLICATION NUMBER: PCT/US99/16180  
;; PRIOR FILING DATE: 1999-07-16  
;; PRIOR APPLICATION NUMBER: 09/350836  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: 09/273447  
;; PRIOR FILING DATE: 1999-03-19  
;; PRIOR APPLICATION NUMBER: 09/122449  
;; PRIOR FILING DATE: 1998-07-24  
;; PRIOR APPLICATION NUMBER: 09/244444  
;; PRIOR FILING DATE: 1999-02-04  
;; PRIOR APPLICATION NUMBER: 09/118,205  
;; PRIOR FILING DATE: 1998-07-16  
;; NUMBER OF SEQ ID NOS: 56  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 48  
;; LENGTH: 2693  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-557-800C-48

Query Match 64.8%; Score 16.2; DB 3; Length 2693;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 AAGTCGAACGGAAGGCTTT 23  
|||||  
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 59  
US-09-608-285A-26/c  
;; Sequence 26, Application US/09608285A  
;; Patent No. 6335013  
;; GENERAL INFORMATION:  
;; APPLICANT: Ford, John  
;; APPLICANT: Mulero, Julio  
;; APPLICANT: Yeung, George  
;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
;; FILE REFERENCE: 28110/36570  
;; CURRENT APPLICATION NUMBER: US/09/608,285A  
;; CURRENT FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: 09/583,231  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 09/557,800  
;; PRIOR FILING DATE: 2000-04-25  
;; PRIOR APPLICATION NUMBER: 09/481,238  
;; PRIOR FILING DATE: 2000-01-11  
;; PRIOR APPLICATION NUMBER: 09/370,265  
;; PRIOR FILING DATE: 1999-08-09  
;; PRIOR APPLICATION NUMBER: PCT/US99/16180  
;; PRIOR FILING DATE: 1999-07-16  
;; PRIOR APPLICATION NUMBER: 09/350,836  
;; PRIOR FILING DATE: 1999-07-09  
;; PRIOR APPLICATION NUMBER: 09/273,447  
;; PRIOR FILING DATE: 1999-03-19  
;; PRIOR APPLICATION NUMBER: 09/244,444  
;; PRIOR FILING DATE: 1999-02-04  
;; PRIOR APPLICATION NUMBER: 09/122,449  
;; PRIOR FILING DATE: 1998-07-24  
;; PRIOR APPLICATION NUMBER: 09/118,205  
;; PRIOR FILING DATE: 1998-07-16  
;; NUMBER OF SEQ ID NOS: 60  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 26  
;; LENGTH: 2762  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; NAME/KEY: CDS  
;; LOCATION: (148)..(1599)  
US-09-608-285A-26

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCTTT 23  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 60  
US-09-608-285A-52/c  
;; Sequence 52, Application US/09608285A  
;; Patent No. 6335013  
;; GENERAL INFORMATION:  
;; APPLICANT: Ford, John  
;; APPLICANT: Mulero, Julio  
;; APPLICANT: Yeung, George  
;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
;; FILE REFERENCE: 28110/36570  
;; CURRENT APPLICATION NUMBER: US/09/608,285A  
;; CURRENT FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-608-285A-52

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAAGGCCTTT 23  
|||||  
DB 659 AAGTCGAACGGAAATGCTCTGT 639

RESULT 61  
US-09-240-639-1/c  
; Sequence 1, Application US/09240639  
; Patent No.: 6350447  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischaut, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/09/240,639  
; CURRENT FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
US-09-240-639-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAAGGCCTTT 23  
|||||  
DB 659 AAGTCGAACGGAAATGCTCTGT 639

RESULT 62  
US-09-370-265-26/c  
; Sequence 26, Application US/09370265  
; Patent No. 6447771

; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE  
; FILE REFERENCE: 2811/35908  
; CURRENT APPLICATION NUMBER: US/09/370,265  
; CURRENT FILING DATE: 1999-08-09  
; EARLIER APPLICATION NUMBER: PCT/US99/16180  
; EARLIER FILING DATE: 1999-07-16  
; EARLIER APPLICATION NUMBER: 09/350,836  
; EARLIER FILING DATE: 1999-07-09  
; EARLIER APPLICATION NUMBER: 09/273,447  
; EARLIER FILING DATE: 1999-03-19  
; EARLIER APPLICATION NUMBER: 09/244,444  
; EARLIER FILING DATE: 1999-02-04  
; EARLIER APPLICATION NUMBER: 09/122,449  
; EARLIER FILING DATE: 1998-07-24  
; EARLIER APPLICATION NUMBER: 09/118,205  
; EARLIER FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (148)..(1599)  
US-09-370-265-26

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAAGGCCTTT 23  
|||||  
DB 659 AAGTCGAACGGAAATGCTCTGT 639

RESULT 63  
US-09-557-800C-26/c  
; Sequence 26, Application US/09557800C  
; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 2762

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-557-800C-26

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 64
US-09-557-800C-52/c
; Sequence 52, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/124449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-52

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 65
US-09-370-625A-26/c
; Sequence 26, Application US/09370625A
; Patent No. 6600032
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES
; FILE REFERENCE: 28110/35908
; CURRENT APPLICATION NUMBER: US/09/370,625A
; CURRENT FILING DATE: 1999-08-09
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; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-625A-26

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 66
US-09-908-510A-1/c
; Sequence 1, Application US/09908510A
; Patent No. 6759214
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120E
; CURRENT APPLICATION NUMBER: US/09/908,510A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-908-510A-1

Query Match      64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 67
US-09-905-744B-1/c
; Sequence 1, Application US/09905744B
; Patent No. 6780410
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; TITLE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120A
; CURRENT APPLICATION NUMBER: US/09/905,744B
; CURRENT FILING DATE: 2001-07-13
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; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
; OTHER INFORMATION:  
US-10-905-744B-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

## RESULT 68

US-10-107-660-1/c  
; Sequence 1, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
US-10-107-660-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

## RESULT 69

US-10-107-576-1/c  
; Sequence 1, Application US/10107576  
; Patent No. 6783959  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; TITLE OF INVENTION: ACIDS  
; FILE REFERENCE: 28110/36120H  
; CURRENT APPLICATION NUMBER: US/10/107,576  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
; OTHER INFORMATION:  
US-10-107-576-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

## RESULT 70

US-09-905-732B-1/c  
; Sequence 1, Application US/09905732B  
; Patent No. 6787328  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120B  
; CURRENT APPLICATION NUMBER: US/09/905,732B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
; OTHER INFORMATION:  
US-09-905-732B-1

Query Match 64.8%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

## RESULT 71

US-09-905-743B-1/c  
; Sequence 1, Application US/09905743B  
; Patent No. 6828423  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND  
; FILE REFERENCE: 28110/36120C  
; CURRENT APPLICATION NUMBER: US/09/905,743B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens

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;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-743B-1

Query Match          64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 72
US-09-905-589-1/c
; Sequence 1, Application US/09905589
; Patent No. 6884872
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905,589
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-905-589-1

Query Match          64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 73
US-10-108-171A-1/c
; Sequence 1, Application US/10108171A
; Patent No. 6899875
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE OF INVENTION: ACIDS
; FILE REFERENCE: 28110/36120F
; CURRENT APPLICATION NUMBER: US/10/108,171A
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
;

US-10-108-171A-1
Query Match          64.8%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 74
US-09-608-285A-50/c
; Sequence 50, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-50

Query Match          64.8%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCGCTTT 23
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 75
US-09-557-800C-50/c
; Sequence 50, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
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/ CURRENT FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: 09/481,238
/ PRIOR FILING DATE: 2000-01-11
/ PRIOR APPLICATION NUMBER: 09/370,265
/ PRIOR FILING DATE: 1999-08-09
/ PRIOR APPLICATION NUMBER: PCT/US99/16180
/ PRIOR FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: 09/350836
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/273447
/ PRIOR FILING DATE: 1999-03-19
/ PRIOR APPLICATION NUMBER: 09/122449
/ PRIOR FILING DATE: 1998-07-24
/ PRIOR APPLICATION NUMBER: 09/244444
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: 09/118,205
/ PRIOR FILING DATE: 1998-07-16
/ NUMBER OF SEQ ID NOS: 56
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 50
/ LENGTH: 2805
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
US-09-557-800C-50

Query Match          64.8%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 76
US-09-608-285A-54/c
; Sequence 54, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
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US-09-608-285A-54

Query Match          64.8%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 77
US-09-557-800C-54/c
; Sequence 54, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
US-09-557-800C-54

Query Match          64.8%; Score 16.2; DB 3; Length 2882;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AAGTCGAACGGAAGGCCTTT 23
   |||||
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 78
US-09-039-866-6
; Sequence 6, Application US/09039866
; Patent No. 6001611
; GENERAL INFORMATION:
; APPLICANT: Will, Stephen G.
; TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/039,866
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 2882
; TYPE: DNA
; ORGANISM: Homo sapiens
/
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,866
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 1023P
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-039-866-6

Query Match          64.0%; Score 16; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAA 16
   |||||
Db 9 GCAAGTCGACGGAAA 24

RESULT 79
US-09-738-274-28
; Sequence 28, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match          64.0%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGACGGAAGGCC 20
   |||||
Db 1 GTCGACGGAAGGCC 16

RESULT 80
US-09-974-300-6612/c
; Sequence 6612, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
```

```
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6612
; LENGTH: 161
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-6612

Query Match          64.0%; Score 16; DB 5; Length 161;
Best Local Similarity 79.2%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAAGCGCTTTTCG 25
   |||||
Db 81 CAAGGCAACGGCAATGCCTTTTCG 58

RESULT 81
US-09-621-976-17351/c
; Sequence 17351, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17351
; LENGTH: 248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17351

Query Match          64.0%; Score 16; DB 3; Length 248;
Best Local Similarity 79.2%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAAGCGCTTTTC 24
   |||||
Db 203 GCAAGCGGACAGAAAGCGCTTTTC 180

RESULT 82
US-09-621-976-17350/c
; Sequence 17350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 17350
; LENGTH: 257
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-17350

Query Match          64.0%; Score 16; DB 3; Length 257;
Best Local Similarity 79.2%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||||| |||||
Db 203 GCAAGCCGACACGAAAGCGCTTTC 180

RESULT 83
US-09-640-211A-60
; Sequence 60, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-60

Query Match          64.0%; Score 16; DB 3; Length 455;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||||| |||||
Db 20 GGAAGAGACCGGAAGGCGCTTTC 43

RESULT 84
US-09-640-211A-1958
; Sequence 1958, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1958

Query Match          64.0%; Score 16; DB 3; Length 455;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||||| |||||
Db 20 GGAAGAGACCGGAAGGCGCTTTC 43

RESULT 85
US-09-252-991A-13661
; Sequence 13661, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13661
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13661

Query Match          64.0%; Score 16; DB 3; Length 465;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||||| |||||
Db 399 GCAGTTGATCGAAGGCGCTTTC 422

RESULT 86
US-09-270-767-13570
; Sequence 13570, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13570
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13570

Query Match          64.0%; Score 16; DB 3; Length 470;
Best Local Similarity 79.2%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||| ||||| |||||
Db 260 GCAGCCCATCGGCAAGGCCATTC 283

RESULT 87
US-09-252-991A-6201
; Sequence 6201, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
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; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6201
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6201

Query Match          64.0%; Score 16; DB 3; Length 552;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
Db 44 CAGGCCGTCGGAAGGCCTTTCG 67

RESULT 88
US-09-949-016-79652
; Sequence 79652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79652
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-79652

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
Db 328 CAAAACGACCGGAATGCTTTTG 351

RESULT 89
US-09-949-016-201683/c
; Sequence 201683, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201683
; LENGTH: 601
```

```
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201683

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25
Db 228 CAAGTCGAATCGAAATTCCTTTGG 205

RESULT 90
US-09-134-001C-1552
; Sequence 1552, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1552
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1552

Query Match          64.0%; Score 16; DB 3; Length 834;
Best Local Similarity 79.2%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
Db 601 GTAACTCGAAGGAAAAAGCCTTTC 624

RESULT 91
US-09-252-991A-13763/c
; Sequence 13763, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13763
; LENGTH: 855
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13763

Query Match          64.0%; Score 16; DB 3; Length 855;
Best Local Similarity 79.2%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
Db 271 GCACGTTGATCGAAGAGGCCTTTC 248
```

RESULT 92  
US-09-252-991A-13865/c  
; Sequence 13865, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 13865  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13865

Query Match 64.0%; Score 16; DB 3; Length 990;  
Best Local Similarity 79.2%; Pred. No. 2.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTTTC 24  
Db 690 GCACGTTGATCGAAGAGGCCTTTC 667

RESULT 93  
US-09-311-170-1  
; Sequence 1, Application US/09311170  
; Patent No. 6121034  
; GENERAL INFORMATION:  
; APPLICANT: Laroche et al., Andre L.  
; TITLE OF INVENTION: Xylanase cxy1  
; FILE REFERENCE: xylanase cxy1  
; CURRENT APPLICATION NUMBER: US/09/311,170  
; CURRENT FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1269  
; TYPE: DNA  
; ORGANISM: Coniothyrium minitans  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1179)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (88)..(180)  
; OTHER INFORMATION: Cellulose-binding domain  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (181)..(273)  
; OTHER INFORMATION: hinge region  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (274)..(1179)  
; OTHER INFORMATION: catalytic domain  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (25)..(75)  
; OTHER INFORMATION: putative signal peptide  
US-09-311-170-1

Query Match 64.0%; Score 16; DB 3; Length 1269;  
Best Local Similarity 79.2%; Pred. No. 3.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTTCG 25  
Db 477 CACGTCGAACGGAAGGCTCGTCG 500  
RESULT 94  
US-09-927-904-6  
; Sequence 6, Application US/09927904  
; Patent No. 6558909  
; GENERAL INFORMATION:  
; APPLICANT: Jensen, Wayne A.  
; TITLE OF INVENTION: HAEMOBARTONELLA PCR METHODS AND MATERIALS  
; FILE REFERENCE: DI-6-C1-1  
; CURRENT APPLICATION NUMBER: US/09/927,904  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/398,577  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,987  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1430  
; TYPE: DNA  
; ORGANISM: Haemobartonella felis  
US-09-927-904-6

Query Match 64.0%; Score 16; DB 3; Length 1430;  
Best Local Similarity 79.2%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24  
Db 35 GCAAGTCGAACGAAGAGGGTTTAC 58

RESULT 95  
US-10-401-337-6  
; Sequence 6, Application US/10401337  
; Patent No. 6759531  
; GENERAL INFORMATION:  
; APPLICANT: Jensen, Wayne A.  
; TITLE OF INVENTION: HAEMOBARTONELLA PCR METHODS AND MATERIALS  
; FILE REFERENCE: DI-6-C1-1  
; CURRENT APPLICATION NUMBER: US/10/401,337  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US/09/927,904  
; PRIOR FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/398,577  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: 60/100,987  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 1430  
; TYPE: DNA  
; ORGANISM: Haemobartonella felis  
US-10-401-337-6

Query Match 64.0%; Score 16; DB 3; Length 1430;  
Best Local Similarity 79.2%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24  
Db 35 GCAAGTCGAACGAAGAGGGTTTAC 58

RESULT 96  
US-09-118-324-1/c  
; Sequence 1, Application US/09118324

```
; Patent No. 6110720
; GENERAL INFORMATION:
; APPLICANT: Li, Xin-Liang
; APPLICANT: Ljungdahl, Lars G.
; APPLICANT: Chen, Huizhong
; TITLE OF INVENTION: Orpinomyces Cellulase CelE Protein and Coding Sequences
; FILE REFERENCE: 32-98sequence listing
; CURRENT APPLICATION NUMBER: US/09/118,324
; CURRENT FILING DATE: 1998-07-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1532
; TYPE: DNA
; ORGANISM: Orpinomyces sp. PC-2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (39)..(1472)
US-09-118-324-1

Query Match          64.0%; Score 16; DB 3; Length 1532;
Best Local Similarity 79.2%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GCAAGTCGAACGGAAGGCCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db      860  GCTAGTGAACCGGAAGTCCTTTC 837

RESULT 97
US-09-252-991A-887
; Sequence 887, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 887
; LENGTH: 1698
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-887

Query Match          64.0%; Score 16; DB 3; Length 1698;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGG 18
      ||||| ||||| ||||| ||||| |||||
Db      361  AAGTCGAACGGAAGG 376

RESULT 98
US-09-533-559-5520
; Sequence 5520, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 1999-03-22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5520
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1710)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-5520

Query Match          64.0%; Score 16; DB 3; Length 1710;
Best Local Similarity 79.2%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GCAAGTCGAACGGAAGGCCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db      807  GCAAGTCGACCGGTAAAGCCCTTC 830

RESULT 99
US-09-799-451-258
; Sequence 258, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunwei
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 258
; LENGTH: 2103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1184)..(1303)
US-09-799-451-258

Query Match          64.0%; Score 16; DB 3; Length 2103;
Best Local Similarity 79.2%; Pred. No. 3.5e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  CAAGTCGAACGGAAGGCCTTTC 25
      ||||| ||||| ||||| ||||| |||||
Db      993  CAAGTCGAATTGAAAGAACTGTCG 1016
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RESULT 100
US-09-543-679A-2542
; Sequence 2542, Application US/09543679A
; Patent No 7034007
; GENERAL INFORMATION:
; APPLICANT: NYCE, Jonathan W.
; TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
; COMPOSITIONS, KIT & METHOD FOR TREATMENT
; OF AIRWAY DISORDERS ASSOCIATED WITH
; BRONCHOCOINSTRUCTION, LUNG INFLAMMATION,
; NUMBER OF SEQUENCES: 3111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: NJ
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-R
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: N/A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 13-Apr-2000
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/127,958
; FILING DATE: 1998-08-03
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-0067191b
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2542:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2542:
US-09-543-679A-2542

Query Match      64.0%; Score 16; DB 5; Length 9900;
Best Local Similarity 79.2%; Pred. No. 4.9e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Search completed: May 19, 2006, 01:01:15
Job time : 93.506 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:46:33 ; Search time 1002.86 Seconds  
(without alignments)  
306.314 Million cell updates/sec

Title: US-10-665-708-21

Perfect score: 25

Sequence: 1 gcaagtcgaacggaaggccttccg 25

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA Main:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	24	96.0	24	10	US-10-665-708-22
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6	23.4	93.6	1455	10	US-10-697-802A-13
7	23.4	93.6	1482	10	US-10-697-802A-5
8	21.8	87.2	1403	10	US-10-522-454-1
9	21.8	87.2	1443	13	US-11-035-236-1
10	21.8	87.2	1443	13	US-11-045-628-1
11	21.8	87.2	1461	10	US-10-697-802A-7
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13	21.8	87.2	1480	16	US-11-228-416-6
14	21.8	87.2	1480	16	US-11-228-416-8
15	21.8	87.2	1480	16	US-11-228-416-9
16	21.8	87.2	1481	16	US-11-228-416-3
17	21.8	87.2	1482	16	US-11-228-416-4
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 2, Appl
					Sequence 6, Appl
					Sequence 13, Appl
					Sequence 5, Appl
					Sequence 1, Appl
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					Sequence 4, Appl

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26	21.4	85.6	1465	7	US-10-029-397A-32	Sequence 32, Appl
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53	19.8	79.2	1464	8	US-10-719-633-7	Sequence 7, Appl
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55	19.8	79.2	1536	7	US-10-029-397A-33	Sequence 33, Appl
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122	17	68.0	5901	16	US-11-136-527-3427	Sequence 3427, Ap	c 195	16.2	64.8	590	6	US-10-762-966-16	Sequence 16, Appl
123	17	68.0	35058	13	US-11-097-143-5575	Sequence 5575, Ap	c 196	16.2	64.8	635	16	US-11-096-568A-8058	Sequence 8058, Ap
c 124	17	68.0	1457619	16	US-11-098-686-8739	Sequence 8739, Ap	c 197	16.2	64.8	637	9	US-10-653-047-7113	Sequence 7113, Ap
c 125	17	68.0	1457619	16	US-11-098-686-8739	Sequence 8739, Ap	c 198	16.2	64.8	638	6	US-10-027-632-292604	Sequence 292604, A
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127	17	68.0	9025608	7	US-10-156-761-1	Sequence 1, Appl	c 200	16.2	64.8	638	6	US-10-027-632-292604	Sequence 292604, A
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c 134	16.6	66.4	537	12	US-10-301-480-821099	Sequence 821099, A	c 207	16.2	64.8	2239	13	US-11-097-143-383	Sequence 383, App
c 135	16.6	66.4	552	4	US-09-925-065A-738727	Sequence 738727, A	c 208	16.2	64.8	2294	7	US-10-286-926-49	Sequence 49, Appl
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c 150	16.6	66.4	1736	5	US-09-925-065A-79105	Sequence 79105, A	c 223	16.2	64.8	2888	10	US-10-491-183-79	Sequence 79, Appl
c 151	16.6	66.4	1736	5	US-09-925-065A-79106	Sequence 79106, A	c 224	16.2	64.8	3200	13	US-11-097-143-35116	Sequence 35116, A
c 152	16.6	66.4	1736	12	US-10-301-480-180343	Sequence 180343, A	c 225	16.2	64.8	4417	13	US-11-097-143-382	Sequence 382, App
c 153	16.6	66.4	1736	12	US-10-301-480-180344	Sequence 180344, A	c 226	16.2	64.8	5498	13	US-11-097-143-10294	Sequence 10294, A
c 154	16.6	66.4	1736	12	US-10-301-480-180345	Sequence 180345, A	c 227	16	64.0	20	11	US-10-831-286A-11940	Sequence 11940, A
c 155	16.6	66.4	1736	12	US-10-301-480-793752	Sequence 793752, A	c 228	16	64.0	24	8	US-10-737-894-10	Sequence 10, Appl
c 156	16.6	66.4	1736	12	US-10-301-480-793753	Sequence 793753, A	c 229	16	64.0	26	3	US-09-738-274-28	Sequence 28, Appl
c 157	16.6	66.4	1736	12	US-10-301-480-793754	Sequence 793754, A	c 230	16	64.0	26	10	US-10-665-708-28	Sequence 28, Appl
c 158	16.6	66.4	2077	13	US-11-097-143-4424	Sequence 4424, Ap	c 231	16	64.0	30	11	US-10-831-286A-27219	Sequence 27219, A
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c 160	16.6	66.4	4456	13	US-11-097-143-4423	Sequence 4423, Ap	c 233	16	64.0	171	9	US-10-029-386-19749	Sequence 19749, A
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255 16 64.0 592 5 US-09-925-065A-800999
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ALIGNMENTS

RESULT 1  
US-09-738-274-21  
; Sequence 21, Application US/09738274  
; Publication No. US20030165824A1

Sequence 71827, A  
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Sequence 71, Appl  
Sequence 71, Appl  
Sequence 60, Appl  
Sequence 1958, Ap  
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Sequence 776918,  
Sequence 80747, A  
Sequence 6, Appli

GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: ROBRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-21

Query Match 100.0%; Score 25; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGAAAGGCCTTTCG 25  
Db 1 GCAAGTCGACGAAAGGCCTTTCG 25

RESULT 2  
US-10-665-708-21  
; Sequence 21, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: ROBRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-21

Query Match 100.0%; Score 25; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.091;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGAAAGGCCTTTCG 25  
Db 1 GCAAGTCGACGAAAGGCCTTTCG 25

RESULT 3

US-09-738-274-22  
; Sequence 22, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-22

Query Match 96.0%; Score 24; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTTCG 25  
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 4  
US-10-665-708-22  
; Sequence 22, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-22

Query Match 96.0%; Score 24; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTTCG 25  
Db 1 CAAGTCGAACGGAAGGCGCTTTTCG 24

RESULT 5  
US-10-697-802A-6  
; Sequence 6, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 6  
; LENGTH: 1449  
; TYPE: DNA  
; ORGANISM: Mycobacterium fortuitum  
US-10-697-802A-6

Query Match 93.6%; Score 23.4; DB 10; Length 1449;  
Best Local Similarity 96.0%; Pred. No. 0.63;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25  
Db 20 GCAAGTCGAACGGAAGGCGCTTTTCG 44

RESULT 6  
US-10-697-802A-13  
; Sequence 13, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 13  
; LENGTH: 1455  
; TYPE: DNA  
; ORGANISM: Mycobacterium mucogenicum  
US-10-697-802A-13

Query Match 93.6%; Score 23.4; DB 10; Length 1455;  
Best Local Similarity 96.0%; Pred. No. 0.63;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTTCG 25  
Db 30 GCAAGTCGAACGGAAGGCGCTTTTCG 54

RESULT 7  
US-10-697-802A-5  
; Sequence 5, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 5  
; LENGTH: 1482  
; TYPE: DNA  
; ORGANISM: Mycobacterium farcinogenes  
US-10-697-802A-5

Query Match 93.6%; Score 23.4; DB 10; Length 1482;  
Best Local Similarity 96.0%; Pred. No. 0.63;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 28 GCAAGTCGAACGGAAGGCGCTTTCG 52  
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## RESULT 8

US-10-522-454-1  
; Sequence 1, Application US/10522454  
; Publication No. US20050244938A1  
; GENERAL INFORMATION:  
; APPLICANT: Hill, Russell T.  
; APPLICANT: Hamann, Mark T.  
; APPLICANT: Peraud, Olivier  
; APPLICANT: Kananah, Noer  
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES  
; FILE REFERENCE: 4115-180  
; CURRENT APPLICATION NUMBER: US/10/522,454  
; PRIOR FILING DATE: 2005-01-20  
; PRIOR APPLICATION NUMBER: PCT/US03/24238  
; PRIOR FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 1403  
; TYPE: DNA  
; ORGANISM: Actinomyces sp.  
US-10-522-454-1

Query Match 87.2%; Score 21.8; DB 10; Length 1403;  
Best Local Similarity 92.0%; Pred. No. 3.7;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
Db 25 GCAAGTCGAGCGGAAGGCGCTTTCG 49  
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## RESULT 9

US-11-035-296-1  
; Sequence 1, Application US/11035296  
; Publication No. US20050203005A1  
; GENERAL INFORMATION:  
; APPLICANT: VICURON PHARMACEUTICALS INC.  
; APPLICANT: LAZZARINI, Ameriga  
; APPLICANT: GASTALDO, Luciano  
; APPLICANT: CANDIANI, Gianpaolo  
; APPLICANT: CICILIATO, Ismaela  
; APPLICANT: LOSI, Daniele  
; APPLICANT: MARINELLI, Flavia  
; APPLICANT: SELVA, Enrico  
; APPLICANT: PARENTI, Franco  
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY  
; FILE REFERENCE: 892,280-195  
; CURRENT APPLICATION NUMBER: US/11/035,296  
; PRIOR FILING DATE: 2005-01-12  
; PRIOR APPLICATION NUMBER: US 10/521,336  
; PRIOR FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658  
; PRIOR FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: EP 03016306.7  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 1443  
; TYPE: DNA  
; ORGANISM: Microbispora sp. ATCC PTA-5024

## US-11-035-296-1

Query Match 87.2%; Score 21.8; DB 13; Length 1443;  
Best Local Similarity 92.0%; Pred. No. 3.7;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
Db 30 GCAAGTCGAGCGGAAGGCGCTTTCG 54  
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## RESULT 10

US-11-045-628-1  
; Sequence 1, Application US/11045628  
; Publication No. US20050233952A1  
; GENERAL INFORMATION:  
; APPLICANT: VICURON PHARMACEUTICALS INC.  
; APPLICANT: LAZZARINI, Ameriga  
; APPLICANT: GASTALDO, Luciano  
; APPLICANT: CANDIANI, Gianpaolo  
; APPLICANT: CICILIATO, Ismaela  
; APPLICANT: LOSI, Daniele  
; APPLICANT: MARINELLI, Flavia  
; APPLICANT: SELVA, Enrico  
; APPLICANT: PARENTI, Franco  
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY  
; FILE REFERENCE: 892,280-500  
; CURRENT APPLICATION NUMBER: US/11/045,628  
; CURRENT FILING DATE: 2005-01-26  
; PRIOR APPLICATION NUMBER: US 11/035,296  
; PRIOR FILING DATE: 2005-01-12  
; PRIOR APPLICATION NUMBER: US 10/521,336  
; PRIOR FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658  
; PRIOR FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: EP 03016306.7  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 1443  
; TYPE: DNA  
; ORGANISM: Microbispora sp. ATCC PTA-5024

Query Match 87.2%; Score 21.8; DB 13; Length 1443;  
Best Local Similarity 92.0%; Pred. No. 3.7;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
|||||  
Db 30 GCAAGTCGAGCGGAAGGCGCTTTCG 54  
|||||

## RESULT 11

US-10-697-802A-7  
; Sequence 7, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; PRIOR FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 7  
; LENGTH: 1461  
; TYPE: DNA  
; ORGANISM: Mycobacterium gordonae  
US-10-697-802A-7

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Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
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Db 20 GCAAGTCGAACGGAAGGCGCTTCG 44

RESULT 12
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: (351)..(351)
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-5

Query Match      87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 13
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
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; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: (351)..(351)
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-6

Query Match      87.2%; Score 21.8; DB 16; Length 1480;
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTCG 25
    |||||
Db 50 GCAAGTCGAACGGAAGGCGCTTCG 74

RESULT 14
US-11-228-416-8
; Sequence 8, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH725 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
```

; LOCATION: (351)..(351)  
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (442)..(442)  
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (443)..(443)  
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1423)..(1423)  
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-8

Query Match 87.2%; Score 21.8; DB 16; Length 1480;  
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
Db 50 GCAAGTCGAGCGGAAGGCCCTTCG 74

RESULT 15  
US-11-228-416-9  
; Sequence 9, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1480  
; TYPE: DNA  
; ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (198)..(198)  
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (351)..(351)  
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (442)..(442)  
; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (443)..(443)  
; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1423)..(1423)  
; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA  
US-11-228-416-9

Query Match 87.2%; Score 21.8; DB 16; Length 1480;  
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
Db 50 GCAAGTCGAGCGGAAGGCCCTTCG 74

RESULT 16  
US-11-228-416-3  
; Sequence 3, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1481  
; TYPE: DNA  
; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (198)..(198)  
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (352)..(352)  
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (443)..(443)  
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (444)..(444)  
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1424)..(1424)  
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-3

Query Match 87.2%; Score 21.8; DB 16; Length 1481;  
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 2;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTCG 25  
Db 50 GCAAGTCGAGCGGAAGGCCCTTCG 74

RESULT 17  
US-11-228-416-4  
; Sequence 4, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15

Query Match 87.2%; Score 21.8; DB 16; Length 1481;  
Best Local Similarity 92.0%; Pred. No. 3.7; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 2;

; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH646 16S ribosomal RNA gene, partial sequence
; NAME/KEY: misc\_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (1425)..(1425)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4

Query Match 87.2%; Score 21.8; DB 16; Length 1482;
Best Local Similarity 92.0%; Pred. No. 3.7; Mismatches 2; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 1 GCAAGTCGAACGGAAGCCCTTCG 25
||||| ||||| ||||| ||||| |||||
Db 50 GCAAGTCGAGCGGAAGGCCCTTCG 74

RESULT 18
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:

; NAME/KEY: misc\_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: (1426)..(1426)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7

Query Match 87.2%; Score 21.8; DB 16; Length 1483;
Best Local Similarity 92.0%; Pred. No. 3.7; Mismatches 2; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 1 GCAAGTCGAACGGAAGCCCTTCG 25
||||| ||||| ||||| ||||| |||||
Db 50 GCAAGTCGAGCGGAAGGCCCTTCG 74

RESULT 19
US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: Primer
US-09-738-972-7

Query Match 85.6%; Score 21.4; DB 3; Length 32;
Best Local Similarity 95.7%; Pred. No. 4.9;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTT 23
||||| ||||| ||||| ||||| |||||
Db 1 GCAAGTCGAACGGAAGGCCCTCT 23

RESULT 20
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14



; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: probe  
US-09-738-972-14

Query Match 85.6%; Score 21.4; DB 3; Length 32;  
Best Local Similarity 95.7%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 32 GCAAGTCGAACGGAAGGCCTCT 10  
|||||

RESULT 21  
US-10-862-026-7  
; Sequence 7, Application US/10862026  
; Publication No. US20040224348A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GPI19-02.UT  
; CURRENT APPLICATION NUMBER: US/10/862,026  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: primer  
US-10-862-026-7

Query Match 85.6%; Score 21.4; DB 9; Length 32;  
Best Local Similarity 95.7%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 1 GCAAGTCGAACGGAAGGCCTCT 23  
|||||

RESULT 22  
US-10-862-026-14/c  
; Sequence 14, Application US/10862026  
; Publication No. US20040224348A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GPI19-02.UT  
; CURRENT APPLICATION NUMBER: US/10/862,026  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: probe  
US-10-862-026-14

Query Match 85.6%; Score 21.4; DB 9; Length 32;  
Best Local Similarity 95.7%; Pred. No. 4.9;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 32 GCAAGTCGAACGGAAGGCCTCT 10  
|||||

RESULT 23  
US-10-478-633A-23  
; Sequence 23, Application US/10478633A  
; Publication No. US20050059000A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKARA BIO INC.  
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for  
; FILE REFERENCE: 663232  
; CURRENT APPLICATION NUMBER: US/10/478,633A  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: JP 2001-177737  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: JP 2001-249689  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 23  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Mycobacterium avium  
US-10-478-633A-23

Query Match 85.6%; Score 21.4; DB 10; Length 560;  
Best Local Similarity 95.7%; Pred. No. 5.5;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 30 GCAAGTCGAACGGAAGGCCTCT 52  
|||||

RESULT 24  
US-10-697-802A-12  
; Sequence 12, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 12  
; LENGTH: 1421  
; TYPE: DNA  
; ORGANISM: Mycobacterium lentiflavum  
US-10-697-802A-12

Query Match 85.6%; Score 21.4; DB 10; Length 1421;  
Best Local Similarity 95.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
|||||  
Db 20 GCAAGTCGAACGGAAGGCCTCT 42  
|||||

RESULT 25  
US-10-697-802A-2  
; Sequence 2, Application US/10697802A

; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 2  
; LENGTH: 1454  
; TYPE: DNA  
; ORGANISM: Mycobacterium avium  
US-10-697-802A-2

Query Match 85.6%; Score 21.4; DB 10; Length 1454;  
Best Local Similarity 95.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
| | | | | | | | | | | | | | | | | | | | | |  
Db 30 GCAAGTCGAACGGAAGGCCTCT 52

## RESULT 26

US-10-029-397A-32  
; Sequence 32, Application US/10029397A  
; Publication No. US20030175709A1

; GENERAL INFORMATION:  
; APPLICANT: MURPHY, GEORGE L.  
; APPLICANT: WHITLEY, J. PENN  
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS  
; FILE REFERENCE: AMBI-0761US  
; CURRENT APPLICATION NUMBER: US/10/029,397A  
; CURRENT FILING DATE: 2002-03-19  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 1465  
; TYPE: DNA  
; ORGANISM: Mycobacterium avium  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (298)..(881)  
; OTHER INFORMATION: N = A, C, G or T/U  
US-10-029-397A-32

Query Match 85.6%; Score 21.4; DB 7; Length 1465;  
Best Local Similarity 95.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 GCAAGTCGAACGGAAGGCCTCT 42

## RESULT 27

US-09-738-274-23  
; Sequence 23, Application US/09738274  
; Publication No. US20030165824A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-23

Query Match 84.0%; Score 21; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTTCG 25  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GTCGAACGGAAGGCCTTTTCG 21

## RESULT 28

US-10-665-708-23  
; Sequence 23, Application US/10665708  
; Publication No. US20050100915A1

; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-23

Query Match 84.0%; Score 21; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 7.4;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GTCGAACGGAAGGCCTTTTCG 25  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GTCGAACGGAAGGCCTTTTCG 21

## RESULT 29

US-10-085-871C-1  
; Sequence 1, Application US/10085871C  
; Publication No. US20030199047A1

; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Chung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.0005  
; CURRENT APPLICATION NUMBER: US/10/085,871C  
; CURRENT FILING DATE: 2002-02-27



Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25  
 Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 34

US-10-727-643-2  
 ; Sequence 2, Application US/10727643  
 ; Publication No. US20050064566A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Fang-Yu  
 ; APPLICANT: Lee, Ming-Liang  
 ; APPLICANT: Anderson, Hong C.  
 ; APPLICANT: Chiu, Chung-Ching  
 ; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin  
 ; FILE REFERENCE: 004135.P005  
 ; CURRENT APPLICATION NUMBER: US/10/727,643  
 ; PRIOR FILING DATE: 2003-12-03  
 ; PRIOR APPLICATION NUMBER: US/10/085,871  
 ; NUMBER OF SEQ ID NOS: 12  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 2  
 ; LENGTH: 1471  
 ; TYPE: DNA  
 ; ORGANISM: Saccharothrix 45494  
 US-10-727-643-2

Query Match 80.8%; Score 20.2; DB 10; Length 1471;  
 Best Local Similarity 88.0%; Pred. No. 21;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25  
 Db 30 GCAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 35

US-10-756-683-1  
 ; Sequence 1, Application US/10756683  
 ; Publication No. US20040180960A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Korea Chungang Educational Foundation  
 ; APPLICANT: Hwang, Byong Kook  
 ; APPLICANT: Lee, Jung Yeop  
 ; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant  
 ; FILE REFERENCE: 4228-102  
 ; CURRENT APPLICATION NUMBER: US/10/756,683  
 ; CURRENT FILING DATE: 2004-01-13  
 ; PRIOR APPLICATION NUMBER: KP 10-2003-0015628  
 ; PRIOR FILING DATE: 2003-03-13  
 ; PRIOR APPLICATION NUMBER: KP 10-2003-0015629  
 ; PRIOR FILING DATE: 2003-03-13  
 ; NUMBER OF SEQ ID NOS: 1  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 1488  
 ; TYPE: DNA  
 ; ORGANISM: Lechevalieria aerocolonigenes  
 US-10-756-683-1

Query Match 80.8%; Score 20.2; DB 9; Length 1488;  
 Best Local Similarity 88.0%; Pred. No. 21;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25  
 Db 42 GCAAGTCGAGCGGTAAGGCCCTTCG 66

RESULT 36

US-10-875-161-2  
 ; Sequence 2, Application US/10875161  
 ; Publication No. US2005009151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chase, Matthew  
 ; APPLICANT: Clayton, Robert  
 ; APPLICANT: Landis, Bryan  
 ; APPLICANT: Banerjee, Amit  
 ; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric  
 ; FILE REFERENCE: S0-3262-2-PR-US  
 ; CURRENT APPLICATION NUMBER: US/10/875,161  
 ; CURRENT FILING DATE: 2004-06-22  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 1514  
 ; TYPE: DNA  
 ; ORGANISM: Rhodococcus opacus  
 ; FEATURE:  
 ; NAME/KEY: rRNA  
 ; LOCATION: (1)..(1514)  
 ; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus  
 ; FEATURE:  
 ; NAME/KEY: misc difference  
 ; LOCATION: (1)..(1514)  
 ; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of  
 ; OTHER INFORMATION: Rhodococcus opacus  
 US-10-875-161-2

Query Match 80.8%; Score 20.2; DB 9; Length 1514;  
 Best Local Similarity 88.0%; Pred. No. 21;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCCTTCG 25  
 Db 53 GCAAGTCGAGCGGTAAGGCCCTTCG 77

RESULT 37

US-10-831-286A-1517  
 ; Sequence 1517, Application US/10831286A  
 ; Publication No. US20060046246A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZENG, QIANDONG  
 ; APPLICANT: CHATELLIER, SONIA  
 ; APPLICANT: MOIR, DONALD T.  
 ; APPLICANT: LACROIX, BRUNA  
 ; APPLICANT: CHILDRESS, DARRELL  
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
 ; FILE REFERENCE: 032796-174.001  
 ; CURRENT APPLICATION NUMBER: US/10/831,286A  
 ; CURRENT FILING DATE: 2004-04-26  
 ; PRIOR APPLICATION NUMBER: 60/464,955  
 ; PRIOR FILING DATE: 2003-04-24  
 ; NUMBER OF SEQ ID NOS: 48788  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1517  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium diphtheriae  
 US-10-831-286A-1517

Query Match 80.0%; Score 20; DB 11; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CAAAGTCGAACGGAAGGCCCT 21  
 Db 1 CAAAGTCGAACGGAAGGCCCT 20

```

RESULT 38
US-10-830-943-11
; Sequence 11, Application US/10830943
; Publication No. US20050009053A1
; GENERAL INFORMATION:
; APPLICANT: Boecker, Sebastian
; APPLICANT: van den Boom, Dirk
; TITLE OF INVENTION: FRAGMENTATION-BASED METHODS AND SYSTEMS
; FILE REFERENCE: 17082-079001
; CURRENT APPLICATION NUMBER: US/10/830,943
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/466,006
; PRIOR FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence
US-10-830-943-11

Query Match      80.0%; Score 20; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCC 20
        |||
Db      50  GCAAGTCGACGGAAGGCC 69

RESULT 39
US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-10-478-633A-24

Query Match      80.0%; Score 20; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCC 20
        |||
Db      42  GCAAGTCGACGGAAGGCC 61

RESULT 40
US-10-697-802A-11
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001

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; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kubicae
US-10-697-802A-11

Query Match      80.0%; Score 20; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCC 20
        |||
Db      14  GCAAGTCGACGGAAGGCC 33

RESULT 41
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium parafricanum
US-10-697-802A-14

Query Match      80.0%; Score 20; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCC 20
        |||
Db      15  GCAAGTCGACGGAAGGCC 34

RESULT 42
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match      80.0%; Score 20; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 43
US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US2003016224A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 2003-04-21
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match 80.0%; Score 20; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 38 GCAAGTCGAACGGAAGGCC 57

RESULT 44
US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match 80.0%; Score 20; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 20 GCAAGTCGAACGGAAGGCC 39

RESULT 45
US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
```

```
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15

Query Match 80.0%; Score 20; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 20 GCAAGTCGAACGGAAGGCC 39

RESULT 46
US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8

Query Match 80.0%; Score 20; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCC 20
    |||||
Db 44 GCAAGTCGAACGGAAGGCC 63

RESULT 47
US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US2003016584A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: Gp107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
```

```
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          79.2%; Score 19.8; DB 3; Length 32;
Best Local Similarity 91.3%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 1 GCAAGTCGAACGGAAGGCCTTT 23

RESULT 48
US-10-665-708-14
; Sequence 14, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GPI07-02.U1
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14

Query Match          79.2%; Score 19.8; DB 10; Length 32;
Best Local Similarity 91.3%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 1 GCAAGTCGAACGGAAGGCCTTT 23

RESULT 49
US-10-697-802A-17
; Sequence 17, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 17
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-697-802A-17

Query Match          79.2%; Score 19.8; DB 10; Length 1416;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 20 GCAAGTCGAACGGAAGGCCTCT 42

RESULT 50
US-10-697-802A-3
; Sequence 3, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 3
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-697-802A-3

Query Match          79.2%; Score 19.8; DB 10; Length 1421;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 20 GCAAGTCGAACGGAAGGCCTCT 42

RESULT 51
US-10-697-802A-10
; Sequence 10, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 10
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
US-10-697-802A-10

Query Match          79.2%; Score 19.8; DB 10; Length 1463;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
Db 19 GCAAGTCGAACGGAAGGCCTCT 41

RESULT 52
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. US2002008226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match          79.2%; Score 19.8; DB 3; Length 1464;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 53
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10719.633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7

Query Match          79.2%; Score 19.8; DB 8; Length 1464;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 20 GCAAGTCGAACGGAAGGCTCT 42

RESULT 54
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match          79.2%; Score 19.8; DB 8; Length 1524;
```

```
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 50 GCAAGTCGAACGGAAGGCTCT 72

RESULT 55
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match          79.2%; Score 19.8; DB 7; Length 1536;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 59 GCAAGTCGAACGGAAGGCTCT 81

RESULT 56
US-10-029-397A-34
; Sequence 34, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match          79.2%; Score 19.8; DB 7; Length 1536;
Best Local Similarity 91.3%; Pred. No. 33;
Matches 21; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTT 23
    |||||
Db 59 GCAAGTCGAACGGAAGGCTCT 81

RESULT 57
US-10-831-286A-8212
; Sequence 8212, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
```



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; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match          77.6%; Score 19.4; DB 11; Length 30;
Best Local Similarity 95.2%; Pred. No. 44;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTT 22
    ||||| ||||| ||||| ||||| ||
Db  1 CAAGTCGAACGGAAGGCGCTT 21

RESULT 58
US-10-438-774-15
; Sequence 15, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: UNWC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 454
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-15

Query Match          77.6%; Score 19.4; DB 7; Length 454;
Best Local Similarity 95.2%; Pred. No. 49;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  5 GTCGAACGGAAGGCGCTTTCG 25
    ||||| ||||| ||||| ||||| ||
Db  1 GTCGAACGGAAGGCGCTTTCG 21

RESULT 59
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 2001-08-08
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGAAGGCGCTTTC 276

RESULT 61
US-09-925-065A-906221
; Sequence 27, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
```

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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 4; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGAAGGCGCTTTC 276

RESULT 60
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match          76.8%; Score 19.2; DB 5; Length 600;
Best Local Similarity 87.5%; Pred. No. 62;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||||| ||||| ||||| |||||
Db  299 GCAAGTCGACCTGAAGGCGCTTTC 276

RESULT 61
US-09-925-065A-906221
; Sequence 27, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
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; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match          76.0%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCC 20
Db  1 CAAGTCGAACGGAAGGCC 19

RESULT 62
US-10-665-708-27
; Sequence 27, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-27

Query Match          76.0%; Score 19; DB 10; Length 23;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCC 20
Db  1 CAAGTCGAACGGAAGGCC 19

RESULT 63
US-10-697-802A-9
; Sequence 9, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 9
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-10-697-802A-9

Query Match          73.6%; Score 18.4; DB 10; Length 1452;
Best Local Similarity 95.0%; Pred.No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCC 20
Db  10 GCAAGTCGAACGGAAGGCC 29

RESULT 64
US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match          72.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred.No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  8 GAACGGAAGCCTTTCG 25
Db  1 GAACGGAAGCCTTTCG 18

RESULT 65
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
```

; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-24

Query Match 72.0%; Score 18; DB 10; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GAACGGAAGGCGTTTCG 25  
Db 1 GAACGGAAGGCGTTTCG 18  
|||||

## RESULT 66

US-10-425-114-30427  
; Sequence 30427, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 30427  
; LENGTH: 1366  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-ZMFLB73019F09\_FLI  
US-10-425-114-30427

Query Match 71.2%; Score 17.8; DB 8; Length 1366;  
Best Local Similarity 90.5%; Pred. No. 3e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22  
Db 896 CAAGTCGAACGGAAGGCGTTT 916  
|||||

## RESULT 67

US-09-917-800A-1684  
; Sequence 1684, Application US/09917800A  
; Patent No. US20020119462A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Molecular  
; FILE REFERENCE: 44921-5038-US  
; CURRENT APPLICATION NUMBER: US/09/917,800A  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: US 60/222,040  
; PRIOR FILING DATE: 2000-07-31

; PRIOR APPLICATION NUMBER: US 60/222,880  
; PRIOR FILING DATE: 2000-11-02  
; PRIOR APPLICATION NUMBER: US 60/290,029  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/290,645  
; PRIOR FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: US 60/292,336  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/295,798  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/297,457  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,884  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,459  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 1740  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1684  
; LENGTH: 4540  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM\_021266  
US-09-917-800A-1684

Query Match 71.2%; Score 17.8; DB 3; Length 4540;  
Best Local Similarity 90.5%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22  
Db 105 CAAGTCGAACGGAAGGCGTTT 125  
|||||

## RESULT 68

US-11-136-527-299  
; Sequence 299, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 299  
; LENGTH: 4770  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-299

Query Match 71.2%; Score 17.8; DB 16; Length 4770;  
Best Local Similarity 90.5%; Pred. No. 3.2e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGTTT 22  
Db 105 CAAGTCGAACGGAAGGCGTTT 125  
|||||

## RESULT 69

US-10-972-079-55955/c  
; Sequence 55955, Application US/10972079  
; Publication No. US20050153317A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: Denise, Sue K.  
; APPLICANT: ROSENFELD, David

```
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55955
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_1
US-10-972-079-55955

Query Match          70.4%; Score 17.6; DB 10; Length 600;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 481 GCAAGGGGGACGGAAGGACTTTC 458

RESULT 70
US-10-972-079-55956/c
; Sequence 55956, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55956
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_2
US-10-972-079-55956

Query Match          70.4%; Score 17.6; DB 10; Length 600;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 114 GCAAGGGGGACGGAAGGACTTTC 91

RESULT 71
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
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```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          70.4%; Score 17.6; DB 4; Length 654;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 401 GGAAGTGAACGGAACGGCCTTTC 424

RESULT 72
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          70.4%; Score 17.6; DB 5; Length 654;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db 401 GGAAGTGAACGGAACGGCCTTTC 424

RESULT 73
US-10-087-192-1004
; Sequence 1004, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
```

; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 2059  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1004  
; LENGTH: 960  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-087-192-1004

Query Match 70.4%; Score 17.6; DB 6; Length 960;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25  
||||| ||||| ||||| ||||| |||||  
Db 811 CAAGTCGAGCAGAAAGTCCTTACG 834

RESULT 74  
US-10-301-480-553054/c  
; Sequence 553054, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 553054  
; LENGTH: 999  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-553054

Query Match 70.4%; Score 17.6; DB 12; Length 999;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24  
||||| ||||| ||||| ||||| |||||  
Db 921 GCAACTGGAACAGAAAGGCGCTTC 898

RESULT 75  
US-10-301-480-1166463/c  
; Sequence 1166463, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1166463  
; LENGTH: 999  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1166463

Query Match 70.4%; Score 17.6; DB 12; Length 999;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24  
||||| ||||| ||||| ||||| |||||  
Db 921 GCAACTGGAACAGAAAGGCGCTTC 898

RESULT 76  
US-10-956-157-9594  
; Sequence 9594, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9594  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-9594

Query Match 70.4%; Score 17.6; DB 10; Length 1400;  
Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25  
||||| ||||| ||||| ||||| |||||  
Db 554 CAAGTCGAATTGAAAGGACTGTCG 577

RESULT 77  
US-10-956-157-4359  
; Sequence 4359, Application US/10956157  
; Publication No. US20050118625A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)  
; CURRENT APPLICATION NUMBER: US/10/956,157  
; CURRENT FILING DATE: 2004-10-04  
; NUMBER OF SEQ ID NOS: 319805  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4359  
; LENGTH: 1786  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-956-157-4359

Query Match 70.4%; Score 17.6; DB 10; Length 1786;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTCG 25  
||||| ||||| ||||| ||||| |||||  
Db 940 CAAGTCGAATTGAAAGGACTGTCG 963

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RESULT 78
US-10-301-480-29919/c
; Sequence 29919, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29919
; LENGTH: 2360
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269,
; LOCATION: 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279,
; LOCATION: 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289,
; LOCATION: 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308,
; LOCATION: 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318,
; LOCATION: 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328,
; LOCATION: 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347,
; LOCATION: 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357,
; LOCATION: 2358, 2359
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-29919
; Query Match 70.4%; Score 17.6; DB 12; Length 2360;
; Best Local Similarity 83.3%; Pred. No. 3.8e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 981 GCAACTGGAACAGAAAGGCGCTTCC 958

RESULT 79
US-10-301-480-643328/c
; Sequence 643328, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643328
; LENGTH: 2360
; TYPE: DNA
; ORGANISM: Mus musculus
; ORGANISM: Mus musculus
US-10-087-192-1003
; Query Match 70.4%; Score 17.6; DB 6; Length 43800;
; Best Local Similarity 83.3%; Pred. No. 4.3e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 25
||||| ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 81
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

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; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2260, 2261, 2262, 2263, 2264, 2265, 2266, 2267, 2268, 2269,
; LOCATION: 2270, 2271, 2272, 2273, 2274, 2275, 2276, 2277, 2278, 2279,
; LOCATION: 2280, 2281, 2282, 2283, 2284, 2285, 2286, 2287, 2288, 2289,
; LOCATION: 2290, 2291, 2292, 2293, 2294, 2295, 2296, 2297, 2298
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2299, 2300, 2301, 2302, 2303, 2304, 2305, 2306, 2307, 2308,
; LOCATION: 2309, 2310, 2311, 2312, 2313, 2314, 2315, 2316, 2317, 2318,
; LOCATION: 2319, 2320, 2321, 2322, 2323, 2324, 2325, 2326, 2327, 2328,
; LOCATION: 2329, 2330, 2331, 2332, 2333, 2334, 2335, 2336, 2337
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2338, 2339, 2340, 2341, 2342, 2343, 2344, 2345, 2346, 2347,
; LOCATION: 2348, 2349, 2350, 2351, 2352, 2353, 2354, 2355, 2356, 2357,
; LOCATION: 2358, 2359
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-643328
; Query Match 70.4%; Score 17.6; DB 12; Length 2360;
; Best Local Similarity 83.3%; Pred. No. 3.8e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCGCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 981 GCAACTGGAACAGAAAGGCGCTTCC 958

RESULT 80
US-10-087-192-1003
; Sequence 1003, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 43800
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1003
; Query Match 70.4%; Score 17.6; DB 6; Length 43800;
; Best Local Similarity 83.3%; Pred. No. 4.3e+02;
; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCGCTTTC 25
||||| ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 81
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

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; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 31297  
; LENGTH: 622  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 18066455  
US-10-767-701-31297

Query Match 68.8%; Score 17.2; DB 8; Length 622;  
Best Local Similarity 86.4%; Pred. No. 5.6e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTCG 25  
||||| ||||| ||||| ||||| |||||  
DB 31 AGTCGAAGGAATGCGCCTTTCG 52

RESULT 82  
US-10-632-27617/c  
; Sequence 27617, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27617  
; LENGTH: 708  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-27617

Query Match 68.8%; Score 17.2; DB 6; Length 708;  
Best Local Similarity 86.4%; Pred. No. 5.7e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||  
DB 415 GCAAGTCGAACGGAAGGCCTT 394

RESULT 83  
US-10-027-632-27618/c  
; Sequence 27618, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27618  
; LENGTH: 708  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-27618

Query Match 68.8%; Score 17.2; DB 6; Length 708;  
Best Local Similarity 86.4%; Pred. No. 5.7e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||  
DB 415 GCAAGTCGAACGGAAGGCCTT 394

RESULT 84  
US-10-027-632-27617/c  
; Sequence 27617, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27617  
; LENGTH: 708  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-27617

Query Match 68.8%; Score 17.2; DB 7; Length 708;  
Best Local Similarity 86.4%; Pred. No. 5.7e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22  
||||| ||||| ||||| ||||| |||||

```
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 85
US-10-027-632-27618/c
; Sequence 27618, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27618
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-27618

Query Match      68.8%; Score 17.2; DB 7; Length 708;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAGCGCCTT 22
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 86
US-10-027-632-151386/c
; Sequence 151386, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151386
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151386

Query Match      68.8%; Score 17.2; DB 7; Length 787;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAGCGCCTT 22
Db      415 GCAAGTCGAACGGGAGCGCCTT 394

RESULT 87
US-10-027-632-151386/c
; Sequence 151386, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151386
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-151386

Query Match      68.8%; Score 17.2; DB 7; Length 787;
Best Local Similarity 86.4%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGGAGCGCCTT 22
Db      494 GCAAGTCGAACGGGAGCGCCTT 473

RESULT 88
US-10-425-114-28596
; Sequence 28596, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
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; SEQ ID NO 28596
; LENGTH: 1735
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4759-017-C5_FLI
US-10-425-114-28596

Query Match          68.8%; Score 17.2; DB 8; Length 1735;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
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Db 1163 GCAAGTCACAGGAAAGGCCTT 1184

RESULT 89
US-10-767-701-13467
; Sequence 13467, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihuei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 13467
; LENGTH: 1754
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS3315_1
US-10-767-701-13467

Query Match          68.8%; Score 17.2; DB 8; Length 1754;
Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
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Db 150 GCAAGTCACAGGAAAGGCCTT 171

RESULT 90
US-09-809-391-59
; Sequence 59, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 1776
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (713)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (862)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
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; LOCATION: (1752)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: SITE
; LOCATION: (1773)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-59

Query Match          68.8%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCCTTTCG 25
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Db 878 CAAGTCGAATTGAAAGRACTGTCG 901

RESULT 91
US-09-882-171-59
; Sequence 59, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
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; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
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7	PRIOR APPLICATION NUMBER: 60/057,761	7	PRIOR FILING DATE: 1997-08-22
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7	PRIOR APPLICATION NUMBER: 60/047,585	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,586	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,590	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,594	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/047,589	7	PRIOR FILING DATE: 1997-05-23
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7	PRIOR APPLICATION NUMBER: 60/047,614	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/043,578	7	PRIOR FILING DATE: 1997-04-11
7	PRIOR APPLICATION NUMBER: 60/043,576	7	PRIOR FILING DATE: 1997-04-11
7	PRIOR APPLICATION NUMBER: 60/047,501	7	PRIOR FILING DATE: 1997-05-23
7	PRIOR APPLICATION NUMBER: 60/043,670	7	PRIOR FILING DATE: 1997-04-11
7	PRIOR APPLICATION NUMBER: 60/056,632	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,664	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,876	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,881	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,909	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,875	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,862	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,887	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/056,908	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/048,964	7	PRIOR FILING DATE: 1997-06-06
7	PRIOR APPLICATION NUMBER: 60/057,650	7	PRIOR FILING DATE: 1997-09-05
7	PRIOR APPLICATION NUMBER: 60/056,884	7	PRIOR FILING DATE: 1997-08-22
7	PRIOR APPLICATION NUMBER: 60/057,669	7	PRIOR FILING DATE: 1997-09-05

Query Match 68.8%; Score 17.2; DB 3; Length 1776;  
Best Local Similarity 79.2%; Pred. No. 5.9e+02;  
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25  
|||||  
DB 878 CAAGTCGAATTGAAAGRACTGTGC 901

RESULT 92  
US-10-164-861-59  
; Sequence 59, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 1776  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (713)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (862)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1752)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1773)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-10-164-861-59

Query Match 68.8%; Score 17.2; DB 7; Length 1776;  
Best Local Similarity 79.2%; Pred. No. 5.9e+02;  
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25  
|||||  
DB 878 CAAGTCGAATTGAAAGRACTGTGC 901

RESULT 93  
US-11-144-947-59  
; Sequence 59, Application US/11144947  
; Publication No. US20060084082A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; CURRENT APPLICATION NUMBER: US/11/144,947  
; CURRENT FILING DATE: 2005-06-06  
; PRIOR APPLICATION NUMBER: 09/882,171  
; PRIOR FILING DATE: 2005-06-03  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/190,068  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 10/164,861

; PRIOR FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,626  
; PRIOR FILING DATE: 1997-03-07  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 1776  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (713)  
; OTHER INFORMATION: n equals a,t,g, or c  
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; NAME/KEY: SITE  
; LOCATION: (862)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1752)  
; OTHER INFORMATION: n equals a,t,g, or c  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1773)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-11-144-947-59

Query Match 68.8%; Score 17.2; DB 16; Length 1776;  
Best Local Similarity 79.2%; Pred. No. 5.9e+02;  
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25  
|||||  
DB 878 CAAGTCGAATTGAAAGRACTGTGC 901

RESULT 94  
US-09-809-391-226  
; Sequence 226, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 226  
; LENGTH: 1791  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-809-391-226

Query Match 68.8%; Score 17.2; DB 3; Length 1791;  
Best Local Similarity 79.2%; Pred. No. 5.9e+02;  
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTTTCG 25  
|||||  
DB 973 CAAGTCGAATTGAAAGRACTGTGC 996

RESULT 95  
US-09-882-171-226  
; Sequence 226, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 166 Human Secreted proteins  
; FILE REFERENCE: P2002F2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/038,621  
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; PRIOR APPLICATION NUMBER: 60/040,626  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
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; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
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Query Match      68.8%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 5.9e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY      2 CAAGTCGAACGGAAGGCGCTTTTCG 25
        |||||
Db      973 CAAGTCGAATTGAAAGRACTGTGC 996
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RESULT 96
US-10-164-861-226
; Sequence 226, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
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; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-226
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; Publication No. US20060084082A1
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
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; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-947-226
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Best Local Similarity 79.2%; Pred. No. 5.9e+02;
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RESULT 98
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; Sequence 553599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
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; LENGTH: 2258
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; ORGANISM: Homo sapiens
US-09-925-065A-553599

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; Sequence 553599, Application US/09925065A
; Publication No. US2005028172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR FILING DATE: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

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Best Local Similarity 86.4%; Pred. No. 5.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
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; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

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Best Local Similarity 86.4%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

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Title: US-10-665-708-21

Perfect score: 25

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Scoring table: IDENTITY\_NUC  
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Searched: 224314 seqs, 35277956 residues

Total number of hits satisfying chosen parameters: 448628

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	16	64.0	2397	7	US-11-217-529-254 Sequence 254, App
4	15.4	61.6	3663	7	US-11-217-529-1369 Sequence 1369, App
5	15.2	60.8	1260	7	US-11-217-529-5375 Sequence 5375, App
6	15.2	60.8	11611	6	US-10-541-993-4 Sequence 4, Appli
7	15	60.0	1157	6	US-10-196-749-391 Sequence 391, App
8	15	60.0	1157	6	US-11-101-316-145 Sequence 145, App
9	15	60.0	2787	7	US-11-217-529-76324 Sequence 76324, A
10	15	60.0	2952	7	US-11-217-529-4946 Sequence 4946, App
11	15	60.0	3093	7	US-11-217-529-3215 Sequence 3215, App
12	14.8	59.2	25	7	US-11-217-529-56270 Sequence 56270, A
13	14.8	59.2	497	6	US-10-488-619-2075 Sequence 2075, App
14	14.8	59.2	599	6	US-10-488-619-2155 Sequence 2155, App
15	14.8	59.2	784	6	US-10-488-619-2156 Sequence 2156, App
16	14.8	59.2	4365	7	US-11-217-529-4529 Sequence 4529, App
17	14.6	58.4	25	7	US-11-217-529-110320 Sequence 110320, A
18	14.6	58.4	471	7	US-11-217-529-77805 Sequence 77805, A
19	14.6	58.4	1350	7	US-11-217-529-730 Sequence 730, App
20	14.6	58.4	2541	7	US-11-217-529-534 Sequence 534, App
21	14.6	58.4	2883	7	US-11-217-529-82268 Sequence 82268, A
22	14.4	57.6	25	7	US-11-217-529-94649 Sequence 94649, A
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c	92	13.6	54.4	903	7	US-10-473-173-107 Sequence 107, App
c	93	13.6	54.4	927	6	US-10-473-173-107 Sequence 3863, Ap
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102	13.6	54.4	2595	7	US-11-217-529-76785	Sequence 76785, A	c 175	13	52.0	822	7	US-11-217-529-380	Sequence 380, App
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104	13.4	53.6	44	7	US-11-326-265-1	Sequence 1, Appli	177	13	52.0	903	7	US-11-217-529-78741	Sequence 78741, Ap
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c 110	13.4	53.6	562	6	US-10-488-619-2770	Sequence 2770, Ap	183	13	52.0	1098	7	US-11-217-529-494	Sequence 494, App
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c 128	13.4	53.6	1716	7	US-11-217-529-2406	Sequence 2406, Ap	201	13	52.0	2016	7	US-11-217-529-2923	Sequence 2923, Ap
c 129	13.4	53.6	1869	7	US-11-217-529-78128	Sequence 78128, A	c 202	13	52.0	2031	7	US-11-217-529-863	Sequence 863, App
130	13.4	53.6	1893	7	US-11-217-529-625	Sequence 625, App	c 203	13	52.0	2115	7	US-11-217-529-76502	Sequence 76502, A
131	13.4	53.6	1983	7	US-11-217-529-82251	Sequence 82251, A	c 204	13	52.0	2193	7	US-11-217-529-81384	Sequence 81384, A
132	13.4	53.6	2175	7	US-10-505-928-500	Sequence 500, App	c 205	13	52.0	2212	6	US-10-196-749-325	Sequence 325, App
133	13.4	53.6	2269	6	US-10-505-928-303	Sequence 303, App	c 206	13	52.0	2217	7	US-11-217-529-80740	Sequence 80740, A
134	13.4	53.6	2277	7	US-11-217-529-81881	Sequence 81881, A	c 207	13	52.0	2283	7	US-11-217-529-3378	Sequence 3378, Ap
c 135	13.4	53.6	2286	7	US-11-217-529-728	Sequence 728, App	c 208	13	52.0	2397	6	US-10-196-749-29	Sequence 29, Appl
136	13.4	53.6	2535	7	US-11-217-529-1209	Sequence 1209, Ap	c 209	13	52.0	2487	7	US-11-217-529-77452	Sequence 77452, A
c 137	13.4	53.6	2871	7	US-11-217-529-76224	Sequence 76224, A	210	13	52.0	2853	7	US-11-217-529-76130	Sequence 76130, A
c 138	13.4	53.6	3354	7	US-11-217-529-75390	Sequence 75390, A	211	13	52.0	3309	7	US-11-217-529-1900	Sequence 1900, Ap
c 139	13.4	53.6	3450	7	US-11-217-529-977	Sequence 977, App	212	13	52.0	3399	7	US-11-217-529-73	Sequence 73, Appl
140	13.4	53.6	3903	7	US-11-217-529-2311	Sequence 2311, App	213	13	52.0	3403	7	US-11-145-307A-74	Sequence 74, Appl
141	13.4	53.6	4293	6	US-11-217-529-76344	Sequence 76344, A	214	13	52.0	3669	7	US-11-181-115-36	Sequence 36, Appl
142	13.4	53.6	4898	6	US-10-505-928-372	Sequence 372, App	c 215	13	52.0	4005	7	US-11-217-529-3980	Sequence 3980, Ap
143	13.4	53.6	5900	6	US-10-505-928-182	Sequence 182, App	216	13	52.0	4308	7	US-11-217-529-82409	Sequence 82409, A
144	13.4	53.6	5957	6	US-10-473-173-106	Sequence 106, App	217	13	52.0	4654	6	US-10-505-528-20	Sequence 20, Appl
145	13.4	53.6	6317	6	US-10-473-173-387	Sequence 387, App	c 218	13	52.0	5775	6	US-10-512-386-55	Sequence 55, Appl
146	13.4	53.6	12918	6	US-10-501-834-4	Sequence 4, Appli	c 219	13	52.0	6105	7	US-11-217-529-1399	Sequence 1399, Ap
147	13.4	53.6	138941	6	US-10-489-730-10	GENERAL INFORMATI	c 220	13	52.0	6557	6	US-10-511-937-388	Sequence 388, App
148	13.2	52.8	278	6	US-10-473-173-309	Sequence 309, App	221	13	52.0	7131	7	US-11-217-529-77074	Sequence 77074, A
149	13.2	52.8	278	6	US-10-488-619-89	Sequence 89, Appl	c 222	13	52.0	8178	6	US-10-473-173-52	Sequence 52, Appl
150	13.2	52.8	492	7	US-11-217-529-173378	Sequence 173378, A	c 223	13	52.0	37426	6	US-10-473-173-32	Sequence 32, Appl
c 151	13.2	52.8	717	7	US-11-217-529-4041	Sequence 4041, Ap	c 224	12.8	51.2	25	7	US-11-217-529-107378	Sequence 107378, A
c 152	13.2	52.8	806	6	US-10-480-619-2939	Sequence 2939, Ap	c 225	12.8	51.2	25	7	US-11-217-529-115745	Sequence 115745, A
153	13.2	52.8	1242	7	US-11-217-529-75628	Sequence 75628, A	c 226	12.8	51.2	25	7	US-11-217-529-152423	Sequence 152423, A
c 154	13.2	52.8	1320	7	US-11-217-529-2321	Sequence 2321, Ap	227	12.8	51.2	76	7	US-11-267-871-640	Sequence 640, App
c 155	13.2	52.8	1377	7	US-11-217-529-4877	Sequence 4877, Ap	c 228	12.8	51.2	76	7	US-11-267-871-640	Sequence 640, App
c 156	13.2	52.8	1446	7	US-11-264-784-35	Sequence 35, Appl	c 229	12.8	51.2	161	6	US-10-488-619-678	Sequence 678, App
157	13.2	52.8	1611	7	US-11-217-529-3860	Sequence 3860, Ap	c 230	12.8	51.2	189	7	US-11-217-529-81593	Sequence 81593, A
158	13.2	52.8	1968	7	US-11-312-958-13	Sequence 13, Appl	231	12.8	51.2	411	6	US-10-861-934-1	Sequence 1, Appli
159	13.2	52.8	2545	6	US-10-511-937-440	Sequence 440, App	232	12.8	51.2	414	6	US-10-861-934-3	Sequence 3, Appli
c 160	13.2	52.8	2545	7	US-11-301-554-1900	Sequence 1900, Ap	233	12.8	51.2	426	6	US-10-861-934-27	Sequence 27, Appli
c 161	13.2	52.8	2850	7	US-11-217-529-79139	Sequence 79139, A	234	12.8	51.2	537	6	US-10-861-934-5	Sequence 5, Appli
c 162	13.2	52.8	3267	7	US-11-217-529-78066	Sequence 78066, A	235	12.8	51.2	602	6	US-10-946-650-47	Sequence 47, Appl
163	13.2	52.8	3330	7	US-11-217-529-3415	Sequence 3415, Ap	c 236	12.8	51.2	617	6	US-10-488-619-1860	Sequence 1860, Ap
164	13.2	52.8	3655	6	US-10-511-937-346	Sequence 346, App	c 237	12.8	51.2	619	6	US-10-488-619-2110	Sequence 2110, Ap
c 165	13.2	52.8	138941	6	US-10-489-730-10	GENERAL INFORMATI	c 238	12.8	51.2	630	6	US-10-488-619-1455	Sequence 1455, Ap
c 166	13	52.0	25	7	US-11-217-529-91576	Sequence 91576, A	239	12.8	51.2	684	7	US-11-217-529-1979	Sequence 1979, Ap
167	13	52.0	25	7	US-11-217-529-152160	Sequence 152160, A	240	12.8	51.2	711	6	US-10-488-619-1859	Sequence 1859, Ap
168	13	52.0	321	7	US-11-217-529-60939	Sequence 60939, A	241	12.8	51.2	792	7	US-11-217-529-77217	Sequence 77217, A
c 169	13	52.0	348	7	US-11-301-554-1019	Sequence 1019, Ap	242	12.8	51.2	828	6	US-10-473-173-120	Sequence 72, Appl
c 170	13	52.0	404	6	US-10-480-619-347	Sequence 347, App	243	12.8	51.2	843	6	US-10-861-934-7	Sequence 7, Appli
c 171	13	52.0	411	7	US-11-217-529-77519	Sequence 77519, A	c 244	12.8	51.2	924	6	US-10-861-934-33	Sequence 33, Appl





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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254

Query Match      64.0%; Score 16; DB 7; Length 2397;
Best Local Similarity 79.2%; Pred. No. 12;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2  CAAGTCGAACGGAAGGCCTTCG 25
Db      397 CACGTCGAGCGGAATGCTATTG 420

RESULT 4
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match      61.6%; Score 15.4; DB 7; Length 3663;
Best Local Similarity 76.0%; Pred. No. 25;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1  GCAAGTCGAACGGAAGGCCTTCG 25
Db      349 GCAAATCTAAGCTAAGGCCTTCG 325

RESULT 5
US-11-217-529-5375/c
; Sequence 5375, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5375
; LENGTH: 1260
; TYPE: DNA
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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5375

Query Match      60.8%; Score 15.2; DB 7; Length 1260;
Best Local Similarity 85.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4  AGTCGACGGAAGGCCTTT 23
Db      415 AGTGAACGGAAGGCCTTT 396

RESULT 6
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4

Query Match      60.8%; Score 15.2; DB 6; Length 11611;
Best Local Similarity 85.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCCTT 22
Db      8479 AAGAAGAACGGAAGGCCTT 8498

RESULT 7
US-10-196-749-391
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; Sequence 391, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P34301C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 391
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-391

Query Match      60.0%; Score 15; DB 6; Length 1157;
Best Local Similarity 78.3%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db     155 CAAGTGGAAACCGGAAGGCGCCTGC 177

RESULT 8
US-11-101-316-145
; Sequence 145, Application US/11101316
; Publication No. US2006009657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; TITLE OF INVENTION: UNDEREXPRESSED IN MELANOMA
; FILE REFERENCE: P32301C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2003-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
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; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 145
; LENGTH: 1157
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-101-316-145

Query Match      60.0%; Score 15; DB 7; Length 1157;
Best Local Similarity 78.3%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 CAAGTCGAACGGAAGGCGCTTTC 24
      ||||| ||||| ||||| ||||| |||||
Db     155 CAAGTGGAAACCGGAAGGCGCCTGC 177

RESULT 9
US-11-217-529-76324
; Sequence 76324, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76324
; LENGTH: 2787
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76324

Query Match      60.0%; Score 15; DB 7; Length 2787;
Best Local Similarity 78.3%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCGCTTT 23
      ||||| ||||| ||||| ||||| |||||
Db     550 GCAAAATCAACGGAAGTTCTGT 572

RESULT 10
US-11-217-529-4946/c
; Sequence 4946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4946
; LENGTH: 2952
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4946

Query Match          60.0%; Score 15; DB 7; Length 2952;
Best Local Similarity 78.3%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  3 AAGTCGAACGGAAGGCGCTTTCG 25
Db  2664 AATTCGATCTGGAAGGCCCTTCG 2642

RESULT 11
US-11-217-529-3215/c
; Sequence 3215, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3215
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3215

Query Match          60.0%; Score 15; DB 7; Length 3093;
Best Local Similarity 78.3%; Pred. No. 39;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTT 23
Db  1580 GCAAGTTGATAAGAAAGCGGTTT 1558

RESULT 12
US-11-217-529-56270/c
; Sequence 56270, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; ;
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-56270

Query Match          59.2%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGG 18
Db  20 GTAAGTCGAATGGAAGG 3

RESULT 13
US-10-488-619-2075
; Sequence 2075, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2075
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2075

Query Match          59.2%; Score 14.8; DB 6; Length 497;
Best Local Similarity 88.9%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGC 19
Db  69 CCAGTCGCACGGAAGGC 86

RESULT 14
US-10-488-619-2156
; Sequence 2156, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2156
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2156

Query Match          59.2%; Score 14.8; DB 6; Length 599;
Best Local Similarity 88.9%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGC 19
Db  537 CCAGTCGCACGGAAGGC 554

RESULT 15
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US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      59.2%; Score 14.8; DB 6; Length 784;
Best Local Similarity 88.9%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CAAGTCGAACGGAAGGC 19
DB      397 CCAAGTCGACGGAAGGC 380

RESULT 16
US-11-217-529-4529/c
; Sequence 4529, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4529
; LENGTH: 4365
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4529

Query Match      59.2%; Score 14.8; DB 7; Length 4365;
Best Local Similarity 88.9%; Pred. No. 51;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GCAAGTCGAACGGAAGG 18
DB      4149 GTAAGTCGAATGAAGG 4132

RESULT 17
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
```

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      58.4%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 30;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      5 GTCCACGGAAGGCGGTGTC 25

RESULT 18
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match      58.4%; Score 14.6; DB 7; Length 471;
Best Local Similarity 81.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 GTCGAACGGAAGGCCTTTCG 25
DB      152 GTCCACGGAAGGCGGTGTC 172

RESULT 19
US-11-217-529-730
; Sequence 730, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
```

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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730

Query Match      58.4%; Score 14.6; DB 7; Length 1350;
Best Local Similarity 81.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db  1128 CAAGCTAACGACAAAGTCCTT 1148

RESULT 20
US-11-217-529-514/c
; Sequence 514, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-514

Query Match      58.4%; Score 14.6; DB 7; Length 2541;
Best Local Similarity 81.0%; Pred. No. 60;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3 AAGTCGAACGGAAGGCCTTT 23
    ||||| ||||| ||||| |||||
Db  2480 AAGTCCAATGTAATGGCCTTT 2460

RESULT 21
US-11-217-529-82268/c
; Sequence 82268, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82268
; LENGTH: 2883
; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82268

Query Match      58.4%; Score 14.6; DB 7; Length 2883;
Best Local Similarity 81.0%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  3 AAGTCGAACGGAAGGCCTTT 23
    ||||| ||||| ||||| |||||
Db  2230 AAGTAGAAGGAACGCGCTTT 2210

RESULT 22
US-11-217-529-94649
; Sequence 94649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94649

Query Match      57.6%; Score 14.4; DB 7; Length 25;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCCTTTC 24
    ||||| ||||| ||||| |||||
Db  1 GCAACGCGACCGGAACACTACTTTC 24

RESULT 23
US-11-217-529-4661
; Sequence 4661, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4661
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4661

Query Match      57.6%; Score 14.4; DB 7; Length 750;
Best Local Similarity 75.0%; Pred. No. 63;
```

```
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| | | | | | | | | |
Db 297 CAAGTCGCATGAAGAGCGCGTTAG 320

RESULT 24
US-09-949-925-62/c
; Sequence 62, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-62

Query Match 57.6%; Score 14.4; DB 1; Length 1452;
Best Local Similarity 75.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| | | | | | | | | |
Db 949 GGAAGTATAAGGTAAGGCGCTTTC 926

RESULT 25
US-11-256-221-1
; Sequence 1, Application US/11256221
; Publication No. US20060094094A1
; GENERAL INFORMATION:
; APPLICANT: Sugio, Tsuyoshi
; APPLICANT: Miura, Akira
; APPLICANT: Parada Valdecantos, Pilar A.
; APPLICANT: Badilla Ohlbaum, Ricardo
; TITLE OF INVENTION: BACTERIA STRAIN WENELN DSM 16786, USE OF SAID BACTERIA FOR
; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE
; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID
; TITLE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA
; FILE REFERENCE: 15053.15U801
; CURRENT APPLICATION NUMBER: US/11/256,221
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: CL 2731-2004
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 1
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Bacteria
US-11-256-221-1

Query Match 57.6%; Score 14.4; DB 7; Length 1531;
Best Local Similarity 93.8%; Pred. No. 70;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCAAGTCGAACGGAAA 16
    ||||| | | | | | | | |
Db 53 GCAAGTCGAACGGTAA 68

RESULT 26
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; APPLICANT: GICQUEL, BRIGITTE
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCObACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
US-11-324-517-36

Query Match 57.6%; Score 14.4; DB 7; Length 1600;
Best Local Similarity 75.0%; Pred. No. 70;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| | | | | | | | | |
Db 1476 CAAGTCGACGGGAAGCGCGTACG 1499

RESULT 27
US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```

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; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

Query Match          57.6%; Score 14.4; DB 7; Length 1872;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| ||||| ||||| ||||| |||||
Db 163 CGATTCGTATGGAATGCGCTTTG 140

RESULT 28
US-11-217-529-1992
; Sequence 1992, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1992
; LENGTH: 1893
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1992

Query Match          57.6%; Score 14.4; DB 7; Length 1893;
Best Local Similarity 75.0%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  1 GCAAGTCGAACGGAAGGCGCTTTC 24
    ||||| ||||| ||||| ||||| |||||
Db 768 GCAAGATGGATGGAAGGCGCTTTC 791

RESULT 29
US-11-217-529-75610/c
; Sequence 75610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75610
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75610

Query Match          57.6%; Score 14.4; DB 7; Length 2013;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| ||||| ||||| ||||| |||||
Db 527 CAATTCATCTGAAAGTCCTTTG 504

RESULT 30
US-11-217-529-3183
; Sequence 3183, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3183
; LENGTH: 2376
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3183

Query Match          57.6%; Score 14.4; DB 7; Length 2376;
Best Local Similarity 75.0%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  2 CAAGTCGAACGGAAGGCGCTTTCG 25
    ||||| ||||| ||||| ||||| |||||
Db 1306 CAAGTCGAAGCTAACGGGATTCG 1329

RESULT 31
US-10-946-650-35
; Sequence 35, Application US/10946650
; Publication No. US20060101535A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: ROTTMANN, WILLIAM H.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: SANDERS, PAUL
; APPLICANT: ZHANG, GARY
; APPLICANT: FITZGERALD, SANDRA JOANNE
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 044463-0348
; CURRENT APPLICATION NUMBER: US/10/946,650
; CURRENT FILING DATE: 2004-09-22
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 2435
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-946-650-35
```



QY 1 GCAAGTCGAACGGAAAGGCCTTC 24

```
Db      838 GAAATTCAAACGGAATAGGCTTC 815
; Sequence 77141, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77141
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77141

Query Match      56.8%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 TCGAACGGAAGGCTTTC 24
Db      187 TCGAAGAGAAAGGCTTTC 169

RESULT 39
US-11-217-529-60921/c
; Sequence 60921, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-60921

Query Match      56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCTTTC 24
Db      22 AATTCGATCTCGAAGGCCCTTC 1

RESULT 40
US-11-217-529-117575/c
; Sequence 117575, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

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```
Db      838 GAAATTCAAACGGAATAGGCTTC 815
; Sequence 75552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75552
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75552

Query Match      56.8%; Score 14.2; DB 7; Length 480;
Best Local Similarity 84.2%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3 AAGTCGAACGGAAGGCTTTC 21
Db      212 AAGACGAATCGAGAGGCTTTC 230

RESULT 37
US-11-217-529-1257/c
; Sequence 1257, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1257
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1257

Query Match      56.8%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      6 TCGAACGGAAGGCTTTC 24
Db      187 TCGAAGAGAAAGGCTTTC 169

RESULT 38
US-11-217-529-77141/c
```

```
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-117575

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 23
   ||||| ||||| ||||| |||||
Db 22 CAGGTCGAAGGTAATGACTT 1

RESULT 41
US-11-217-529-152173
; Sequence 152173, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152173
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152173

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 23
   ||||| ||||| ||||| |||||
Db 4 CAAGTTCTCGGAAGGCCTCT 25

RESULT 42
US-11-217-529-188129
; Sequence 188129, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
```

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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-188129

Query Match          56.0%; Score 14; DB 7; Length 25;
Best Local Similarity 77.3%; Pred. No. 61;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTT 22
   ||||| ||||| ||||| |||||
Db 1 GAAACTCTACCTGAAGGCCTT 22

RESULT 43
US-11-139-257-9
; Sequence 9, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Hapde, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; TITLE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-139-257-9

Query Match          56.0%; Score 14; DB 7; Length 150;
Best Local Similarity 77.3%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTT 23
   ||||| ||||| ||||| |||||
Db 10 CATGACAAACGCAAGGCCTTT 31

RESULT 44
US-11-139-257-14
; Sequence 14, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Hapde, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; TITLE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Positive internal control
```

```
US-11-139-257-14
Query Match          56.0%; Score 14; DB 7; Length 210;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 40 CATGACAAACGGCAAGGCTTTT 61

RESULT 45
US-11-139-257-12
; Sequence 12, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Control Sequence
US-11-139-257-12

Query Match          56.0%; Score 14; DB 7; Length 213;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 41 CATGACAAACGGCAAGGCTTTT 62

RESULT 46
US-11-217-529-81114
; Sequence 81114, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81114
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81114

Query Match          56.0%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTT 22
```

```
Db 16 GCCAGTCGAAAGAAAGGGCTT 37

RESULT 47
US-11-217-529-81538
; Sequence 81538, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81538
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81538

Query Match          56.0%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 89;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 90 CAAGTTCTTCGAAAGGCCTCT 111

RESULT 48
US-11-217-529-79564/c
; Sequence 79564, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79564
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79564

Query Match          56.0%; Score 14; DB 7; Length 381;
Best Local Similarity 77.3%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
Db 108 CAAGTCGATCGGAAGTGACTCT 87

RESULT 49
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```
US-11-217-529-78815
; Sequence 78815, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78815
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78815

Query Match          56.0%; Score 14; DB 7; Length 438;
Best Local Similarity 77.3%; Pred. No. 92;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTC 24
    ||||| ||||| ||||| |||||
Db 1 ATGTCGAAGGAAGGTTTGC 22

RESULT 50
US-11-217-529-2487
; Sequence 2487, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2487
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-2487

Query Match          56.0%; Score 14; DB 7; Length 579;
Best Local Similarity 77.3%; Pred. No. 96;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCCAACTAAAGGACTTT 107
    ||||| ||||| ||||| |||||
Db 86 CAATTCCAACTAAAGGACTTT 107

RESULT 51
US-11-217-529-81387
; Sequence 81387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
```

```
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81387
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81387

Query Match          56.0%; Score 14; DB 7; Length 666;
Best Local Similarity 77.3%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTC 24
    ||||| ||||| ||||| |||||
Db 374 AAGTGAATGGAAGGCTCTCC 395

RESULT 52
US-11-217-529-4416
; Sequence 4416, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4416
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4416

Query Match          56.0%; Score 14; DB 7; Length 837;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTC 24
    ||||| ||||| ||||| |||||
Db 176 AAGTCAAGGAAGATGTCATTTC 197

RESULT 53
US-11-217-529-174359
; Sequence 174359, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
```

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; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174359
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-174359

Query Match          56.0%; Score 14; DB 7; Length 984;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCCTT 22
    ||||| ||||| ||||| |||||
Db 835 GAAACTCTACCTGAAGGCCTT 856

RESULT 54
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7

Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 55
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9
```

```
Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 56
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH Variant RC-35
US-10-975-697-11

Query Match          56.0%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCCTTTTCG 25
    ||||| ||||| ||||| |||||
Db 1014 AGTCGAAAGACTGGCCTTTTCG 1035

RESULT 57
US-11-217-529-78457/c
; Sequence 78457, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHITIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78457
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-78457

Query Match          56.0%; Score 14; DB 7; Length 1194;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAAGTCGAACGGAAGGCCTTT 23
    ||||| ||||| ||||| |||||
Db 980 CAGGTCGAAGGGTAATGACTTT 959
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RESULT 58
US-10-196-749-223/c
; Sequence 223, Application US/10196749
; Publication No. US200600948641
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 223
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-223

Query Match      56.0%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCGCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 59
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529

Query Match      56.0%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCGCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 58
US-10-196-749-223/c
; Sequence 223, Application US/10196749
; Publication No. US200600948641
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 223
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-223

Query Match      56.0%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCGCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      807 AAGGCGCCGGAAGGCGGTGC 786

RESULT 59
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```

```
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match      56.0%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3  AAGTCGAACGGAAGGCGCTTTC 24
      ||| ||| ||| ||| ||| ||| |||
Db      971 AAGTCTAACGGTAATACCTTGC 950

RESULT 60
US-09-949-925-78/c
; Sequence 78, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1212)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-78

Query Match      56.0%; Score 14; DB 1; Length 1931;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GCAAGTCGAACGGAAGGCGCTT 22
      ||| ||| ||| ||| ||| ||| |||
Db      253 GCTCATCGAAGGGAAGGCATT 232

RESULT 61
US-09-949-925-12/c
```

; Sequence 12, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P203P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; PRIOR FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 1932  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-949-925-12

Query Match 56.0%; Score 14; DB 1; Length 1932;  
Best Local Similarity 77.3%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22  
||| ||||| ||||| |||  
Db 253 GCTCATCGAAGGGAAGGCATT 232

RESULT 62  
US-11-217-529-77876  
; Sequence 77876, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77876  
; LENGTH: 1950  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; US-11-217-529-77876

Query Match 56.0%; Score 14; DB 7; Length 1950;  
Best Local Similarity 77.3%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 ACTCGAACGGAAGGCCTTTCG 25  
| | | | | | | | | | | | | | | | | | | | |  
Db 1230 ACTGGAAGTGAAGGCTTTCG 1251

RESULT 63  
US-11-217-529-82283/c  
; Sequence 82283, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 82283  
; LENGTH: 2436  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; US-11-217-529-82283

Query Match 56.0%; Score 14; DB 7; Length 2436;  
Best Local Similarity 77.3%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22  
| | | | | | | | | | | | | | | | | | | | |  
Db 1922 GAAACTTGAAGGGAAGGCCTT 1901

RESULT 64  
US-11-217-529-522  
; Sequence 522, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 522  
; LENGTH: 2511  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; US-11-217-529-522

Query Match 56.0%; Score 14; DB 7; Length 2511;  
Best Local Similarity 77.3%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGACGGAAGGCCTT 23  
||| ||||| ||||| |||  
Db 357 CAACTCCAATGGAAGGAGCGTT 378



```
RESULT 65
US-11-217-529-75493
; Sequence 75493, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75493
; LENGTH: 2700
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75493

Query Match          56.0%; Score 14; DB 7; Length 2700;
Best Local Similarity 77.3%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTTTC 24
||||| ||||| ||||| ||||| |||||
Db 691 AAGTCATACAGAAAGCCGATC 712

RESULT 66
US-11-217-529-3368/c
; Sequence 3368, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3368
; LENGTH: 2706
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3368

Query Match          56.0%; Score 14; DB 7; Length 2706;
Best Local Similarity 77.3%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCTTT 23
||||| ||||| ||||| ||||| |||||
Db 1768 CAAGACCAGAGTAAGGCCTTT 1747

RESULT 67
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-29

Query Match          56.0%; Score 14; DB 6; Length 6805;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCCTTTTCG 25
||||| ||||| ||||| ||||| |||||
Db 1258 AGTCGAAGACTGGCCCTTTCG 1237

RESULT 68
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-31

Query Match          56.0%; Score 14; DB 6; Length 7330;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCCTTTTCG 25
||||| ||||| ||||| ||||| |||||
Db 1258 AGTCGAAGACTGGCCCTTTCG 1237

RESULT 69
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
```

```
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:glyA overexpression
;
US-10-520-210-25

Query Match          56.0%; Score 14; DB 6; Length 7701;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      4 AGTCGAACGGAAGGCCTTTCG 25
Db      1263 AGTCGAAGACTGGGCCTTTCG 1242

RESULT 70
US-10-520-210-24/c
; Sequence 24, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 7926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:serA overexpression
;
US-10-520-210-24

Query Match          56.0%; Score 14; DB 6; Length 7926;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      4 AGTCGAACGGAAGGCCTTTCG 25
Db      1263 AGTCGAAGACTGGGCCTTTCG 1242

RESULT 71
US-11-297-317-15
; Sequence 15, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
```

```
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-G1 HuAb-VHQ
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO:12 (VHQ) from 3921-4274)
US-11-297-317-15

Query Match          56.0%; Score 14; DB 7; Length 8687;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCCTT 22
Db      6871 GCAATTCTGAAGGAAGTCCTT 6892

RESULT 72
US-11-297-317-16
; Sequence 16, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Aversa
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballido Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldanha
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 8687
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-G1 HuAb-VHE
; OTHER INFORMATION: (Complete DNA Sequence of a humanised heavy chain expression vect
; OTHER INFORMATION: or comprising SEQ ID NO: 11 (VHE) from 3921-4274)
US-11-297-317-16

Query Match          56.0%; Score 14; DB 7; Length 8687;
Best Local Similarity 77.3%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GCAAGTCGAACGGAAGGCCTT 22
Db      6871 GCAATTCTGAAGGAAGTCCTT 6892

RESULT 73
US-11-297-317-18
; Sequence 18, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
```

; APPLICANT: Gregorio Aversa  
; APPLICANT: Frank Kolbinger  
; APPLICANT: Jose M. Carballido Herrera  
; APPLICANT: Andras Aszodi  
; APPLICANT: Jose W. Saldaña  
; APPLICANT: Bruce M. Hall  
; TITLE OF INVENTION: Therapeutic binding molecules  
; FILE REFERENCE: Not Yet Known  
; CURRENT APPLICATION NUMBER: US/11/297,317  
; CURRENT FILING DATE: 2005-12-08  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 9362  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-K HuAb-VL1 hum  
; OTHER INFORMATION: V2  
; OTHER INFORMATION: (Complete DNA Sequence of a humanised light chain expression vect  
; OTHER INFORMATION: or comprising SEQ ID NO: 13 (humV2=VLm) from 3926-4246)  
US-11-297-317-18

Query Match 56.0%; Score 14; DB 7; Length 9362;  
Best Local Similarity 77.3%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22  
Db 7548 GCAATTCGAAAGGAAAGTCCTT 7569

## RESULT 74

US-11-297-317-17  
; Sequence 17, Application US/11297317  
; Publication No. US2006008825A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregorio Aversa  
; APPLICANT: Frank Kolbinger  
; APPLICANT: Jose M. Carballido Herrera  
; APPLICANT: Andras Aszodi  
; APPLICANT: Jose W. Saldaña  
; APPLICANT: Bruce M. Hall  
; TITLE OF INVENTION: Therapeutic binding molecules  
; FILE REFERENCE: Not Yet Known  
; CURRENT APPLICATION NUMBER: US/11/297,317  
; CURRENT FILING DATE: 2005-12-08  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 17  
; LENGTH: 9400  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Nucleotide sequence of the expression vector HCMV-K HuAb-VL1 hum  
; OTHER INFORMATION: V1  
; OTHER INFORMATION: (Complete DNA Sequence of a humanised light chain expression vect  
; OTHER INFORMATION: or comprising SEQ ID NO: 14 (humV1=VLh) from 3964-4284  
US-11-297-317-17

Query Match 56.0%; Score 14; DB 7; Length 9400;  
Best Local Similarity 77.3%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22  
Db 7586 GCAATTCGAAAGGAAAGTCCTT 7607

## RESULT 75

US-10-541-993-4/c

; Sequence 4, Application US/10541993  
; Publication No. US20060099670A1  
; GENERAL INFORMATION:  
; APPLICANT: Matuschek, Markus  
; APPLICANT: Heinekamp, Thorsten  
; APPLICANT: Schmidt, Andre  
; APPLICANT: Brakhage, Axel  
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus  
; FILE REFERENCE: 13311-00010-US  
; CURRENT APPLICATION NUMBER: US/10/541,993  
; CURRENT FILING DATE: 2005-07-08  
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100  
; PRIOR FILING DATE: 2004-01-09  
; PRIOR APPLICATION NUMBER: DE 103 00 649.4  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: DE 103 41 272.7  
; PRIOR FILING DATE: 2003-09-08  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 11611  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Vector  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (227)..(227)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (318)..(318)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (526)..(526)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (8946)..(8946)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (10028)..(10028)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-541-993-4

Query Match 56.0%; Score 14; DB 6; Length 11611;  
Best Local Similarity 77.3%; Pred. No. 1.5e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCAAGTCGACGGAAGGCCTT 22  
Db 5488 GCAATTCGAAAGGAAAGTCCTT 5467

## RESULT 76

US-10-519-335-37/c  
; Sequence 37, Application US/10519335  
; Publication No. US20060099210A1  
; GENERAL INFORMATION:  
; APPLICANT: Cavarec, Laurent  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Destenaves, Benoit  
; APPLICANT: Gonthier, Catherine  
; APPLICANT: Elias, Isabelle  
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN T  
; FILE REFERENCE: G-194US03PCT  
; CURRENT APPLICATION NUMBER: US/10/519,335  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 60/391,359

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; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60402)..(60402)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61110)..(61110)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98207)..(98207)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98208)..(98208)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98209)..(98209)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98210)..(98210)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98211)..(98211)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99743)..(99743)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108055)..(108055)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109094)..(109094)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109125)..(109125)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (118900)..(118900)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119024)..(119024)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119053)..(119053)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119115)..(119115)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119121)..(119121)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119123)..(119123)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (141674)..(141674)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142063)..(142063)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142137)..(142137)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (142967)..(142967)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143077)..(143077)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143506)..(143506)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143587)..(143587)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (143629)..(143629)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (149079)..(149079)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5363)..(5363)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8080)..(8080)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10296)..(10296)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14528)..(14528)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15336)..(15336)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15457)..(15457)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16288)..(16288)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16306)..(16306)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16316)..(16316)
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OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (16357)..(16397)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (56012)..(56012)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (57662)..(57662)  
OTHER INFORMATION: n = a or c or g or t  
FEATURE:  
NAME/KEY: 5'UTR  
LOCATION: (1)..(54)  
OTHER INFORMATION: exon 1  
FEATURE:  
NAME/KEY: exon  
LOCATION: (55)..(124)  
OTHER INFORMATION: exon 1  
FEATURE:  
NAME/KEY: exon  
LOCATION: (91147)..(91244)  
OTHER INFORMATION: exon 2  
FEATURE:  
NAME/KEY: exon  
LOCATION: (93669)..(93834)  
OTHER INFORMATION: exon 3  
FEATURE:  
NAME/KEY: exon  
LOCATION: (96310)..(96422)  
OTHER INFORMATION: exon 4  
FEATURE:  
NAME/KEY: exon  
LOCATION: (99546)..(99723)  
OTHER INFORMATION: exon 5  
FEATURE:  
NAME/KEY: exon  
LOCATION: (125441)..(125605)

Query Match 56.0%; Score 14; DB 6; Length 151830;  
Best Local Similarity 77.3%; Pred. No. 1.7e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCTTT 23  
DB 127951 CAAGGCGATCACAGGGCTTT 127930

RESULT 77  
US-10-506-549-3/c  
; Sequence 3, Application US/10506549  
; Publication No. US20060100417A1  
; GENERAL INFORMATION:  
; APPLICANT: APPLERA CORPORATION  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; AND USES THEREOF  
; FILE REFERENCE: CL001361-US  
; CURRENT APPLICATION NUMBER: US/10/506,549  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 60/361,343  
; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 394191  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(394191)

OTHER INFORMATION: n = A,T,C or G  
US-10-506-549-3

Query Match 56.0%; Score 14; DB 6; Length 394191;  
Best Local Similarity 77.3%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 AGTCGAACGGAAGGCTTTTCG 25  
DB 388331 AGGCAATGGAAAGGCTTTAG 388310

RESULT 78  
US-11-217-529-4473/c  
; Sequence 4473, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4473  
; LENGTH: 987  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-4473

Query Match 55.2%; Score 13.8; DB 7; Length 987;  
Best Local Similarity 72.0%; Pred. No. 1.3e+02;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 GCAAGTCGAACGGAAGGCTTTTCG 25  
DB 745 GCAAGGCGACTGCGAAGGCGTCTAG 721

RESULT 79  
US-11-217-529-82631  
; Sequence 82631, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 82631  
; LENGTH: 1200  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-82631

Query Match 55.2%; Score 13.8; DB 7; Length 1200;  
Best Local Similarity 72.0%; Pred. No. 1.3e+02;

Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGCCCTTTCG 25  
Db 558 GCACGGCGACCTGAAACTCTTTCG 582

RESULT 80  
US-10-473-173-97  
; Sequence 97, Application US/10473173  
; Publication No. US2006008822A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN ANDEL INSTITUTE  
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell  
; FILE REFERENCE: 38345-170094  
; CURRENT APPLICATION NUMBER: US/10/473,173  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 498  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 97  
; LENGTH: 1212  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-473-173-97

Query Match 55.2%; Score 13.8; DB 6; Length 1212;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAG 17  
Db 1002 GCAAGTCGAACGGAAG 1018

RESULT 81  
US-11-529-75992  
; Sequence 75992, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 75992  
; LENGTH: 1236  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-529-75992

Query Match 55.2%; Score 13.8; DB 7; Length 1236;  
Best Local Similarity 88.2%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGG 18  
Db 1176 CAAGTCGAAGGGAATG 1192

RESULT 82  
US-11-217-529-79704

; Sequence 79704, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 79704  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-79704

Query Match 55.2%; Score 13.8; DB 7; Length 1380;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGC 19  
Db 1061 AAGTCGAACGGAAGGC 1077

RESULT 83  
US-11-217-529-2853  
; Sequence 2853, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2853  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2853

Query Match 55.2%; Score 13.8; DB 7; Length 1647;  
Best Local Similarity 88.2%; Pred. No. 1.4e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAG 17  
Db 189 GCACATCGAACGGAAG 205

RESULT 84  
US-11-217-529-80937  
; Sequence 80937, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO

```
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80937
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80937

Query Match      55.2%; Score 13.8; DB 7; Length 1647;
Best Local Similarity 72.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      1230 GCATTCGATGAGAAAGGCATTTG 1254

RESULT 85
US-10-196-749-275
; Sequence 275, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 275
; LENGTH: 1915
; TYPE: DNA
```

```
; ORGANISM: Homo Sapien
US-10-196-749-275

Query Match      55.2%; Score 13.8; DB 6; Length 1915;
Best Local Similarity 72.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      560  GCAAGTCGAGTGATGAGCCTGTG 584

RESULT 86
US-11-217-529-173838
; Sequence 173838, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173838
; LENGTH: 2157
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173838

Query Match      55.2%; Score 13.8; DB 7; Length 2157;
Best Local Similarity 72.0%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  GCAAGTCGACGGAAGGCCTTTG 25
Db      1981 GCAAGTCAATTTCAATGCCTGTG 2005

RESULT 87
US-11-217-529-76817
; Sequence 76817, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76817
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76817

Query Match      55.2%; Score 13.8; DB 7; Length 2454;
Best Local Similarity 72.0%; Pred. No. 1.5e+02;
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Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25  
Db 1598 GGAAGCCGACAGTCAGGCGCTTACG 1622

## RESULT 88

US-10-505-928-84

; Sequence 84, Application US/10505928  
; Publication No. US2006008532A1  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
; FILE REFERENCE: 28967/39178  
; CURRENT APPLICATION NUMBER: US/10/505,928  
; CURRENT FILING DATE: 2004-08-27  
; PRIOR APPLICATION NUMBER: US 60/363,019  
; PRIOR FILING DATE: 2002-03-07  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: PatentIn 3.2  
; SEQ ID NO 84  
; LENGTH: 3588  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-505-928-84

Query Match 55.2%; Score 13.8; DB 6; Length 3588;  
Best Local Similarity 72.0%; Pred. No. 1.6e+02;  
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCAAGTCGAACGGAAGGCCTTTTCG 25  
Db 377 GCACGCTCTCGGAAGACCTGCGC 401

## RESULT 89

US-11-217-529-98883

; Sequence 98883, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 98883  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-98883

Query Match 54.4%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AAGTCGAACGGAAGGCCTT 22  
Db 6 AAGTCACACGCAAGGCCTT 25

## RESULT 90

US-11-217-529-130040/c

; Sequence 130040, Application US/11217529

; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 130040  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-130040

Query Match 54.4%; Score 13.6; DB 7; Length 25;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCT 21  
Db 21 CAAGTCGATCGGAAGTGACT 2

## RESULT 91

US-10-488-619-2026

; Sequence 2026, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2026  
; LENGTH: 523  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-2026

Query Match 54.4%; Score 13.6; DB 6; Length 523;  
Best Local Similarity 80.0%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCCTTT 23  
Db 257 AATCAAAAGGAAGGACTTT 276

## RESULT 92

US-11-217-529-4440

; Sequence 4440, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529



; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 4440  
 ; LENGTH: 903  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-4440

Query Match 54.4%; Score 13.6; DB 7; Length 903;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCGAACGGAAGGCTTTTCG 25  
 DB 268 TCGAACGGAAGAGACTTTGG 287

RESULT 93  
 US-10-473-173-107/c  
 ; Sequence 107, Application US/10473173  
 ; Publication No. US20060088231  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VAN ANDEL INSTITUTE  
 ; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell  
 ; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification  
 ; FILE REFERENCE: 38345-170094  
 ; CURRENT APPLICATION NUMBER: US/10/473,173  
 ; CURRENT FILING DATE: 2003-09-29  
 ; PRIOR APPLICATION NUMBER: US 60/279,411  
 ; PRIOR FILING DATE: 2001-03-29  
 ; NUMBER OF SEQ ID NOS: 498  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 107  
 ; LENGTH: 927  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-473-173-107

Query Match 54.4%; Score 13.6; DB 6; Length 927;  
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CAAGTCGAACGGAAGGCT 21  
 DB 564 CAGGAAGCAGGAAGGCT 545

RESULT 94  
 US-11-217-529-3863  
 ; Sequence 3863, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 3863  
 ; LENGTH: 1224  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus

US-11-217-529-3863  
 Query Match 54.4%; Score 13.6; DB 7; Length 1224;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GTCGAACGGAAGGCTTTTC 24  
 DB 309 GTCGAAGGAAGGCTTGC 328

RESULT 95  
 US-11-217-529-78935  
 ; Sequence 78935, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 78935  
 ; LENGTH: 1242  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-78935

Query Match 54.4%; Score 13.6; DB 7; Length 1242;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 TCGAACGGAAGGCTTTTCG 25  
 DB 63 TCGAACAGTAAGGCTTTTG 82

RESULT 96  
 US-11-217-529-2620  
 ; Sequence 2620, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 2620  
 ; LENGTH: 1443  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-2620

Query Match 54.4%; Score 13.6; DB 7; Length 1443;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 GCAAGTCGAACGGAAGGCC 20
Db 249 GGAAGTGAAGGGGAAGGCC 268

RESULT 97
US-11-217-529-76764
; Sequence 76764, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76764
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76764

Query Match 54.4%; Score 13.6; DB 7; Length 1479;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 AGTCGAACGGAAGGCCCTT 23
Db 7 AGTCGAACACTACAGGCCCTT 26

RESULT 98
US-10-505-928-419
; Sequence 419, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 419
; LENGTH: 1667
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-419

Query Match 54.4%; Score 13.6; DB 6; Length 1667;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CAAGTCGAACGGAAGGCCCT 21
Db 370 CAAGTCGAGCGGCAAGCACT 389

RESULT 99
US-11-217-529-82107
; Sequence 82107, Application US/11217529
; Publication No. US20060099612A1
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; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82107
; LENGTH: 1797
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82107
```

```
Query Match 54.4%; Score 13.6; DB 7; Length 1797;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy 2 CAAGTCGAACGGAAGGCCCT 21
Db 485 CAAGCTCAACGGATAGGCCT 504
```

```
RESULT 100
US-11-217-529-5081
; Sequence 5081, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5081
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5081
```

```
Query Match 54.4%; Score 13.6; DB 7; Length 2040;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
Qy 4 AGTCGAACGGAAGGCCCTTT 23
Db 62 AGACGAACCTTAAAGGCATTT 81
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Search completed: May 19, 2006, 05:38:11
Job time : 18.512 secs
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 282.94 Seconds  
(without alignments)  
591.412 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24

Sequence: i caagtcgaacggaagccttcg 24

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

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1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

15: Geneseqn2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	24	100.0	24	10	ADG88353
3	24	100.0	24	14	AEA08228
4	24	100.0	25	4	AAD11271
5	24	100.0	25	10	ADG88352
6	24	100.0	25	14	AEA08227
7	22.4	93.3	500	13	ADZ20587
8	22.4	93.3	1449	14	AEA22405
9	22.4	93.3	1455	14	AEA22412
10	22.4	93.3	1482	14	AEA22404
11	21	87.5	22	4	AAD11273
12	21	87.5	22	10	ADG88354
13	21	87.5	22	14	AEA08229
14	20.8	86.7	50	12	ADP94057
15	20.8	86.7	166	2	AAX32481
16	20.8	86.7	460	8	ABZ76674
17	20.8	86.7	497	14	ABE72673
18	20.8	86.7	500	14	AED64356

92	18.8	78.3	211	14	AEB98761	Aeb98761 Mycobacte	165	16.6	69.2	4456	4	ABL04788	AbL04788 Drosophil
93	18.8	78.3	349	13	ADV99481	Adv99481 Meningiti	c 166	16.6	69.2	18900	13	ADM00484	Adw00484 Escherich
94	18.8	78.3	1271	23	AAV24293	Aav24293 Mycobacte	167	16.4	68.3	25	2	AAV24418	Aav24418 Target se
95	18.8	78.3	1416	14	AEA22416	Aea22416 Mycobacte	168	16.4	68.3	25	2	AAV13026	Aas13026 Mycobacte
96	18.8	78.3	1421	14	AEA22402	Aea22402 Mycobacte	169	16.4	68.3	25	4	AAS30718	Aas30718 Mycobacte
97	18.8	78.3	1463	14	AEA22409	Aea22409 Mycobacte	170	16.4	68.3	25	4	AAS30716	Aas30716 Mycobacte
98	18.8	78.3	1464	3	AAZ35571	Aaz35571 Mycobacte	171	16.4	68.3	549	4	ABL15533	AbL15533 Drosophil
99	18.8	78.3	1464	5	AAS11027	Aas11027 Mycobacte	172	16.4	68.3	1456	15	AEQ07725	Aeg07725 Nocardioid
100	18.8	78.3	1469	13	ADR90574	Adr90574 M kansasi	173	16.4	68.3	5503	4	ABL15532	AbL15532 Drosophil
101	18.8	78.3	1524	4	AAS30719	Aas30719 Mycobacte	174	16.2	67.5	587	8	ABZ53802	AbZ53802 Aspergill
102	18.8	78.3	1536	10	ADB61681	AdB61681 16S rRNA	c 175	16.2	67.5	590	8	ABQ83792	Abq83792 Normal co
103	18.8	78.3	1536	10	ADB61682	AdB61682 16S rRNA	176	16.2	67.5	637	3	AAF14590	Aaf14590 Aspergill
104	18.8	78.3	1537	10	ADF41649	Adf41649 Mycobacte	177	16.2	67.5	637	13	ADU58631	Adu58631 Aspergill
c 105	18.8	78.3	36241	10	ADB74385	AdB74385 Mycobacte	178	16.2	67.5	637	14	AD296634	Ad296634 Aspergill
106	18.8	78.3	36470	10	ADB74374	AdB74374 Mycobacte	c 179	16.2	67.5	685	14	AEB88183	Aeb88183 Human CDN
107	18.8	78.3	110000	4	AAI99682_14	Continuation (15 o	c 180	16.2	67.5	755	14	AEB88269	Aeb88269 Human DNA
108	18.8	78.3	110000	4	RAI99683_14	Continuation (15 o	c 181	16.2	67.5	788	3	AAC33114	Aac33114 Arabidops
109	18.4	76.7	36	14	ADU69991	Adu69991 LAMP reac	c 182	16.2	67.5	790	14	AEB88271	Aeb88271 Human DNA
110	18.4	76.7	37	14	ADU69989	Adu69989 LAMP reac	c 183	16.2	67.5	813	14	AEB88267	Aeb88267 Human DNA
111	18.4	76.7	39	14	ADU69984	Adu69984 LAMP reac	c 184	16.2	67.5	972	6	ABK77386	Abk77386 Bacillus
112	18.4	76.7	39	14	ADU69983	Adu69983 LAMP reac	c 185	16.2	67.5	1049	13	ADS95257	Ads95257 Murine th
113	18.4	76.7	39	14	ADU69985	Adu69985 LAMP reac	c 186	16.2	67.5	1049	13	ADV68114	Adv68114 Biologica
114	18.4	76.7	39	14	AEB98765	Aeb98765 Mycobacte	c 187	16.2	67.5	1498	4	AAF63387	Aaf63387 cDNA enco
115	18.4	76.7	39	14	AEB98779	Aeb98779 Mycobacte	c 188	16.2	67.5	1588	4	AAF63423	Aaf63423 Human CD3
116	18.4	76.7	39	15	AEF95350	Aef95350 Nucleic a	c 189	16.2	67.5	1735	13	ADX53856	Adx53856 Plant ful
117	18.4	76.7	41	14	ADU69960	Adu69960 LAMP reac	c 190	16.2	67.5	1902	13	ADT48449	Adt48449 Bacterial
118	18.4	76.7	41	14	ADU69958	Adu69958 LAMP reac	c 191	16.2	67.5	2226	13	ACN43714	Acn43714 Human dia
119	18.4	76.7	42	14	ADU69959	Adu69959 LAMP reac	c 192	16.2	67.5	2239	4	ABL02095	AbL02095 Drosophil
120	18.4	76.7	42	14	ADU69957	Adu69957 LAMP reac	c 193	16.2	67.5	2294	4	AAF63419	Aaf63419 Human CD3
121	18.2	75.8	1158	14	ADW16249	Adw16249 DNA copy	c 194	16.2	67.5	2371	4	AAF63416	Aaf63416 Human CD3
122	18	75.0	19	4	AAD11274	Aad11274 Mycobacte	c 195	16.2	67.5	2497	4	AAF63421	Aaf63421 Human CD3
123	18	75.0	19	10	ADG88355	Adg88355 Mycobacte	c 196	16.2	67.5	2597	13	ACN43713	Acn43713 Human dia
124	18	75.0	19	14	AEA08230	Aea08230 Mycobacte	c 197	16.2	67.5	2648	6	ABT05471	Abt05471 DNA of NO
125	18	75.0	50	2	AAx99197	Aax99197 M. sorofu	c 198	16.2	67.5	2693	3	AAF63418	Aaf63418 Human CD3
c 126	18	75.0	1137	9	AAD57239	Aad57239 Human CGD	c 199	16.2	67.5	2693	4	ABT05470	Abt05470 DNA of NO
127	17.8	74.2	1366	13	ADU59584	Adu59584 Plant ful	c 200	16.2	67.5	2729	12	ADQ87074	Adq87074 Human tum
128	17.8	74.2	1418	8	ABZ22595	Abz22595 Rhodococc	c 201	16.2	67.5	2736	6	ABL39778	AbL39778 Human NS
129	17.8	74.2	4540	6	ABK63777	Abk63777 Rat sequ	c 202	16.2	67.5	2762	3	AAA96066	Aaa96066 Human ect
c 130	17.6	73.3	465	10	ADB58396	AdB58396 Toxicity-	c 203	16.2	67.5	2762	4	AAF63422	Aaf63422 Human CD3
132	17.6	73.3	960	11	ACN44517	Acn44517 Mouse mRN	c 204	16.2	67.5	2762	4	AAF63386	Aaf63386 Human CD3
133	17.6	73.3	1561	13	ADR07240	Adr07240 Full leng	c 205	16.2	67.5	2762	6	AAD31693	Aad31693 Human CD3
134	17.6	73.3	1763	15	AE888040	Aee88040 Human cDN	c 206	16.2	67.5	2762	12	ADQ99441	Adq99441 Human CD3
135	17.6	73.3	1787	4	AAH14162	Aah14162 Human cDN	c 207	16.2	67.5	2762	13	ADR69170	Adr69170 Human CD3
136	17.6	73.3	1792	12	ADQ84493	Adq84493 Human tum	c 208	16.2	67.5	2762	13	ADR69004	Adr69004 Human CD3
137	17.6	73.3	1792	12	ADQ85308	Adq85308 Human tum	c 209	16.2	67.5	2762	13	ACN40734	Acn40734 Tumour-as
138	17.6	73.3	43800	11	ACN44516	Acn44516 Mouse gen	c 210	16.2	67.5	2762	13	ADs17884	AdS17884 Human CD3
139	17.4	72.5	36	14	ADU69990	Adu69990 LAMP reac	c 211	16.2	67.5	2762	13	ADR87780	Adr87780 Human CD3
140	17.4	72.5	1452	14	AEA22408	Aea22408 Mycobacte	c 212	16.2	67.5	2762	13	ADR65838	Adr65838 Human pro
141	17.2	71.7	1417	12	ADJ87468	Adj87468 Tomato Le	c 213	16.2	67.5	2762	13	ADR65522	Adr65522 Human pro
142	17.2	71.7	1776	2	AAV59559	Aav59559 Human sec	c 214	16.2	67.5	2762	13	ADs09773	AdS09773 Human the
143	17.2	71.7	1776	6	ABs73546	AbS73546 Human cDN	c 215	16.2	67.5	2762	14	ADV16894	Adv16894 Human CD3
144	17.2	71.7	1776	9	ACD82689	AcD82689 cDNA sequ	c 216	16.2	67.5	2762	14	ADZ66963	Adz66963 Human CD3
145	17.2	71.7	1776	9	AD122774	Adi22774 cDNA enco	c 217	16.2	67.5	2762	14	ADZ74432	Adz74432 Human CD3
146	17.2	71.7	1776	12	ADH73776	Adh73776 Human sec	c 218	16.2	67.5	2805	4	AAF63420	Aaf63420 Human CD3
147	17.2	71.7	1791	6	ABs73713	AbS73713 Human cDN	c 219	16.2	67.5	2837	5	AA87012	Aa87012 DNA enco
148	17.2	71.7	1791	6	ABs73713	AbS73713 Human cDN	c 220	16.2	67.5	2882	4	AAF63424	Aaf63424 Human CD3
149	17.2	71.7	1791	9	ACD82856	AcD82856 cDNA sequ	c 221	16.2	67.5	2888	10	ADC14273	Adc14273 Human enz
150	17.2	71.7	1791	10	ADI22941	Adi22941 cDNA enco	c 222	16.2	67.5	3200	4	ABL25250	AbL25250 Drosophil
151	17.2	71.7	1791	12	ADH73943	Adh73943 Human sec	c 223	16.2	67.5	3757	4	ABL14492	AbL14492 Drosophil
c 152	17.2	71.7	2919	13	ADS59960	AdS59960 Bacterial	c 224	16.2	67.5	4417	4	ABL02094	AbL02094 Drosophil
153	17	70.8	23	2	AAV59060	Aav59060 Primer KY	c 225	16.2	67.5	5498	4	ABL08702	AbL08702 Drosophil
154	17	70.8	23	2	ADFA1650	Adf1650 Mycobacte	c 226	16.2	67.5	5656	4	ABL14490	AbL14490 Drosophil
155	17	70.8	23	10	ADR05075	Adr05075 Mycobacte	c 227	16.2	67.5	13206	4	ABL14494	AbL14494 Drosophil
156	17	70.8	23	13	ADR05075	Adr05075 Mycobacte	c 228	16.2	67.5	110000	14	AEB35724_2	Continuation (3 of
157	17	70.8	50	2	AAx99200	Aax99200 M. intrac	c 229	16.2	67.5	110000	14	AEB35724_3	Continuation (4 of
158	16.8	69.2	1452	13	ADR90573	Adr90573 M intrac	c 230	16.2	67.5	110000	14	AEB39175_23	Continuation (25 o
c 159	16.6	69.2	36538	10	ABV75558	Abv75558 Saccharop	c 231	16.2	67.5	110000	14	AEB39175_24	Continuation (25 o
160	16.6	69.2	508	5	AA834274	Aas34274 Human cDN	c 232	16.2	67.5	110000	14	AEB42401_23	Continuation (24 o
c 161	16.6	69.2	671	13	ADQ79174	Adq79174 Novel can	c 233	16	66.7	17	14	ADU70004	AdU70004 LAMP reac
162	16.6	69.2	780	6	ABQ90469	Abq90469 M. capnoul	c 234	16	66.7	26	4	AAD11278	Aad11278 Mycobacte
163	16.6	69.2	1392	8	ACA23504	Aca23504 Prokaryot	c 235	16	66.7	26	10	ADG88359	Adg88359 Mycobacte
164	16.6	69.2	1436	14	ADW16288	Adw16288 DNA copy	c 236	16	66.7	26	14	AEA08234	Aea08234 Mycobacte
	16.6	69.2	2077	4	ABL04789	AbL04789 Drosophil	c 237	16	66.7	60	6	AAL42509	Aal42509 Self-asse

238	16	66.7	60	6	AA142505	AA142505 Self-asse
239	16	66.7	161	6	ABK79321	ABK79321 Bacillus
c 240	16	66.7	330	4	AA527929	AA527929 Novel cDN
241	16	66.7	330	10	ADG40833	ADG40833 Human res
242	16	66.7	330	11	ADI96607	ADI96607 Human res
c 243	16	66.7	339	6	ABN18591	ABN18591 Human ORF
c 244	16	66.7	360	6	ABQ92667	ABQ92667 Human imm
c 245	16	66.7	417	11	ABD04111	ABD04111 Pseudomon
246	16	66.7	463	8	ABZ76675	ABZ76675 Streptomy
247	16	66.7	463	8	ABZ76673	ABZ76673 Streptomy
248	16	66.7	496	5	AA587009	AA587009 DNA encod
249	16	66.7	500	14	ABE72672	ABE72672 Streptosp
c 250	16	66.7	506	12	ACH77915	ACH77915 Human gen
251	16	66.7	552	11	ABD07597	ABD07597 Pseudomon
252	16	66.7	553	13	ADQ55635	ADQ55635 Novel can
253	16	66.7	639	8	ABZ53337	ABZ53337 Aspergill
254	16	66.7	913	15	AEF74691	AEF74691 Human pol
255	16	66.7	981	8	ACA27357	ACA27357 Prokaryot
256	16	66.7	1221	13	ADT43292	ADT43292 Bacterial
257	16	66.7	1269	3	AA99893	AA99893 C. minita
258	16	66.7	1420	14	ADW16254	ADW16254 DNA copy
259	16	66.7	1449	4	AAF32669	AAF32669 Human cDN
260	16	66.7	1468	14	AED50856	AED50856 M. haemof
261	16	66.7	1476	14	ABE94382	ABE94382 Streptomy
c 262	16	66.7	1487	14	ABE94381	ABE94381 Streptomy
263	16	66.7	1698	11	ABD02283	ABD02283 Pseudomon
264	16	66.7	1705	2	AA975593	AA975593 Extended
265	16	66.7	1705	12	ADP18860	ADP18860 Human sec
266	16	66.7	1712	10	ADC29975	ADC29975 Human nov
267	16	66.7	1766	10	ADC29974	ADC29974 Human nov
268	16	66.7	1770	4	AAH15708	AAH15708 Human cDN
269	16	66.7	1797	4	AAH76747	AAH76747 Human COP
c 270	16	66.7	1822	4	AAH17113	AAH17113 Human cDN
c 271	16	66.7	1857	4	AA544870	AA544870 Human con
c 272	16	66.7	1857	10	ADC31910	ADC31910 Human nov
c 273	16	66.7	1857	10	ADC31911	ADC31911 Human nov
274	16	66.7	1934	4	AA544698	AA544698 Human ful
c 275	16	66.7	2000	11	ACL36279	ACL36279 Rice stre
276	16	66.7	2103	6	ABZ11376	ABZ11376 Human pol
277	16	66.7	2103	12	ADMA43894	ADMA43894 Novel hum
278	16	66.7	2106	11	ABD08113	ABD08113 Pseudomon
c 279	16	66.7	2199	8	ACA43833	ACA43833 Prokaryot
c 280	16	66.7	2325	4	AA551444	AA551444 Pseudomon
c 281	16	66.7	2325	8	ACA19423	ACA19423 Prokaryot
c 282	16	66.7	2427	11	ABD04295	ABD04295 Pseudomon
283	16	66.7	2556	11	ABD04470	ABD04470 Pseudomon
284	16	66.7	2633	10	ADD29575	ADD29575 Human tum
c 285	16	66.7	3689	13	ADR14442	ADR14442 Human NF-
286	16	66.7	4839	4	ABL14642	ABL14642 Drosophil
c 287	16	66.7	31248	9	ACC58250	ACC58250 Coumermyc
288	16	66.7	35058	4	ABL05556	ABL05556 Drosophil
c 289	16	66.7	35359	9	ACC58251	ACC58251 Coumermyc
c 290	16	66.7	36063	10	ADB74391	ADB74391 Mycobacte
c 291	16	66.7	89328	6	ABL61995	ABL61995 Colon ade
c 292	16	66.7	110000	6	ABA03041_07	Continuation (8 of
c 293	16	66.7	152141	8	ACA64961	ACA64961 Human BCR
294	15.8	65.8	330	4	AA182750	AA182750 Human pol
295	15.8	65.8	375	11	ACH95596	ACH95596 Klebsiell
c 296	15.8	65.8	381	5	AA577874	AA577874 DNA encod
c 297	15.8	65.8	510	14	ABE04097	ABE04097 Cryptococ
c 298	15.8	65.8	510	14	ABE04098	ABE04098 Cryptococ
c 299	15.8	65.8	510	14	ABE04147	ABE04147 Cryptococ
c 300	15.8	65.8	510	14	ABE04146	ABE04146 Cryptococ

## ALIGNMENTS

RESULT 1  
 AAD11272  
 ID AAD11272 standard; DNA; 24 BP.  
 XX  
 AC AAD11272;

XX	24-SEP-2001	(first entry)	
DT	Mycobacterium 16S rRNA amplifying primer #16.		
XX	Mycobacterium 16S rRNA; 16S ribosomal RNA; amplification;		
DE	Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.		
XX	Mycobacterium sp.		
KW	WO200144510-A2.		
OS	21-JUN-2001.		
XX	17-DEC-1999; 99WO-US030346.		
XX	17-DEC-1999; 99WO-US030346.		
XX	(GENP-) GEN-PROBE INC.		
PA	(INMR ) BIOMERIEUX SA.		
PI	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;		
XX	WPI; 2001-398170/42.		
XX	Detecting Mycobacterium species, involves in vitro amplification of 16S		
PT	rRNA or DNA encoding RNA in nucleic acid amplification mixture using		
PT	specific primers, and detecting the amplified nucleic acid.		
XX	Claim 1; Page 36; 44pp; English.		
XX	The invention relates to a method of detecting Mycobacterium species,		
CC	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA		
CC	encoding 16S rRNA in an in vitro nucleic acid amplification mixture		
CC	comprising a polymerase, and at least two primers, and then detecting the		
CC	amplified nucleic acid. The method is relatively simple and useful for		
CC	detecting the presence of various Mycobacterium species in a biological		
CC	sample, and thus important for diagnosis of infections resulting from		
CC	them. The method is especially important for screening opportunistic		
CC	infections caused by M. tuberculosis or a Mycobacterium other than		
CC	tuberculosis (MOTT). The present sequence is a PCR primer used for		
CC	amplifying Mycobacterium 16S rRNA		
XX	Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;		
XX	Query Match 100.0%; Score 24; DB 4; Length 24;		
XX	Best Local Similarity 100.0%; Pred. No. 0.1; Indels 0; Gaps 0;		
XX	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 CAAGTCGAACGGAAGGCGCTTTCG 24		
Db	1 CAAGTCGAACGGAAGGCGCTTTCG 24		
XX	RESULT 2		
XX	ADG88353		
ID	ADG88353 standard; DNA; 24 BP.		
XX	ADG88353;		
AC	ADG88353;		
XX	11-MAR-2004 (first entry)		
DT	Mycobacterium amplifying PCR primer #22.		
XX	In vitro amplification; PCR; primer; ss.		
OS	Mycobacterium celatum.		
XX	US2003165824-A1.		
PN	04-SEP-2003.		
PD	15-DEC-2000; 2000US-00738274.		

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XX PR 17-DEC-1999; 99US-0172190P.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2003-898044/82.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample comprises performing in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PS Claim 1; SEQ ID NO 22; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample comprises performing an in vitro
XX CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX CC detecting the amplified Mycobacterium nucleic acid. The present sequence
XX CC is Mycobacterium amplifying PCR primer.
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
DB 1 CAAGTCGAACGGAAGGCGCTTTCG 24
RESULT 3
ID AEA08228 standard; DNA; 24 BP.
XX AC AEA08228;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX KW PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX PA (BREN/) BRENTANO S T.
XX PA (JUCK/) JUCKER M T.
XX PA (DELG/) DELGADO F D.
XX PA (CLEU/) CLEUZAT P.
XX PA (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2005-345392/35.
XX PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX PT in a biological sample, comprises using in vitro nucleic acid
XX PT amplification and detection of amplified products.
XX PR 17-DEC-1999; 99US-0172190P.
XX PS Claim 1; SEQ ID NO 22; 20pp; English.
XX CC The present invention relates to a method of detecting Mycobacterium
XX CC species present in a biological sample. The method involves using in
XX CC vitro nucleic acid amplification and detection of amplified products. The
XX CC invention is useful for diagnostic detection of pathogenic bacteria such
XX CC as Mycobacterium species. The present sequence is the Mycobacterium
XX CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S rRNA)
XX CC amplifying non-T7 PCR primer.
XX SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
DB 1 CAAGTCGAACGGAAGGCGCTTTCG 24
RESULT 4
ID AAD11271 standard; DNA; 25 BP.
XX AC AAD11271;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #15.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
XX PA (INMR ) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2001-398170/42.
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
XX PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX PT specific primers, and detecting the amplified nucleic acid.
XX PS Claim 1; Page 36; 44pp; English.
XX CC The invention relates to a method of detecting Mycobacterium species,
XX CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX CC comprising a polymerase, and at least two primers, and then detecting the
XX CC amplified nucleic acid. The method is relatively simple and useful for
XX CC detecting the presence of various Mycobacterium species in a biological
XX CC sample, and thus important for diagnosis of infections resulting from
XX CC them. The method is especially important for screening opportunistic
XX CC infections caused by M. tuberculosis or a Mycobacterium other than
XX CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX CC amplifying Mycobacterium 16S rRNA
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 100.0%; Score 24; DB 4; Length 25;

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Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 5
ADG88352
ID ADG88352 standard; DNA; 25 BP.
AC ADG88352;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #21.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
FN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
DR WPI; 2003-898044/82.
XX
CC Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample comprises performing in vitro nucleic acid
amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 21; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products.
XX
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
detecting the amplified Mycobacterium nucleic acid. The present sequence
is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 6
AEA08227
ID AEA08227 standard; DNA; 25 BP.
AC AEA08227;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX
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Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
PCR; primer; ss.
Mycobacterium celatum.
US2005100915-A1.
12-MAY-2005.
18-SEP-2003; 2003US-00665708.
17-DEC-1999; 99US-0172190P.
15-DEC-2000; 2000US-00738274.
(BREN/) BRENTANO S T.
(JUCK/) JUCKER M T.
(DELG/) DELGADO F D.
(CLEU/) CLEUZIAT P.
(RODR/) RODRIGUE M.
Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
WPI; 2005-345392/35.
Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
in a biological sample, comprises using in vitro nucleic acid
amplification and detection of amplified products.
Claim 8; SEQ ID NO 21; 21pp; English.
The present invention relates to a method of detecting Mycobacterium
species present in a biological sample. The method involves using in
vitro nucleic acid amplification and detection of amplified products. The
invention is useful for diagnostic detection of pathogenic bacteria such
as Mycobacterium species. The present sequence is the Mycobacterium
celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 24; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCGCTTTCG 24
Db 2 CAACTCGAACGGAAGGCGCTTTCG 25

RESULT 7
ADZ20587
ID ADZ20587 standard; DNA; 500 BP.
XX
AC ADZ20587;
XX
DT 16-JUN-2005 (first entry)
DE Formaldehyde decomposition related Mycobacterium sp. DNA.
XX
KW decomposition; formaldehyde; ds.
XX
OS Mycobacterium sp.
XX
FN JP2003284548-A.
XX
PD 07-OCT-2003.
XX
PF 27-MAR-2002; 2002JP-00089307.
XX
PR 27-MAR-2002; 2002JP-00089307.
XX
PA (KUMO-) KUMONOTO KEN PREFECTURE.
(MITS-) MITSUWA CORP YG.
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PA (MITS-) MITSUWA BIPRO KK.  
 XX WPI; 2004-172963/17.  
 XX Decomposing formaldehyde by Mycobacterium and/or growth medium of the  
 PT cells.  
 PT  
 XX Example 1; SEQ ID NO 1; 20pp; Japanese.  
 XX  
 CC The invention relates to a novel method for decomposing formaldehyde by  
 CC using microbial cells that belong to Mycobacterium sp. or Fusarium  
 CC oxysporum, and/or the growth medium of the microbial cells. The invention  
 CC further comprises: microbial cells which belong to Mycobacterium sp.  
 CC having the ability to decompose formaldehyde; a formaldehyde  
 CC decomposition agent comprising Mycobacterium sp. and/or the growth medium  
 CC of the microbial cells; and a formaldehyde decomposition agent comprising  
 CC F. oxysporum and/or its growth medium. The method is useful for  
 CC decomposing formaldehyde in sea water by Mycobacterium sp. or F.  
 CC oxysporum that is deposited under FERM P-818690 or FERM P-18403,  
 CC respectively. This polynucleotide sequence represents the Mycobacterium  
 CC sp. DNA of the invention.  
 XX  
 SQ Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 13; Length 500;  
 Best Local Similarity 95.8%; Pred. No. 0.85;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCGCTTCG 24  
 DB 54 CAAGTCGAACGGAAGGCGCTTCG 77  
 RESULT 8  
 AEA22405  
 ID AEA22405 standard; DNA; 1449 BP.  
 XX  
 AC AEA22405;  
 XX  
 DT 25-AUG-2005 (first entry)  
 DE  
 DE Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.  
 XX  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium fortuitum.  
 XX  
 XX US2005130168-A1.  
 PN  
 PD 16-JUN-2005.  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX 31-OCT-2003; 2003US-00697802.  
 XX  
 XX (HANK/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 PI  
 XX WPI; 2005-424597/43.  
 DR  
 XX  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 PT  
 XX Disclosure; SEQ ID NO 6; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations; and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;  
 Query Match 93.3%; Score 22.4; DB 14; Length 1449;  
 Best Local Similarity 95.8%; Pred. No. 0.95;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CRAAGTCGAACGGAAGGCGCTTCG 24  
 DB 21 CAAGTCGAACGGAAGGCGCTTCG 44  
 RESULT 9  
 AEA22412  
 ID AEA22412 standard; DNA; 1455 BP.  
 XX  
 AC AEA22412;  
 XX  
 DT 25-AUG-2005 (first entry)  
 DE  
 DE Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.  
 XX  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium mucogenicum.  
 XX  
 XX US2005130168-A1.  
 PN  
 PD 16-JUN-2005.  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX 31-OCT-2003; 2003US-00697802.  
 XX  
 XX (HANK/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 PI  
 XX WPI; 2005-424597/43.  
 DR  
 XX  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 PT  
 XX Disclosure; SEQ ID NO 13; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product



CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an APB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations, and a first reverse primer having consecutive bases of an  
 CC APB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 SQ Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 14; Length 1455;  
 Best Local Similarity 95.8%; Pred. No. 0.95;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 |||||  
 Db 31 CAAGTCGAACGGAAGGCGCTTTCG 54

RESULT 10  
 AEA22404  
 ID AEA22404 standard; DNA; 1482 BP.  
 XX  
 AC AEA22404;  
 XX  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 XX  
 DE Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.  
 XX  
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium farcinogenes.  
 XX  
 XX US2005130168-A1.  
 PN  
 XX 16-JUN-2005.  
 PD  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX 31-OCT-2003; 2003US-00697802.  
 PR  
 XX (HANX//) HAN X.  
 PA (PHAM//) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 PI  
 XX WPI; 2005-424597/43.  
 DR  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.  
 XX  
 XX Disclosure; SEQ ID NO 5; 74pp; English.

CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an APB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations, and a first reverse primer having consecutive bases of an  
 CC APB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 SQ Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;

Query Match 93.3%; Score 22.4; DB 14; Length 1482;  
 Best Local Similarity 95.8%; Pred. No. 0.95;  
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 |||||  
 Db 29 CAAGTCGAACGGAAGGCGCTTTCG 52

RESULT 11  
 AAD11273  
 ID AAD11273 standard; DNA; 22 BP.  
 XX  
 AC AAD11273;  
 XX  
 DT 24-SEP-2001 (first entry)  
 XX  
 DE Mycobacterium 16S rRNA amplifying primer #17.  
 XX  
 KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
 KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.  
 XX  
 OS Mycobacterium sp.  
 XX  
 XX WO200144510-A2.  
 PN  
 XX 21-JUN-2001.  
 PD  
 XX 17-DEC-1999; 99WO-US030346.  
 PF  
 XX 17-DEC-1999; 99WO-US030346.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA (INMR ) BIOMERIEUX SA.  
 XX  
 XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 PI WPI; 2001-398170/42.  
 XX  
 XX Detecting Mycobacterium species, involves in vitro amplification of 16S

PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
 PT specific primers, and detecting the amplified nucleic acid.  
 XX  
 PS Claim 1; Page 36; 44pp; English.  
 XX  
 CC The invention relates to a method of detecting Mycobacterium species,  
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
 CC comprising a polymerase, and at least two primers, and then detecting the  
 CC amplified nucleic acid. The method is relatively simple and useful for  
 CC detecting the presence of various Mycobacterium species in a biological  
 CC sample, and thus important for diagnosis of infections resulting from  
 CC them. The method is especially important for screening opportunistic  
 CC infections caused by *M. tuberculosis* or a Mycobacterium other than  
 CC *tuberculosis* (MOTT). The present sequence is a PCR primer used for  
 CC amplifying Mycobacterium 16S rRNA  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 87.5%; Score 21; DB 4; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GTCGAACGGAAGGCTTTTCG 24  
 DB 1 GTCGAACGGAAGGCTTTTCG 21  
 RESULT 12  
 ADG88354  
 ID ADG88354 standard; DNA; 22 BP.  
 XX  
 AC ADG88354;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Mycobacterium amplifying PCR primer #23.  
 XX  
 KW In vitro amplification; PCR; primer; ss.  
 XX  
 OS Mycobacterium celatum.  
 XX  
 PN US2003165824-A1.  
 XX  
 PD 04-SEP-2003.  
 XX  
 PF 15-DEC-2000; 2000US-00738274.  
 XX  
 PR 17-DEC-1999; 99US-0172190P.  
 XX  
 PA (BREN/) BRENTANO S T.  
 PA (JUCK/) JUCKER M T.  
 PA (DELG/) DELGADO F D.  
 PA (CLEU/) CLEUZIAT P.  
 PA (RODR/) RODRIGUE M.  
 XX  
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 XX  
 DR WPI; 2003-898044/82.  
 XX  
 CC Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 CC in a biological sample comprises performing in vitro nucleic acid  
 CC amplification and detection of amplified products.  
 XX  
 PS Claim 1; SEQ ID NO 23; 20pp; English.  
 XX  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample comprises performing an in vitro  
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
 CC is Mycobacterium amplifying PCR primer.  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 87.5%; Score 21; DB 10; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GTCGAACGGAAGGCTTTTCG 24  
 DB 1 GTCGAACGGAAGGCTTTTCG 21  
 RESULT 13  
 AEA08229  
 ID AEA08229 standard; DNA; 22 BP.  
 XX  
 AC AEA08229;  
 XX  
 DT 14-JUL-2005 (first entry)  
 XX  
 DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.  
 KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;  
 KW PCR; primer; ss.  
 XX  
 OS Mycobacterium celatum.  
 XX  
 PN US2005100915-A1.  
 XX  
 PD 12-MAY-2005.  
 XX  
 PF 18-SEP-2003; 2003US-00665708.  
 XX  
 PR 17-DEC-1999; 99US-0172190P.  
 PR 15-DEC-2000; 2000US-00738274.  
 XX  
 PA (BREN/) BRENTANO S T.  
 PA (JUCK/) JUCKER M T.  
 PA (DELG/) DELGADO F D.  
 PA (CLEU/) CLEUZIAT P.  
 PA (RODR/) RODRIGUE M.  
 XX  
 PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 XX  
 DR WPI; 2005-345392/35.  
 XX  
 CC Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 CC in a biological sample, comprises using in vitro nucleic acid  
 CC amplification and detection of amplified products.  
 XX  
 PS Claim 8; SEQ ID NO 23; 21pp; English.  
 XX  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample. The method involves using in  
 CC vitro nucleic acid amplification and detection of amplified products. The  
 CC invention is useful for diagnostic detection of pathogenic bacteria such  
 CC as Mycobacterium species. The present sequence is the Mycobacterium  
 CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)  
 CC amplifying non-T7 PCR primer.  
 XX  
 SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 87.5%; Score 21; DB 14; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GTCGAACGGAAGGCTTTTCG 24  
 DB 1 GTCGAACGGAAGGCTTTTCG 21  
 RESULT 14  
 ADF94057  
 ID ADF94057 standard; DNA; 50 BP.  
 XX

AC ADF94057;  
 XX 11-MAR-2004 (first entry)  
 XX Microorganism detection probe, SEQ ID 150.  
 DE Probe; detection; identification; microorganism; food; drug;  
 XX 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
 KW Mycobacterium gordonae.  
 XX WO2003106676-A1.  
 PN 24-DEC-2003.  
 XX 16-JUN-2003; 2003WO-JP007620.  
 PF 14-JUN-2002; 2002JP-00174564.  
 PR (HISF ) HITACHI SOFTWARE ENG CO LTD.  
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
 XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
 XX Shimadzu M, Kobayashi I, Ishiko H;  
 XX WPI; 2004-071565/07.  
 DR 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
 PT microorganism for specific detection and identification of the  
 PT microorganism in foods and drug compositions.  
 XX Claim 2; SEQ ID NO 150; 150pp; Japanese.  
 XX The present invention relates to probes (ADF93908-ADF94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADF94060 and ADF94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Moraxella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguinis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.  
 XX Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;  
 SQ Query Match 86.7%; Score 20.8; DB 12; Length 50;  
 Best Local Similarity 91.7%; Pred. No. 4;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCGCTTCG 24  
 |||||||  
 DB 4 CAAGTCGAACGGAAGGCGCTTCG 27

RESULT 15  
 AAX32481  
 ID AAX32481 standard; DNA; 166 BP.  
 XX AAX32481;  
 AC AAX32481;  
 XX 22-JUN-1999 (first entry)  
 DT Preferred probe of the invention.  
 DE 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.  
 KW Synthetic.  
 XX Streptomyces ambofaciens.  
 OS WO9914361-A1.  
 PN 25-MAR-1999.  
 XX 16-SEP-1998; 98WO-EP006038.  
 PF 18-SEP-1997; 97US-0059295P.  
 PR 16-DEC-1997; 97US-0069748P.  
 XX (MERI ) MERCK SHARP & DOHME ESPANA SAE.  
 PA Genilloud O, Mellado RP, Parro V, Rodriguez V;  
 XX WPI; 1999-229548/19.  
 DR New probes used for detection of maduromycetes bacteria and to  
 PT differentiate between maduromycetes and streptomycetes.  
 PT Disclosure; Fig 1; 22pp; English.  
 PS The invention relates to a novel nucleic acid probe hybridises to a  
 CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria  
 CC under hybridisation conditions, and does not hybridise to nucleic acids  
 CC encoding a portion of 16S rRNA of streptomycetes under identical  
 CC hybridisation conditions. The probes can be used for detecting the  
 CC presence of maduromycetes bacteria in a sample and for differentiating  
 CC between maduromycetes and streptomycetes bacteria in a sample. The  
 CC present sequence represents a preferred probe of the invention  
 XX Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;  
 SQ Query Match 86.7%; Score 20.8; DB 2; Length 166;  
 Best Local Similarity 91.7%; Pred. No. 4.5;  
 Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCGCTTCG 24  
 |||||||  
 DB 57 CAAGTCGAACGGAAGGCGCTTCG 80  
 RESULT 16  
 ABZ76674  
 ID ABZ76674 standard; DNA; 460 BP.  
 XX ABZ76674;  
 AC 30-APR-2003 (first entry)  
 DT Microtetraspora recticatena IPO14525 DNA sequence SEQ ID NO:5.  
 DE Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;  
 XX antilipaeamic; microorganism; gene; ds.  
 KW Nonomuraea recticatena.  
 OS WO200299109-A1.  
 XX

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XX PD 12-DEC-2002.
XX PF
XX PR 30-MAY-2002; 2002WO-JP005252.
XX PR
XX PR 01-JUN-2001; 2001JP-00166412.
XX PR
XX PA (SAOC ) MERCIAN CORP.
XX PI
XX PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ieshiki K;
XX DR WPI; 2003-148672/14.
XX DR
XX PT Novel Streptomyces sp. produced polypeptide for hydroxylation of
XX PT compactin at 6beta-position and its encoded DNA, applicable in
XX PT constructing transformant microbes to synthesize pravastatin for treating
XX PT hyperlipidemia.
XX PS
XX PS Disclosure; Page 50-51; 67pp; Japanese.
XX CC
XX CC The present invention describes a DNA sequence which contains a base
XX CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,
XX CC or a DNA hybridizable with the DNA under stringent conditions and
XX CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-
XX CC position. Also described: (1) DNA containing base sequences from bases
XX CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA
XX CC hybridizable with the DNA under stringent conditions and encoding a
XX CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
XX CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
XX CC sequence based on the polypeptide but with some amino acids deleted,
XX CC substituted or added and having hydroxylase activity on compactin at the
XX CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
XX CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
XX CC process for producing pravastatin by culturing the transformant
XX CC microorganism before isolating the culture liquor or cells, and addition
XX CC of compactin for reaction to give pravastatin for recovery; and (6)
XX CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (I) has
XX CC antilipemic activity. The polypeptide and its encoded DNA are applicable
XX CC in constructing transformant microorganisms to synthesize pravastatin for
XX CC treating hyperlipidemia. With the recombinant microorganisms,
XX CC pravastatin can be produced efficiently, with much less galpha
XX CC hydroxylated epimer formed. The present sequence represents a
XX CC Microtetraspora recticatenata IPO14525 nucleotide sequence, which is given
XX CC in the exemplification of the present invention
XX PD
XX SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;
Query Match 86.7%; Score 20.8; DB 8; Length 460;
Best Local Similarity 91.7%; Pred. No. 5;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
Db 31 CAAGTCGAGCGGAAGGCCCTTTCG 54
RESULT 17
AEB72673
ID AEB72673 standard; DNA; 497 BP.
XX AC
XX AC AEB72673;
XX DT
XX DT 06-OCT-2005 (first entry)
XX DE
XX DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX KW cyclosporin; cyclosporin A; ds.
XX OS
XX OS Streptosporangium sp.
XX PN JP2005198543-A.
XX PD
XX PD 28-JUL-2005.
XX PS
XX PS Disclosure; SEQ ID NO 1; 30pp; Japanese.
XX CC
XX CC The invention relates to a novel method for producing a cyclosporin
XX CC derivative. The method involves incubating cyclosporin A in the presence
XX CC of a strain belonging to Dactylosporangium, Streptomyces, Nocardia,
XX CC Pseudonocardia or Streptosporangium or its cultured microbial cells and
XX CC extracting the cyclosporin derivative from the incubated microbial cells and
XX CC cyclosporin derivative is used as a reference standard for quantitative
XX CC measurement of cyclosporin A and its metabolite in blood and urine. This
XX CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in
XX CC the cyclosporin production method of the invention.
XX SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;
Query Match 86.7%; Score 20.8; DB 14; Length 497;
Best Local Similarity 91.7%; Pred. No. 5.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
Db 54 CAAGTCGAGCGGAAGGCCCTTTCG 77
RESULT 18
AED64356
ID AED64356 standard; DNA; 500 BP.
XX AC
XX AC AED64356;
XX DT
XX DT 12-JAN-2006 (first entry)
XX DE
XX DE Rhodococcus sp. 16S rDNA, SEQ ID 1.
XX KW 16S ribosomal RNA; 16S rRNA; ds.
XX OS
XX OS Rhodococcus sp.; Z-35-1 strain.
XX PN JP2005304498-A.
XX PD
XX PD 04-NOV-2005.
XX PF
XX PF 22-MAR-2005; 2005JP-00081977.
XX PR
XX PR 23-MAR-2004; 2004JP-00083956.
XX PA (SANY-) SANYO FINE KK.
XX PI
XX PI Isobe K, Matsura A, Sakaguchi T;
XX DR WPI; 2005-762911/78.
XX PT
XX PT Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its
XX PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino
XX PT protecting group of L- or D-lysine, by utilizing oxidase derived from
XX PT Rhodococcus.
XX PS
XX PS Disclosure; SEQ ID NO 1; 30pp; Japanese.
```

XX The present invention relates to a method (M1) for producing alpha-L- or  
CC -D-amino adipic acid semialdehyde derivatives. The method involves  
CC oxidatively deaminating the aminomethyl group of the alpha-amino  
CC protecting group of L- or D-lysine into an aldehyde group, by utilizing  
CC an oxidase derived from Rhodococcus. The present sequence was used to  
XX illustrate the invention.

SQ Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;  
Query Match 86.7%; Score 20.8; DB 14; Length 500;  
Best Local Similarity 91.7%; Pred. No. 5.1;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTTTCG 24  
||||||| ||| |||||||||  
Db 54 CAACTCGAGCGGTAAAGGCTTTTCG 77  
||||||| ||| |||||||||

RESULT 19  
AD080217/c  
ID AD080217 standard; DNA; 1343 BP.  
XX  
AC AD080217;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Rhodococcus sp. GR-002 strain 16S rDNA.  
XX  
KW cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;  
KW catalase test positive; nitrate-reduction ability positive;  
KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;  
KW alkali phosphatase positive; beta-glucuronidase negative;  
KW beta-galactosidase negative; alpha-glucosidase positive;  
KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;  
KW FERM P-18804; waste engine oil; aromatic hydrocarbon;  
KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.  
XX  
OS Rhodococcus sp.  
XX  
PN JP2004113197-A.  
XX  
PD 15-APR-2004.  
XX  
PF 27-SEP-2002; 2002JP-00284521.  
XX  
PR 27-SEP-2002; 2002JP-00284521.  
XX  
PA (GEIT-) GEITO KK.  
XX  
DR WPI; 2004-322544/30.  
XX  
XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain  
PT having biochemical properties e.g. gram positive bacillus, catalase test  
PT positive, pyrazinamidase negative, useful for degrading waste engine oil.  
XX  
PS Claim 2; SEQ ID NO 1; 13pp; Japanese.

XX The invention relates to a novel cyclic hydrocarbon degrading agent from  
CC the Rhodococcus genus. The cyclic hydrocarbon degrading agent having  
CC biochemical properties such as: gram positive bacillus, catalase test  
CC positive, nitrate-reduction ability positive, pyrazinamidase negative,  
CC pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-  
CC glucuronidase negative, beta-galactosidase negative, alpha-glucosidase  
CC positive, N-acetyl-beta-glucosaminidase negative, urease positive. The  
CC novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having  
CC the accession number FERM P-18804. The cyclic hydrocarbon degrading agent  
CC is useful for processing a cyclic hydrocarbon-containing substance, such  
CC as a waste engine oil. The novel Rhodococcus microorganism is useful for  
CC degrading cyclic hydrocarbons containing aromatic hydrocarbons,  
CC cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.  
CC This polynucleotide represents the novel Rhodococcus microorganism 16S  
CC rDNA sequence of the invention.

XX  
SQ Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;  
Query Match 86.7%; Score 20.8; DB 12; Length 1343;  
Best Local Similarity 91.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTTTCG 24  
||||||| ||| |||||||||  
Db 1293 CAACTCGAGCGGTAAAGGCTTTTCG 1270  
||||||| ||| |||||||||

RESULT 20  
ADW16264  
ID ADW16264 standard; DNA; 1390 BP.  
XX  
AC ADW16264;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE DNA copy of the N\_albus 16S ribosomal RNA EN46 isolate Seq 16.  
XX  
KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;  
KW disease resistance; insect resistance; crop improvement;  
KW plant growth factor; antibacterial; antimicrobial; fungicide;  
KW insecticide; nematocide.  
XX  
OS Nocardioides albus.  
XX  
PN WO2005003328-A1.  
XX  
PD 13-JAN-2005.  
XX  
PF 07-JUL-2004; 2004WO-AU0000914.  
XX  
PR 07-JUL-2003; 2003US-0485241P.  
PR 22-SEP-2003; 2003US-0504703P.  
XX  
PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.  
XX  
PI Franco CMM, Coombs JT;  
XX  
DR WPI; 2005-091806/10.  
XX  
PT Improving plant productivity comprises introducing into the plant or  
PT propagation material an endophytic actinomycete that facilitates  
PT induction of at least one characteristic related to improved  
PT productivity.  
XX  
PS Claim 1; SEQ ID NO 16; 235pp; English.

XX This invention relates to a novel method for improving plant  
CC productivity. Specifically, it refers to introducing into the plant or  
CC propagation material an endophytic actinomycetes or variant thereof,  
CC where the actinomycetes facilitate induction of a characteristic related  
CC to improved productivity. The present invention further describes  
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin  
CC or cytokinin that are able to induce disease resistance in plants i.e.  
CC provide disease bio-control capabilities against pathogen infection.  
CC Accordingly, the method facilitates the improvement of cereal crop  
CC productivity including increasing germination by up-regulating plant  
CC growth promoting activities, as well as improving plant vigor or flower  
CC and fruit yield. Furthermore, the new actinomycete or metabolite is  
CC useful in the manufacture of a medicament for the therapeutic and/or  
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.  
CC plant. As such, this method provides plant protectants and plant growth  
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,  
CC insecticide and nematocide activities. This polynucleotide is the DNA  
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

SQ Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;  
Query Match 86.7%; Score 20.8; DB 14; Length 1390;

Best Local Similarity 91.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24  
||||| ||||| ||||| ||||| |||||  
Db 4 CAAGTCGAGCGGAAGGCCCTTCG 27

RESULT 21  
ADJ38609  
ID ADJ38609 standard; DNA; 1403 BP.  
XX AC  
XX ADJ38609;  
XX 06-MAY-2004 (first entry)  
XX Micromonospora sp. M42 16S rRNA, SEQ ID 1.  
DE XX  
XX Protozoacide; Tuberculostatic; Antitubercular; Antimalarial;  
KW Cerebroprotective; Actinomycete; manzamine; 16S rRNA; antibiotic; ds.  
XX OS  
XX Micromonospora sp. M42.  
XX WO2004013297-A2.  
XX 12-FEB-2004.  
XX 01-AUG-2003; 2003WO-US024238.  
XX 01-AUG-2002; 2002US-0400330P.  
XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY.  
PA (UMIS ) UNIV MISSISSIPPI.  
XX Hill RT, Hamann MT, Peraud O, Kasanah N;  
XX WPI; 2004-169330/16.  
XX New isolated actinomycete useful for producing antibiotics produces  
PT manzamine having antituberculosis and antimalarial activity.  
XX Claim 19; SEQ ID NO 1; 46pp; English.  
XX The present invention relates to an isolated actinomycete (A1) producing  
CC manzamine, which comprises a 16S rRNA (ADJ38609). (A1) is useful for  
CC producing manzamine by fermentation, which involves culturing (A1) having  
CC manzamine producing ability in a culture medium suitable for the growth  
CC of manzamine compounds and production of manzamine and separating the  
CC manzamine from the culturing medium. (A1) is useful for producing  
CC antibiotics.  
XX Sequence 1403 BP; 304 A; 361 C; 484 G; 254 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 12; Length 1403;  
Best Local Similarity 91.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24  
||||| ||||| ||||| ||||| |||||  
Db 26 CAAGTCGAGCGGAAGGCCCTTCG 49

RESULT 22  
ADW16290  
ID ADW16290 standard; DNA; 1427 BP.  
XX AC  
XX ADW16290;  
XX 07-APR-2005 (first entry)  
XX DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.  
DE 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;

KW disease resistance; insect resistance; crop improvement;  
KW plant growth factor; antibacterial; antimicrobial; fungicide;  
KW insecticide; nematocide.  
XX Actinomycetales.  
XX WO2005003328-A1.  
XX 13-JAN-2005.  
XX 07-JUL-2004; 2004WO-AU000914.  
XX 07-JUL-2003; 2003US-0485241P.  
XX 22-SEP-2003; 2003US-0504703P.  
XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.  
XX Franco CMW, Coombs JT;  
XX WPI; 2005-091806/10.  
XX Improving plant productivity comprises introducing into the plant or  
PT propagation material an endophytic actinomycete that facilitates  
PT induction of at least one characteristic related to improved  
PT productivity.  
XX Example 18; Fig 19; 235pp; English.  
XX This invention relates to a novel method for improving plant  
CC productivity. Specifically, it refers to introducing into the plant or  
CC propagation material an endophytic actinomycetes or variant thereof,  
CC where the actinomycetes facilitate induction of a characteristic related  
CC to improved productivity. The present invention further describes  
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin  
CC or cytokinin that are able to induce disease resistance in plants i.e.  
CC provide disease bio-control capabilities against pathogen infection.  
CC Accordingly, the method facilitates the improvement of cereal crop  
CC productivity including increasing germination by up-regulating plant  
CC growth promoting activities, as well as improving plant vigor or flower  
CC and fruit yield. Furthermore, the new actinomycete or metabolite is  
CC useful in the manufacture of a medicament for the therapeutic and/or  
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.  
CC plant. As such, this method provides plant protectants and plant growth  
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,  
CC insecticide and nematocide activities. This polynucleotide is the DNA  
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.  
XX Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1427;  
Best Local Similarity 91.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTCG 24  
||||| ||||| ||||| ||||| |||||  
Db 25 CAAGTCGAGCGGAAGGCCCTTCG 48

RESULT 23  
ADZ35975  
ID ADZ35975 standard; DNA; 1440 BP.  
XX AC  
XX ADZ35975;  
XX 30-JUN-2005 (first entry)  
XX Verrucosisspora sp. AB-18-032 16S rRNA gene.  
XX ds; antibiotic; antimalarial; protozoacide; 16S rRNA;  
KW polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;  
KW vitamin; abyssomicin B; abyssomicin C; abyssomicin D;  
KW Staphylococcus aureus infection; protozoal infection;  
KW plasmodium infection; Leishmania infection; chagas disease;

Gram positive bacteria infection; mrsa infection .

Verrucosisporea sp. AB-18-032.

WO2005033114-A1.

14-APR-2005.

23-SEP-2004; 2004WO-EP010661.

01-OCT-2003; 2003DE-01047472.

11-NOV-2003; 2003DE-01053300.

(UYTU-) UNIV TUEBINGEN.

Fiedler H, Suesemuth R, Zaehner H, Bull A;

WPI; 2005-296122/30.

New abyssomicin polycyclic macrolactone compounds, useful as antibiotics and antiprotzoal agents effective against multiresistant strains, prepared using bacteria of genus Verrucosisporea.

Disclosure; SEQ ID NO 1; 47pp; German.

This invention describes novel polycyclic macrolactones and their derivatives, prepared using bacteria of genus Verrucosisporea and designated abyssomicins. The polycyclic macrolactones have at least one oxo-bicyclo system as a partial structure and at least one Michael system as a double bond system. The polycyclic macrolactones are prepared by culturing Verrucosisporea strain AB 18-032, recovering a culture supernatant from the culture, optionally preparing a culture filtrate and optionally isolating one or more polycyclic macrolactones from the supernatant and/or filtrate. Alternatively the microorganism is cultured followed by isolating one or more polycyclic macrolactones from the microorganism. The Verrucosisporea strain AB 18-032 was isolated from marine sediment collected at a depth of 1000m in Sagami Bay in the Japanese Sea and is deposited as DSM No. 15899. The polycyclic macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an essential component in the biosynthesis of folic acid) from chorismic acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is essential to the life of microorganisms, especially prokaryotes and protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of folic acid in mammals (including humans), and thus have no adverse effects on mammalian cells. Three polycyclic macrolactones are specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin D. Abyssomicin C strongly inhibited growth of methicillin-resistant Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus aureus strain Mu50. The products of the invention are useful as antibiotics (especially effective against Gram positive bacteria) and antiprotzoal agents, specifically effective against bacteria and protozoa resistant (especially multi-resistant) to conventional antibiotics. Typically polycyclic macrolactones are useful for combating tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping sickness and Chagas disease) and infections caused by resistant Gram positive bacteria such as methicillin- and vancomycin-resistant Staphylococcus aureus strains. Polycyclic macrolactones are also useful as disinfectants (especially in hospitals and other medical establishments) and as lead structures for the development of further active agents. This sequence represents the Verrucosisporea strain AB 18-032 16S rRNA DNA which is used to phylogenically classify the bacterial strain.

Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1440;  
Best Local Similarity 91.7%; Pred. No. 5.7;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

||||| ||||||| ||||||| ||||||| |||||||

DB 1 CAAAGTCGACGGAAGGCGCTTTCG 24

RESULT 24

ADX38843

ID ADX38843 standard; DNA; 1443 BP.

XX

AC ADX38843;

XX

DT 05-MAY-2005 (first entry)

XX

DE Microbispora 16S rDNA.

XX

XX antibiotic; bacterial infection; animal growth; 16S rDNA; ds;

KW antibacterial; anabolic.

XX

OS Microbispora sp. ATCC PTA-5024.

XX

PN WO2005014628-A1.

XX

PD 17-FEB-2005.

XX

PF 12-JUL-2004; 2004WO-EP007658.

XX

PR 18-JUL-2003; 2003EP-00016306.

XX

PA (VICU-) VICURON PHARM INC.

XX

PI Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;

PI Marinelli F, Selva E, Parenti F;

XX

DR WPI; 2005-173079/18.

XX

New antibiotic 107891 complex comprising Factor A1 and Factor A2 and having specified physico-chemical characteristics, used to form medicament for the treatment or prevention of bacterial infections, or used as animal growth promoter.

Disclosure; SEQ ID NO 1; 85pp; English.

The invention relates to an antibiotic 107891 complex comprising Factor A1 and Factor A2. The antibiotic is used to form a pharmaceutical composition used as medicament for the treatment or prevention of bacterial infections, or as animal growth promoter. The present sequence represents the Microbispora 16S rDNA.

Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

Query Match 86.7%; Score 20.8; DB 14; Length 1443;

Best Local Similarity 91.7%; Pred. No. 5.7;

Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAGGCGCTTTCG 24

||||| ||||||| ||||||| ||||||| |||||||

DB 31 CAAAGTCGACGGAAGGCGCTTTCG 54

RESULT 25

AEA22406

ID AEA22406 standard; DNA; 1461 BP.

XX

AC AEA22406;

XX

DT 25-AUG-2005 (first entry)

XX

DE Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.

XX

KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX

OS Mycobacterium gordonae.

XX

PN US2005130168-A1.

XX

PD 16-JUN-2005.

XX

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PF 31-OCT-2003; 2003US-00697802.
XX
XX
PR 31-OCT-2003; 2003US-00697802.
XX
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.
XX
XX Disclosure; SEQ ID NO 7; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complementary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complementary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an AFB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations, or (iii) a first forward primer having consecutive bases of
CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium goodii 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1461 BP; 319 A; 350 C; 500 G; 292 T; 0 U; 0 Other;
SQ
Query Match 86.7%; Score 20.8; DB 14; Length 1461;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTCG 24
Db 21 CAAGTCGAACGGAAGGCCTTCG 44

RESULT 26
AED35651
ID AED35651 standard; DNA; 1483 BP.
XX
XX AED35651;
XX
XX 15-DEC-2005 (first entry)
XX
XX Pseudonocardia sp. 727713 melanocortin receptor modulator WS727713.
DE
DE ds; melanocortin receptor; cosmetics; brain injury; cerebroprotective;
XX inflammation; renal disease; nephrotropic; ischemia;
XX cardiovascular disease; vasotrophic; reperfusion injury; inflammation;
XX hepatitis; hepatotropic; virucide; sepsis; septic shock; Antibacterial;
XX immunosuppressive; respiratory distress syndrome; Respiratory-Gen.;

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KW respiratory disease; rheumatoid arthritis; arthritis; Antirheumatic;
KW Antiarthritic; immune disorder; gout; Antigout; osteoarthritis;
KW osteopathic; nephritis; genitourinary disease; nephrotropic;
KW hypersensitivity; Antiallergic; inflammatory bowel disease;
KW Gastrointestinal-Gen.; gastrointestinal disease; Endocrine-Gen.;
KW genitourinary disease; female sexual dysfunction;
KW male sexual dysfunction; Gynecological; transplant rejection; Analgesic;
KW pain; neurological disease; HIV infection; Anti-HIV; hypopigmentation;
KW Dermatological; dermatological disease; tinea; Fungicide;
KW Eating-Disorders-General.; Cardiovacular-Gen.; Anorectic;
KW nutritional disorder; psychiatric disorder; fever; Antipyretic;
KW temperature disorder; functional bowel disorder; obesity; pancreatitis;
KW fibroid; scar tissue; keloid; scleroderma; graft versus host disease;
KW liver cirrhosis; pulmonary fibrosis; nephropathy; Ophthalmological;
KW uveitis; Behcet's disease; hematological disease; sarcoidosis; vasculitis;
KW infection; antimicrobial; celiac disease; melanoma; neoplasm; Cytostatic;
KW Anabolic.
XX
XX Pseudonocardia sp. 727713.
XX WO2005097973-A1.
PN
XX
XX 20-OCT-2005.
PD
XX
XX 22-MAR-2005; 2005WO-JP005653.
PF
XX
XX 08-APR-2004; 2004AU-00901919.
PR
XX
XX (FUJI ) FUJISAWA PHARM CO LTD.
PA
XX
XX Otsuka T, Ueda H, Fujie K, Muramatsu H, Hashimoto M, Takase S;
XX WPI; 2005-703551/72.
XX
XX New pure WS727713 compound which is a melanocortin receptor modulator
PT useful as antiinflammatory and for treating e.g. hypoxic shock, acute
XX respiratory distress syndrome, rheumatic arthritis and melanoma invasion.
XX
XX Disclosure; SEQ ID NO 1; 41pp; English.
PS
XX
XX This invention describes a novel compound WS727713 isolated from
CC Pseudonocardia sp. 727713 in a leaf litter sample. The compound is
CC capable of modulating the melanocortin receptor and has a potent anti-
CC inflammatory effect. The compound can be used as a medicament or a
CC cosmetic for treating or preventing ischemic or reperfusion injury, brain
CC shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis,
CC gouty arthritis, aortic regurgitation, juvenile chronic arthritis,
CC osteoarthritis, nephritis, induction of tolerance, contact
CC hypersensitivity, inflammatory bowel disease, sexual dysfunction,
CC transplantation, pain, disease progression of HIV, post inflammatory hypo
CC pigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever,
CC functional bowel disease, obesity, satiety effect, diabetes mellitus,
CC modulation of dermal exocrine function, canities (canities
CC circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic
CC scars, keloids, localized scleroderma, systematic sclerosis, sclerodermic
CC graft versus host disease of the skin, cirrhosis of the liver, idiopathic
CC and bleomycin induced lung fibrosis, cyclosporin induced nephropathy),
CC uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis,
CC microbial infections, celiac disease, vulvar vestibulitis syndrome,
CC melanoma invasion or anorexia in human or an animal.
XX
XX Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;
SQ
Query Match 86.7%; Score 20.8; DB 14; Length 1483;
Best Local Similarity 91.7%; Pred. No. 5.7;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTCG 24
Db 32 CAAGTCGAACGGAAGGCCTTCG 55

```



RESULT 27										
ADR90327	ADR90327 standard; DNA; 1511 BP.									
XX	ID	AC	AC	AC	AC	AC	AC	AC	AC	AC
XX	ADR90327;									
XX	16-DEC-2004	(first entry)								
XX	Rhodococcus sp. M-15	bioremediation-related 16S rDNA.								
XX	alkane; petroleum; bioremediation;	16S ribosomal RNA; 16S rRNA; ds.								
XX	Rhodococcus sp.									
XX	JP2004261126-A.									
XX	24-SEP-2004.									
XX	03-MAR-2003;	2003JP-00056155.								
XX	03-MAR-2003;	2003JP-00056155.								
XX	(EBAR )	EBARA CORP.								
XX	WPI;	2004-665486/65.								
XX	Evaluating the ability of an environmental sample to degrade alkanes for	providing alkane degrading bacteria, comprises measuring alkane degrading								
XX	bacteria having high resolving power of alkane present in petroleum.									
XX	Claim 1;	SEQ ID NO 3; 33pp; Japanese.								
XX	The invention relates to a novel method for evaluating the ability of an	environmental sample to degrade alkanes. The method comprises measuring								
XX	the number of alkane-degrading bacteria present in the sample, where the	bacteria have high resolving power of a type of alkane present in								
XX	petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of	the invention may be useful for evaluating the ability of an								
XX	environmental sample to degrade alkanes and thus, for providing alkane-	degrading bacteria to be utilised in bioremediation of an environment								
XX	contaminated with petroleum. The method is rapid and simple. The current	sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S								
XX	ribosomal RNA gene (rDNA) of the invention.									
XX	Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;									
XX	Query Match	86.7%; Score 20.8; DB 13; Length 1511;								
XX	Best Local Similarity	91.7%; Pred. No. 5.7;								
XX	Matches 22; Conservative	0; Mismatches 2; Indels 0; Gaps 0;								
QY	1	CAAGTCGAACGGAAAGGCGTTTCG 24								
Db	51	CAAGTCGAGCGGTAAGGCGTTTCG 74								
RESULT 28										
ADR90325	ADR90325 standard; DNA; 1511 BP.									
XX	ID	AC	AC	AC	AC	AC	AC	AC	AC	AC
XX	ADR90325;									
XX	16-DEC-2004	(first entry)								
XX	Rhodococcus sp. M-13	bioremediation-related 16S rDNA.								
XX	alkane; petroleum; bioremediation;	16S ribosomal RNA; 16S rRNA; ds.								
XX	Rhodococcus sp.									
XX	JP2004261126-A.									
XX	24-SEP-2004.									





Query Match	86.7%;	Score 20.8;	DB 14;	Length 84222;	
Best Local Similarity	91.7%;	Pred. No. 8.8;			
Matches	22;	Conservative	0;	Mismatches	2;
Indels	0;	Gaps	0;		
Qy	1	CAAGTCGAACGGAAGGCGCTTTTCG	24		
Db	15395	CAAGTCGAGCGGAAGGCGCTTTCG	15372		
RESULT 32					
AAD11024/c					
ID	AAD11024 standard; DNA; 32 BP.				
XX					
AC	AAD11024;				
XX					
XX					
DT	24-SEP-2001 (first entry)				
XX					
XX	Probe #4 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.				
DE					
XX					
XX	Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;				
KW	in vitro amplification; MAC infection; probe; ss.				
XX					
XX	Mycobacterium sp.				
OS					
XX					
PN	W0200144511-A2.				
XX					
XX					
PD	21-JUN-2001.				
XX					
XX					
PF	15-DEC-2000; 2000WO-US033872.				
XX					
XX					
PR	15-DEC-1999; 99US-0171202P.				
XX					
XX					
PA	(GENP-) GEN-PROBE INC.				
XX					
PA	(BREN/) BRENTANO S T.				
XX					
PA	(LANK/) LANKFORD R L.				
XX					
XX					
PI	Brentano ST, Lankford RL;				
XX					
DR	WPI; 2001-398171/42.				
XX					
XX					
PT	Detecting Mycobacterium avium complex organisms, comprises using in vitro				
XX					
PT	nucleic acid amplification with amplification oligonucleotides specific				
XX					
PT	for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial				
XX					
PT	species.				
XX					
XX					
PS	Claim 11; Page 27; 27pp; English.				
XX					
XX					
CC	The present invention relates to a method for detecting Mycobacterium				
XX					
CC	avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.				
XX					
CC	tuberculosis, M. paratuberculosis) present in a biological sample. The				
XX					
CC	method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding				
XX					
CC	16S rRNA obtained from a biological sample containing nucleic acid from a				
XX					
CC	MAC species in an in vitro nucleic acid amplification mixture comprising				
XX					
CC	a polymerase activity and a pair of primers to produce an amplified				
XX					
CC	nucleic acid and detecting amplified nucleic acid. The method is useful				
XX					
CC	for in vitro diagnostic detection of pathogenic bacteria, particularly				
XX					
CC	detecting infections caused by MAC organisms, distinguished from other				
XX					
CC	closely-related Mycobacterium species. The present sequence is a probe				
XX					
CC	used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA				
XX					
SQ	Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;				
Query Match 85.0%; Score 20.4; DB 4; Length 32;					
Best Local Similarity 95.5%; Pred. No. 5.9;					
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1	CAAGTCGAACGGAAGGCGCTTTT	22		
Db	31	CAAGTCGAACGGAAGGCGCTCT	10		
RESULT 33					
AAD11017					

```

OS Mycobacterium avium.
XX WO9935284-A1.
XX PN
XX PD
XX 15-JUL-1999.
XX
XX 30-DEC-1997; 97WO-BR0000087.
XX PF
XX PR 30-DEC-1997; 97WO-BR0000087.
XX PA
XX (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX Peregrino Ferreira PC, Geessien Kroon E;
XX PI Bernardes Margutti Pinto ME, Aleixo AW;
XX XX
XX WPI; 1999-444201/37.
XX
XX Detection of mycobacteria by shift mobility assay.
XX PT
XX Disclosure; Fig 7; 20pp; English.
XX
XX The invention describes a new method for diagnosis, identification and
XX characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX DNA amplification and shift mobility assay. The method is based on
XX divergence in sequences found in 16S rRNA to identify mycobacteria
XX species, since a remarkable shift of heteroduplex bands are obtained
XX between single stranded and homoduplex bands in UPAGE. The method is
XX fast, simple and can produce information not easily obtained when
XX compared with other detection methods. The sensitivity of other assays
XX suffer due to the tendency of the denatured PCR product strands to
XX reassociate and exclude oligonucleotide probes, and stearic interference
XX between the bound oligonucleotides and the solid support which impede
XX hybridization to nucleic acids in solution. Sequences AAX99193-237
XX represent 16S rRNA gene regions of some mycobacterial species
XX
XX Sequence 50 BP; 15 A; 12 C; 14 G; 9 T; 0 U; 0 Other;
XX
XX Query Match 85.0%; Score 20.4; DB 2; Length 50;
XX Best Local Similarity 95.5%; Pred. No. 6.2;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGGCCTTT 22
XX |||||
XX Db 10 CAAGTCGAACGGAAGGCCTCT 31
XX
XX RESULT 35
XX AAX99196
XX ID AAX99196 standard; DNA; 50 BP.
XX AC
XX AC AAX99196;
XX XX
XX DT 28-SEP-1999 (first entry)
XX DE
XX DE M. fortuitum 16S rRNA gene fragment.
XX KW
XX KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX OS
XX OS Mycobacterium fortuitum.
XX PN
XX PN WO9935284-A1.
XX PD
XX PD 15-JUL-1999.
XX
XX 30-DEC-1997; 97WO-BR0000087.
XX PF
XX PR 30-DEC-1997; 97WO-BR0000087.
XX PA
XX (UYMI-) UNIV FEDERAL MINAS GERAIS.
XX
XX

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PI Peregrino Ferreira PC, Geessien Kroon E;
PI Bernardes Margutti Pinto ME, Aleixo AW;
XX
XX WPI; 1999-444201/37.
XX
XX Detection of mycobacteria by shift mobility assay.
XX PT
XX Disclosure; Fig 7; 20pp; English.
XX
XX The invention describes a new method for diagnosis, identification and
XX characterisation of Mycobacterium tuberculosis or any other mycobacteria
XX by using polymerase chain reaction (PCR) and shift mobility assay (SMA)
XX in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,
XX DNA amplification and shift mobility assay. The method is based on
XX divergence in sequences found in 16S rRNA to identify mycobacteria
XX species, since a remarkable shift of heteroduplex bands are obtained
XX between single stranded and homoduplex bands in UPAGE. The method is
XX fast, simple and can produce information not easily obtained when
XX compared with other detection methods. The sensitivity of other assays
XX suffer due to the tendency of the denatured PCR product strands to
XX reassociate and exclude oligonucleotide probes, and stearic interference
XX between the bound oligonucleotides and the solid support which impede
XX hybridization to nucleic acids in solution. Sequences AAX99193-237
XX represent 16S rRNA gene regions of some mycobacterial species
XX
XX Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;
XX
XX Query Match 85.0%; Score 20.4; DB 2; Length 50;
XX Best Local Similarity 95.5%; Pred. No. 6.2;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 CAAGTCGAACGGAAGGCCTTT 22
XX |||||
XX Db 10 CAAGTCGAACGGAAGGCCTCT 31
XX
XX RESULT 36
XX ADF94050
XX ID ADF94050 standard; DNA; 50 BP.
XX AC
XX AC ADF94050;
XX XX
XX DT 11-MAR-2004 (first entry)
XX DE
XX DE Microorganism detection probe, SEQ ID 143.
XX KW
XX KW Probe; detection; identification; microorganism; food; drug;
XX 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.
XX OS
XX OS Mycobacterium avium.
XX PN
XX PN WO2003106676-A1.
XX PD
XX PD 24-DEC-2003.
XX
XX 16-JUN-2003; 2003WO-JP007620.
XX PF
XX PF 14-JUN-2002; 2002JP-00174564.
XX PR
XX XX
XX (HISF) HITACHI SOFTWARE ENG CO LTD.
XX PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.
XX
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;
XX Shimadzu M, Kobayashi I, Ishiko H;
XX WPI; 2004-071565/07.
XX
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a
XX microorganism for specific detection and identification of the
XX microorganism in foods and drug compositions.
XX
XX Claim 2; SEQ ID NO 143; 150pp; Japanese.
XX

```

CC The present invention relates to probes (ADP93908-ADP94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADP94060 and ADP94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.

XX SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 50;  
 Best Local Similarity 95.5%; Pred. No. 6.2;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 Db 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 37  
 AEB98762  
 ID AEB98762 standard; DNA; 209 BP.  
 XX AC AEB98762;  
 XX DT 06-OCT-2005 (first entry)  
 XX DE Mycobacterium avium partial 16S rDNA sequence, SEQ ID 4.  
 XX KW microorganism detection; mycobacterium infection; antibacterial; ds.  
 XX OS Mycobacterium avium.  
 XX PI JP2005204582-A.  
 XX PN 04-AUG-2005.  
 XX PF 23-JAN-2004; 2004JP-00015195.  
 XX PR 23-JAN-2004; 2004JP-00015195.  
 XX PA (ASAH ) ASahi Kasei KK.  
 XX PI Oda N;  
 XX DR WPI; 2005-526965/54.  
 XX PT New single-stranded oligonucleotide, useful for amplifying the nucleic  
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and  
 PT Mycobacterium kansasii.

XX Example 1; SEQ ID NO 4; 14pp; Japanese.

XX The invention relates to a novel single-stranded oligonucleotide used in  
 CC a detection method of an atypical mycobacteria group. The invention  
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a  
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the  
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the  
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the  
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of  
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.  
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful  
 CC in medical applications. This polynucleotide represents a Mycobacterium  
 CC avium partial 16S rDNA sequence amplified by the LAMP method of the  
 CC invention.

XX SQ Sequence 209 BP; 48 A; 48 C; 70 G; 43 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 14; Length 209;  
 Best Local Similarity 95.5%; Pred. No. 7.3;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 Db 40 CAAGTCGAACGGAAGGCCTCT 61

RESULT 38  
 ABT23571  
 ID ABT23571 standard; DNA; 560 BP.

XX AC ABT23571;  
 XX DT 22-MAY-2003 (first entry)  
 XX DE Stabilising reagent method related oligo SEQ ID No 23.  
 XX KW Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;  
 KW specific amplification; pathogenic microorganism; chimeric;  
 XX genetic engineering; clinical medicine; ss.  
 XX OS Mycobacterium avium.  
 XX PN WO2002101042-A1.  
 XX PD 19-DEC-2002.  
 XX PF 12-JUN-2002; 2002WO-JP005832.  
 XX PR 12-JUN-2001; 2001JP-00177737.  
 XX PR 20-AUG-2001; 2001JP-00249689.  
 XX PA (TAKI ) TAKARA BIO INC.  
 XX PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;  
 PI Enoki T, Asada K, Kato I;  
 XX WPI; 2003-148805/14.

Method for stabilizing and storing reaction reagents for specific  
 PT amplification and detection of nucleic acids particularly in e.g.  
 PT identifying pathogenic microorganisms or viruses in sample.

XX Example 15; Page 109; 177pp; Japanese.

XX The invention relates to a novel stabilising reaction reagent for use in  
 CC the amplification and/or detection of a target nucleic acid comprising:  
 CC preparing a reaction mixture with e.g. a nucleic acid as template, at  
 CC least 1 primer and RNaseH; and incubation of the reaction mixture for a  
 CC defined period of time to form a reaction product during the  
 CC amplification of such target nucleic acid. The method is useful for  
 CC stabilising and long-term storage of reaction reagents for highly  
 CC sensitive and specific amplification and detection of nucleic acids

CC particularly in identifying pathogenic microorganisms or viruses in a  
CC sample using chimeric oligonucleotide primers, which is useful in genetic  
CC engineering and clinical medicine. This polynucleotide sequence  
CC represents an oligo relating to the novel stabilising reaction reagent  
CC method of the invention

XX  
SQ Sequence 560 BP; 117 A; 134 C; 198 G; 111 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 10; Length 560;  
Best Local Similarity 95.5%; Pred. No. 8.1;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22  
|||  
Db 31 CAAGTCGAACGGAAGGCCTCT 52

RESULT 39

AEA22411

ID AEA22411 standard; DNA; 1421 BP.

XX AEA22411;

XX 25-AUG-2005 (first entry)

XX Mycobacterium lentiflavum 16S rRNA sequence SEQ ID NO:12.

XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX Mycobacterium lentiflavum.

XX US2005130168-A1.

XX 16-JUN-2005.

XX 31-OCT-2003; 2003US-00697802.

XX 31-OCT-2003; 2003US-00697802.

XX (HANX/) HAN X.

XX (PHAM/) PHAM A S.

XX Han X, Pham AS;

XX WPI; 2005-424597/43.

XX Determining a bacterium species comprises providing oligonucleotide

XX primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.

XX Disclosure; SEQ ID NO 12; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium

XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)

XX extracting a genomic nucleotide from the bacterium to provide a

XX nucleotide template; (c) annealing a region of a nucleotide template to a

XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a

XX complementary fashion, the primer set designed to provide a product

XX having a predetermined size dictated by a complementary primer set; (d)

XX amplifying the region of the nucleotide template to produce the product;

XX and (e) determining a species of a bacterium in a nucleotide sequence of

XX the product. Also described is an alternative method (M2) for determining

XX a bacterium species comprising: (a) providing a specimen or a sample

XX having a template; (b) providing a pair of primers selected from: (i) a

XX first forward primer having consecutive bases of an AFB-f comprising any

XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments

XX or variations, and a first reverse primer having consecutive bases of an

XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)

XX or their fragments or variations, (ii) a second forward primer having

XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21

XX bp (AEA22489-AEA22516) or their fragments or variations, and a second

XX reverse primer having consecutive bases of an UB-r comprising any of the

XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or

XX variations, or (iii) a first forward primer having consecutive bases of

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
CC comparing the product from the specimen with a nucleotide sequence from a  
CC database to determine the bacterium species present in the specimen. The  
CC methods are useful for determining a bacterium species. The present  
CC sequence represents a Mycobacterium lentiflavum 16S rRNA nucleotide  
CC sequence, which is used in the exemplification of the present invention.

XX  
SQ Sequence 1421 BP; 306 A; 344 C; 487 G; 284 T; 0 U; 0 Other;

Query Match 85.0%; Score 20.4; DB 14; Length 1421;  
Best Local Similarity 95.5%; Pred. No. 8.9;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22

|||  
Db 21 CAAGTCGAACGGAAGGCCTCT 42

RESULT 40

ADK66476

ID ADK66476 standard; RNA; 1431 BP.

XX ADK66476;

XX 06-MAY-2004 (first entry)

XX Corynebacterium 16S rRNA sequence.

XX ss; 16S rRNA; microorganism detection; clinical sample;

XX pharmaceutical composition.

XX Corynebacterium sp.

XX WO2004009839-A2.

XX 29-JAN-2004.

XX 16-JUL-2003; 2003WO-EP007717.

XX 18-JUL-2002; 2002DE-01032776.

XX 14-FEB-2003; 2003DE-01007732.

XX (HENK ) HENKEL KGAA.

XX (VERM-) VERMICON AG.

XX Saettler A, Jassoy C, Scholtyssek R, Maischein V, Nieveler S;

XX Weiss A, Trebesius K, Beilmohr C, Ludwig W, Bamberg RR, Schleifer K;

XX Muellner S, Adomat C, Bergmaier I;

XX WPI; 2004-123402/12.

XX New oligonucleotides for specific detection of microorganisms, useful

XX e.g. for detecting or quantifying microbes on the skin, in foods,

XX clinical samples or water, by in situ hybridization.

XX Disclosure; Page 66-67; 67pp; German.

XX The present invention provides a number of oligonucleotides for the

XX specific detection of microorganisms. The oligonucleotides are used to

XX detect and/or quantify microorganisms, especially on the skin, in foods

XX or the environment (water, soil and air), from waste waters or biofilms,

XX in clinical samples (body fluids or tissues), and in pharmaceutical or

XX cosmetic compositions. The present sequence is a Corynebacterium 16S rRNA

XX sequence.

XX  
SQ Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 1431;

Best Local Similarity 81.8%; Pred. No. 8.9;

Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CAAGTCGAACGGAAGGCCTTT 22
   |||||:|||||:|||||:
Db 31 CAAGUCGAACGGAAGGCCUCU 52

RESULT 41
ADK66445
ID ADK66445 standard; RNA; 1431 BP.
XX
AC ADK66445;
XX
DT 06-MAY-2004 (first entry)
XX
DE Corynebacterium 16S rRNA sequence.
XX
KW ss; 16S rRNA; microorganism detection; skin; acne.
XX
OS Corynebacterium sp.
XX
PN W02004009843-A2.
XX
PD 29-JAN-2004.
XX
PF 16-JUL-2003; 2003WO-EP007718.
XX
PR 18-JUL-2002; 2002DE-01032775.
XX
PR 14-FEB-2003; 2003DE-01006616.
XX
PA (HENK ) HENKEL KGAA.
XX
PI Saettler A, Jassoy C, Scholtyssek R, Maischein V, Nieveler S;
PI Weiss A, Trebesius K, Beimehr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX
DR WPI; 2004-123405/12.
XX
PT Kit for detection of microorganisms on skin, useful e.g. for diagnosis of
PT infection, comprises specific oligonucleotides for in situ hybridization.
XX
PS Disclosure; Page 62-63; 63pp; German.
XX
CC The present invention relates to a kit for detecting microorganisms that
CC contains at least one oligonucleotide specific for at least one species,
CC or group of species, that is present on the skin. The kit is used to
CC detect and/or quantify microorganisms that are present on the skin; e.g.
CC for early diagnosis of secondary infection in cases of acne. The present
CC sequence is a Corynebacterium 16S rRNA sequence.
XX
SQ Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 85.0%; Score 20.4; DB 12; Length 1431;
Best Local Similarity 81.8%; Pred. No. 8.9;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   |||||:|||||:|||||:
Db 31 CAAGUCGAACGGAAGGCCUCU 52

RESULT 42
AAQ37639
ID AAQ37639 standard; rRNA; 1449 BP.
XX
AC AAQ37639;
XX
DT 25-MAR-2003 (revised)
DT 18-JUN-1993 (first entry)
XX
DE Mycobacterium genavense 16S rRNA.
XX
KW Detection; rapid; immunosuppressed patients; AIDS; ss.
XX
OS Mycobacterium genavense.

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   |||||:|||||:|||||:
Db 48 CAAGTCGAACGGAAGGCCTCT 69

RESULT 43
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   |||||:|||||:|||||:
Db 48 CAAGTCGAACGGAAGGCCTCT 69

Query Match 85.0%; Score 20.4; DB 2; Length 1449;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
   |||||:|||||:|||||:
Db 48 CAAGTCGAACGGAAGGCCTCT 69

RESULT 43
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX
AC AEA22401;
XX
DT 25-AUG-2005 (first entry)
XX
DE Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
OS Mycobacterium avium.
XX
PN US2005130168-A1.
XX
PD 16-JUN-2005.
XX
PF 31-OCT-2003; 2003US-00697802.
XX
PR 31-OCT-2003; 2003US-00697802.
XX
PA (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
PI Han X, Pham AS;
XX
DR WPI; 2005-424597/43.
XX

```



PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 PS Disclosure; SEQ ID NO 2; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;  
 Query Match 85.0%; Score 20.4; DB 14; Length 1454;  
 Best Local Similarity 95.5%; Pred. No. 8.9;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 DB 31 CAAGTCGAACGGAAGGCCTCT 52  
 |||||  
 RESULT 44  
 ADB61680  
 ID ADB61680 standard; DNA; 1465 BP.  
 XX  
 AC ADB61680;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE 16S rRNA of Mycobacterium avium DNA sequence.  
 XX  
 KW enriching mRNA; high quality bacterial mRNA; bacterial gene expression;  
 KW poly-A tail; mRNA purification; oligo-dT capture;  
 KW prokaryote mRNA purification; bridging oligonucleotide; targeting region;  
 KW capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;  
 KW eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;  
 KW 28S eukaryotic rRNA bridging oligonucleotide; ds.  
 XX  
 OS Mycobacterium avium.  
 XX  
 PN WO2003054162-A2.  
 XX  
 PD 03-JUL-2003.  
 XX  
 PF 19-DEC-2002; 2002WO-US041014.  
 XX  
 PR 20-DEC-2001; 2001US-00029397.

XX (AMBI-) AMBION INC.  
 PA Murphy GL, Whitley JP;  
 XX  
 PI WPI; 2003-663255/62.  
 XX  
 DR Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a  
 XX bridging oligonucleotide comprising bridging region and a targeting  
 PT region complementary to a targeted nucleic acid, and a capture  
 PT oligonucleotide.  
 XX  
 PS Claim 4; Page 168; 208pp; English.  
 XX  
 CC This invention relates to a novel method for isolating, depleting or  
 CC separating a targeted nucleic acid, such as rRNA, from a sample  
 CC comprising targeted and non-targeted nucleic acids. It effects a way of  
 CC enriching for non-targeted nucleic acids such as mRNAs. Isolating  
 CC sufficient quantities of high quality bacterial mRNA is a demanding  
 CC process which impedes analysis of bacterial gene expression in the  
 CC presence of host cells. A small percentage of bacterial mRNAs may be poly  
 CC -A tailed, but these are targeted for degradation and tend to be  
 CC unstable. As a result, the commonly employed method for mRNA purification  
 CC with eukaryotic cells, oligo-dT capture, is ineffective. The present  
 CC invention provides an alternative, more suitable method for mRNA  
 CC purification from prokaryotes. The method of the invention comprises the  
 CC incubation of a sample with a bridging oligonucleotide (containing a  
 CC targeting region) and subsequently incubating with a capture  
 CC oligonucleotide allowing the isolation of the target from the sample. The  
 CC method is useful for depleting or isolating targeted nucleic acid, for  
 CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S  
 CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may  
 CC comprise any one of 64 fully defined sequences as given in the  
 CC specification. The present sequence is that of a DNA sequence which  
 CC represents the sequence of 16S rRNA of Mycobacterium avium related to the  
 CC invention.  
 XX  
 SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;  
 Query Match 85.0%; Score 20.4; DB 10; Length 1465;  
 Best Local Similarity 95.5%; Pred. No. 8.9;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 DB 21 CAAGTCGAACGGAAGGCCTCT 42  
 |||||  
 RESULT 45  
 ADR90572  
 ID ADR90572 standard; DNA; 1472 BP.  
 XX  
 AC ADR90572;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE M avium 16S rRNA gene sequence SeqID1.  
 XX  
 KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;  
 KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.  
 XX  
 OS Mycobacterium avium.  
 XX  
 PH Key Location/Qualifiers  
 FT variation 893 /\*tag= a  
 FT variation 1312 /\*tag= b  
 FT variation 1393 /\*tag= c  
 XX  
 PN JP2004254591-A.  
 XX

```

PD 16-SEP-2004.
XX
XX
XX 26-FEB-2003; 2003JP-00048654.
XX
PR 26-FEB-2003; 2003JP-00048654.
XX
XX (MITP ) MITSUBISHI YUKA BCL KK.
XX
XX WPI; 2004-664464/65.
XX
XX Differentiating acid-fast bacterium e.g., Mycobacterium avium complex,
XX useful for detecting mutant of M.avium complex, and for grouping strains
XX of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast
XX bacterium.
XX
XX Claim 3; SEQ ID NO 1; 23pp; Japanese.
XX
XX This invention relates to a novel method of differentiating acid-fast
XX bacterium, which involves detecting a mutation in the 16S rRNA gene of
XX the acid-fast bacterium. The method is useful for differentiating acid-
XX fast bacterium such as M avium complex (MAC) or M kansasii, in particular
XX for detecting mutants of MAC, and for grouping strains of M kansasii. The
XX method is also useful for carrying out taxonomic-tree analysis of
XX atypical-mycobacteria and enables detection of MAC accurately and
XX reliably. The present sequence is that of a Mycobacterium 16S rRNA gene
XX which may be used in the method of the invention.
XX
XX Sequence 1472 BP; 323 A; 348 C; 500 G; 298 T; 0 U; 3 Other;
SQ
Query Match 85.0%; Score 20.4; DB 13; Length 1472;
Best Local Similarity 95.5%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCTT 22
Db 31 CAAGTCGAACGGAAGGCCTCT 52
RESULT 46
AEB98771
ID AEB98771 standard; DNA; 39 BP.
XX
XX AC AEB98771;
XX
XX 06-OCT-2005 (first entry)
XX
XX Mycobacterium avium identification LAMP primer, SEQ ID 13.
XX
XX microorganism detection; mycobacterium infection; antibacterial; primer;
XX PCR; ss; LAMP.
XX
XX Mycobacterium avium.
XX Synthetic.
XX
XX JP2005204582-A.
XX
XX 04-AUG-2005.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX (ASAH ) ASahi KASEI KK.
XX
XX Oda N;
XX
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX
XX Claim 1; SEQ ID NO 13; 14pp; Japanese.
XX
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
XX a detection method of an atypical mycobacteria group. The invention
XX further includes: amplifying the nucleic acid of Mycobacterium avium by a
XX loop-mediated isothermal amplification (LAMP) method; amplifying the
XX nucleic acid of M. intracellulare by a LAMP method; amplifying the
XX nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
XX nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
XX M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
XX kansasii by a LAMP method. The single-stranded oligonucleotide is useful
XX in medical applications. This oligo sequence represents a loop-mediated
XX isothermal amplification (LAMP) primer used in the exemplification of the
XX invention.
XX
XX Sequence 39 BP; 10 A; 11 C; 10 G; 8 T; 0 U; 0 Other;
SQ
Query Match 83.3%; Score 20; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAGGCCT 20
Db 20 CAAGTCGAACGGAAGGCCT 39
RESULT 47
AAT45276
ID AAT45276 standard; rRNA; 1391 BP.
XX
XX AC AAT45276;
XX
XX 12-SEP-1997 (first entry)
XX
XX Corynebacterium diphtheriae 16S rRNA.
XX
XX Ribosomal RNA; species specific; detection; reverse transcription;
XX primer; hybridisation probe; identification; ss.
XX
XX Corynebacterium diphtheriae.
XX
XX Key Location/Qualifiers
XX misc_feature 38..59
XX /tag= a
XX /note= "Defined as nucleotides 72-100"
XX misc_feature 153..170
XX /tag= b
XX /note= "Defined as nucleotides 195-215"
XX misc_feature 415..431
XX /tag= c
XX /note= "Defined as nucleotides 466-494"
XX misc_feature 544..567
XX /tag= d
XX /note= "Defined as nucleotides 544-567"
XX misc_feature 773..787
XX /tag= e
XX /note= "Defined as nucleotides 838-853"
XX misc_feature 793..808
XX /tag= f
XX /note= "Defined as nucleotides 859-875"
XX misc_feature 946..965
XX /tag= g
XX /note= "Defined as nucleotides 1013-1032"
XX
XX FR2733755-A1.
XX
XX 08-NOV-1996.
XX
XX 03-MAY-1995; 95FR-00005494.
XX
XX 03-MAY-1995; 95FR-00005494.
XX (INMR ) BIO MERIEUX.
XX

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PI Mabilat C, Ruimy R;
XX WPI; 1997-001738/01.
XX
XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for
XX identifying Corynebacterium spp.
XX
XX Claim 1; Fig 1; 60pp; French.
XX
XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were
XX amplified from 28 strains of 25 different species of Corynebacterium by
XX PCR using primers specific for eubacteria. The amplification products
XX were sequenced and the sequences were aligned for comparison. It was
XX found that certain regions, i.e. those corresponding to nucleotides 72-
XX 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S
XX ribosomal RNA of C. diphtheriae (refer to features table for the present
XX sequence), vary considerably between different species. Probes and
XX primers comprising at least 5 nucleotides from one of these species-
XX specific sequences, including the present sequence, or their complements,
XX are useful to distinguish between different Corynebacterium species. DNA
XX versions of the probes and primers are also included
XX
XX Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match      83.3%; Score 20; DB 2; Length 1391;
Best Local Similarity 90.0%; Pred. No. 14;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20
Db 30 CAAGUCGAACGGAAGGCCU 49

RESULT 48
ABN86276
ID ABN86276 standard; DNA; 1457 BP.
XX
XX ABN86276;
XX
XX 08-OCT-2002 (first entry)
XX
XX G. polyisoprenivorans P8219 16S rDNA sequence #2.
XX
XX Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.
XX
XX Gordonia polyisoprenivorans.
XX
XX JP2002142754-A.
XX
XX 21-MAY-2002.
XX
XX 08-NOV-2000; 2000JP-00341214.
XX
XX 08-NOV-2000; 2000JP-00341214.
XX
XX (IMBI-) IMB KK.
XX
XX WPI; 2002-561124/60.
XX
XX A Gordonia sp. microorganism, useful in the eradication of the
XX environmental hormone of phthalic acid esters for environmental
XX protection.
XX
XX Disclosure; Fig 2A-D; 21pp; Japanese.
XX
XX The invention relates to a Gordonia sp. microorganism, capable of
XX eradication of the environmental hormone of phthalic acid alkyl esters.
XX The microorganism is used in the eradication of phthalic acid esters for
XX environmental protection. The present sequence represents an alternate G.
XX polyisoprenivorans P8219 16S rDNA sequence
XX
XX Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

Query Match      82.5%; Score 19.8; DB 6; Length 1457;
Best Local Similarity 91.3%; Pred. No. 17;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
Db 41 CAAGTCGAACGGAAGGCCCTGC 63

RESULT 50
AAS59540/c
ID AAS59540 standard; DNA; 2743 BP.
XX
XX AAS59540;
XX
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein encoding DNA #35.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant; ds.
XX

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OS Propionibacterium acnes.
XX WO200181581-A2.
XX 01-NOV-2001.
XX 20-APR-2001; 2001WO-US012865.
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Claim 1; SEQ ID NO 35; 1069pp; English.
XX
XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
XX Propionibacterium acnes immunogenic polypeptides. The proteins and their
XX associated DNA sequences are used in the treatment, prevention and
XX diagnosis of medical conditions caused by P. acnes. The disorders include
XX SAPHO syndrome (synovitis, acne, pustulosis, hyperostosis and
XX osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
XX infections of bone, joints and the central nervous system, however it is
XX particularly involved in the inflammatory lesions associated with acne
XX vulgaris. A method for detecting the presence or absence of P. acnes in a
XX patient comprises contacting a sample with a binding agent that binds to
XX the proteins of the invention and determining the amount of bound protein
XX in the sample. The polypeptides may be used as antigens in the production
XX of antibodies specific for P. acnes proteins. These antibodies can be
XX used to downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). This sequence encodes the
XX polypeptides shown in AAU47822-AAU47846. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
XX
XX Query Match 82.5%; Score 19.8; DB 4; Length 2743;
XX Best Local Similarity 91.3%; Pred. No. 19;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CAAGTCGAACGGAAGGCGCTTTC 23
XX |||||
XX Db 2592 CAAGTCGAACGGAAGGCGCTTGC 2570
XX
XX RESULT 51
XX ID ACF64469/c
XX AC ACF64469;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX Propionibacterium acnes DNA contig sequence #35.
XX
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine; ds.
XX
XX OS Propionibacterium acnes.
XX
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PN WO2003033515-A1.
XX 24-APR-2003.
XX 11-OCT-2002; 2002WO-US032727.
XX 15-OCT-2001; 2001US-00978825.
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallieue-Douglas J;
XX WPI; 2003-381789/36.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
XX
XX Claim 1; SEQ ID NO 35; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention
XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes
XX polypeptide and an isolated T cell population comprising T cells prepared
XX via this method; a vaccine composition (comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or
XX antigen-presenting cells that express the polypeptide); a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a
XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne
XX vulgaris, or for stimulating an immune response specific for a P. acnes
XX protein. The polynucleotides can also be used as probes or primers for
XX nucleic acid hybridisation. The vaccine composition is useful for the
XX stimulation of an immune response against P. acnes, or for treating acne,
XX and the kit is useful for performing a diagnostic assay. The present
XX sequence represents a P. acnes DNA contig which is specifically claimed
XX in the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;
XX
XX Query Match 82.5%; Score 19.8; DB 8; Length 2743;
XX Best Local Similarity 91.3%; Pred. No. 19;
XX Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CAAGTCGAACGGAAGGCGCTTTC 23
XX |||||
XX Db 2592 CAAGTCGAACGGAAGGCGCTTGC 2570
XX
XX RESULT 52
XX AAX99198
XX ID AAX99198 standard; DNA; 50 BP.
XX
XX AC AAX99198;
XX
XX 28-SEP-1999 (first entry)
XX
XX M. smegmatis 16S rRNA gene fragment.
XX
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA; ss.
XX shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
```

OS	Mycobacterium smegmatis.
XX	
PI	Peregrino Ferreira PC, Geessien Kroon E;
PN	Bernardes Margutti Pinto ME, Aleixo AW;
XX	
PD	WPI; 1999-444201/37.
XX	
PF	Detection of mycobacteria by shift mobility assay.
XX	
PR	Disclosure; Fig 7; 20pp; English.
XX	
PA	(UWMI-) UNIV FEDERAL MINAS GERAIS.
XX	
PI	Peregrino Ferreira PC, Geessien Kroon E;
PI	Bernardes Margutti Pinto ME, Aleixo AW;
XX	
DR	WPI; 1999-444201/37.
XX	
PT	Detection of mycobacteria by shift mobility assay.
XX	
PS	Disclosure; Fig 7; 20pp; English.
XX	
CC	The invention describes a new method for diagnosis, identification and characterisation of Mycobacterium tuberculosis or any other mycobacteria by using polymerase chain reaction (PCR) and shift mobility assay (SMA) in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction, DNA amplification and Shift mobility assay. The method is based on divergence in sequences found in 16S rRNA to identify mycobacteria species, since a remarkable shift of heteroduplex bands are obtained between single stranded and homoduplex bands in UPAGE. The method is fast, simple and can produce information not easily obtained when compared with other detection methods. The sensitivity of other assays reassociate and exclude oligonucleotide probes, and stearic interference between the bound oligonucleotides and the solid support which impede hybridization to nucleic acids in solution. Sequences AAX99193-237 represent 16S rRNA gene regions of some mycobacterial species
XX	
SQ	Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;
	Query Match 80.8%; Score 19.4; DB 2; Length 50;
	Best Local Similarity 90.9%; Pred. No. 19;
	Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 CAAGTCGAACGGAAAGGCCTTT 22 
Db	10 CAAGTCGAACGGAAAGNCCTT 31
	RESULT 53
	ADS75567
ID	AUS75567 standard; DNA; 535 BP.
XX	
AC	ADS75567;
XX	
DT	02-DEC-2004 (first entry)
XX	
DE	Rhodococcus equi TB-60 16S rDNA sequence, SEQ ID 1.
XX	
KW	Urethane; polyurethane; 16S rDNA; ds.
XX	
OS	Rhodococcus equi; TB-60.
XX	
PN	WO2004078952-A1.
XX	
PD	16-SEP-2004.
XX	
PF	03-MAR-2004; 2004WO-JP002691.
XX	
PR	03-MAR-2003; 2003JP-00055421.
XX	
PA	(NISC-) JAPAN SCI & TECHNOLOGY AGENCY.
XX	
PI	Kambe T, Shigeno Y;
XX	
DR	WPI; 2004-728402/71.
XX	
PT	Novel microorganism or its mutant belonging to Rhodococcus genus and having ability to cleave urethane bond, useful for plastic disposal and recycling of urethane compounds.
XX	
PS	Example 2; SEQ ID NO 1; 26pp; Japanese.
XX	
PA	The present invention relates to a novel Rhodococcus equi TB-60 strain

```

CC microorganism: (I) or its mutant, which can cleave urethane bonds. (I) is
CC useful for decomposing urethane compounds which involves contacting (I)
CC with urethane compound. The urethane compound is a raw material of
CC polyurethane or is polyurethane. (I) is useful in plastic disposal and
CC recycling of urethane compounds by decomposing urethane compounds. The
CC present sequence is a 16S rDNA sequence from the microorganism of the
CC invention.
XX
SQ Sequence 535 BP; 118 A; 131 C; 191 G; 95 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 13; Length 535;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
Db 52 CAAGTCGAGCGGTAAAGGCCCTTCG 75

RESULT 55
ADF56670
ID ADF56670 standard; DNA; 1437 BP.
XX
XX AC ADF56670;
XX
DT 12-FEB-2004 (first entry)
XX
DE YS-44442 16S rDNA, SEQ ID 1.
XX
XX Pravastatin; HMG-CoA reductase inhibitor;
XX 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
XX Saccharothrix sp.
XX
XX JP2003250532-A.
XX
XX 09-SEP-2003.
XX
XX 22-FEB-2002; 2002JP-00046750.
XX
XX 22-FEB-2002; 2002JP-00046750.
XX (YUNG-) YUNG SHIN PHARM IND CO LTD.
XX
XX WPI; 2004-046768/05.
XX
XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
XX mutants useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 18pp; Japanese.
XX
XX The present invention relates to microorganisms (I) Saccharothrix genus
XX YS-44442 and YS-45494 strains and their mutants. Also claimed is a method
XX (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
XX 3-methyl glutaryl (HMG)-CoA reductase inhibitors.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 12; Length 1437;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 56
ADG64519
ID ADG64519 standard; DNA; 1437 BP.
XX
XX AC ADG64519;
XX
DT 02-JUN-2005 (first entry)
XX
XX Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.

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```

DT 11-MAR-2004 (first entry)
XX
XX Saccharothrix strain YS-44442 16S rDNA sequence.
XX
XX Microorganism; Saccharothrix; YS-44442; YS-45494;
XX 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
XX pravastatin; fermentation; compactin; lovastatin;
XX blood cholesterol level; antilipemic; 16S rDNA; ds.
XX Saccharothrix sp.
XX
XX US2003199047-A1.
XX
XX 23-OCT-2003.
XX
XX 27-FEB-2002; 2002US-00085871.
XX
XX 27-FEB-2002; 2002US-00085871.
XX (LEEP/) LEE F.
XX (LEEM/) LEE M.
XX (HONG/) HONG A C.
XX (CHIU/) CHIU S.
XX
XX Lee F, Lee M, Hong AC, Chiu S;
XX WPI; 2004-041353/04.
XX
XX Novel microorganism strains YS-44442 and YS-45494 of Saccharothrix,
XX useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 16pp; English.
XX
XX The present invention relates to the isolation of novel microorganism
XX strains of Saccharothrix designated YS-44442 and YS-45494. Also disclosed
XX is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
XX inhibitors such as pravastatin. The Saccharothrix strains YS-44442 and YS
XX -45494 are useful for producing pravastatin. The method involves
XX cultivating the strains at a suitable condition to generate a
XX fermentation broth, feeding compactin into the broth, fermenting the
XX broth for a period of time to convert the compactin to pravastatin, and
XX isolating the pravastatin from the broth. The fermentation broth is
XX cultivated for less than 2 days, preferably for 18 hours. The
XX fermentation broth is derived from a seed culture of the microorganism
XX which is cultivated at a suitable condition for 18-48 hours before
XX inoculation into the broth. The broth is fermented for less than 5 days,
XX preferably 3 days, most preferably less than 24 hours. The method of the
XX invention is useful for isolating HMG-CoA reductase inhibitor such as
XX pravastatin, compactin or lovastatin, preferably pravastatin. The
XX pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
XX cholesterol levels. The present sequence represents Saccharothrix strain
XX YS-44442 16S rDNA sequence.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;

Query Match      80.0%; Score 19.2; DB 12; Length 1437;
Best Local Similarity 87.5%; Pred. No. 34;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTTCG 24
Db 31 CAAGTCGAGCGGTAAAGGCCCTTCG 54

RESULT 57
ADY86147
ID ADY86147 standard; DNA; 1437 BP.
XX
XX AC ADY86147;
XX
XX 02-JUN-2005 (first entry)
XX
XX Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.

```

XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;  
 KW metabolic disorder; ds.  
 XX OS Saccharothrix; YS-44442.  
 XX PN US2005064566-A1.  
 XX PD 24-MAR-2005.  
 XX PF 03-DEC-2003; 2003US-00727643.  
 XX PR 27-FEB-2002; 2002US-00085871.  
 XX PA (LEEF/) LEE F.  
 XX PA (LEEM/) LEE M.  
 XX PA (HONG/) HONG A. C.  
 XX PA (CHIU/) CHIU S.  
 XX PI Lee F, Lee M, Hong AC, Chiu S;  
 XX WPI; 2005-252680/26.  
 XX PT Isolation of pravastatin, used to treat hypercholesterolemia, comprises  
 PT adding ammonium sulfate into a first solution to form precipitate,  
 PT isolating and dissolving the precipitate to form a second solution and  
 PT followed by extracting.  
 XX PS Example 1; SEQ ID NO 1; 19pp; English.  
 XX CC The present invention relates to two new microorganism strains of  
 CC Saccharothrix, designated as YS-44442 and YS-45494. The invention also  
 CC provides a method of isolating pravastatin from Saccharothrix sp and an  
 CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A  
 CC (HMG CoA) reductase inhibitor. The invention is useful for the  
 CC preparation of pravastatin which is useful in the treatment of  
 CC hypercholesterolemia. The present sequence is the Saccharothrix YS-44442  
 CC 16s rDNA.  
 XX SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;  
 Query Match 80.0%; Score 19.2; DB 14; Length 1437;  
 Best Local Similarity 87.5%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCTTTTCG 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 31 CAAGTCGAGCGTAAGGCTTTTCG 54  
 RESULT 58  
 ADC61232  
 ID ADC61232 standard; DNA; 1439 BP.  
 XX AC ADC61232;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.  
 XX KW Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;  
 KW 16s rDNA; ds.  
 XX OS Rhodococcus erythropolis.  
 XX PN WO2003020890-A2.  
 XX PD 13-MAR-2003.  
 XX PF 29-AUG-2002; 2002WO-US027549.  
 XX PR 29-AUG-2001; 2001US-0315546P.  
 XX

PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
 XX Bramucci MG, Brzosowicz PC, Kostichka KN, Nagarajan V;  
 PI Rouviere PE, Thomas SM;  
 XX WPI; 2003-313085/30.  
 DR Novel nucleic acid fragment useful for converting ketone substrates to  
 XX the corresponding lactone or ester, is isolated from Rhodococcus,  
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase  
 PT polypeptide.  
 XX PS Claim 54; SEQ ID NO 6; 225pp; English.  
 XX CC The invention relates to a novel isolated nucleic acid fragment  
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase  
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 531, 493, 539,  
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;  
 CC a nucleic acid molecule that hybridises with the above sequence under the  
 CC hybridisation conditions; or their complements. The BV monooxygenase  
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV  
 CC monooxygenase polypeptide, by probing a genomic library with the  
 CC fragment, identifying a DNA clone that hybridises with the fragment, and  
 CC sequencing the genomic fragment that comprises the above identified  
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase  
 CC polypeptide. The genes and their products are useful for converting  
 CC suitable ketone substrates to the corresponding lactone or ester. This  
 CC polynucleotide sequence represents the 16s rDNA gene from Arthrobacter  
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.  
 XX SQ Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;  
 Query Match 80.0%; Score 19.2; DB 10; Length 1439;  
 Best Local Similarity 87.5%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCTTTTCG 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 32 CAATTCGAGCGTAAGGCTTTTCG 55  
 RESULT 59  
 ADF56671  
 ID ADF56671 standard; DNA; 1471 BP.  
 XX AC ADF56671;  
 XX DT 12-FEB-2004 (first entry)  
 XX DE YS-45494 16s rDNA, SEQ ID 2.  
 XX KW Pravastatin; HMG-CoA reductase inhibitor;  
 KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16s rDNA; ds.  
 XX OS Saccharothrix sp.  
 XX PN JP2003250532-A.  
 XX PD 09-SEP-2003.  
 XX PF 22-FEB-2002; 2002JP-00046750.  
 XX PR 22-FEB-2002; 2002JP-00046750.  
 XX PA (YUNG-) YUNG SHIN PHARM IND CO LTD.  
 XX DR WPI; 2004-046768/05.  
 XX PT Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their  
 XX mutants useful for producing pravastatin.  
 XX PS Example 1; SEQ ID NO 2; 19pp; Japanese.  
 XX

CC cholesterol levels. The present sequence represents *Saccharothrix* strain

RESULT 62



AED47485  
 ID AED47485 standard; DNA; 1477 BP.  
 XX  
 AC AED47485;  
 XX  
 DT 15-DEC-2005 (first entry)  
 XX  
 DE Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.  
 XX  
 KW Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.;  
 KW Uropathic; binding inhibitor; muscarinic acetylcholine receptor;  
 KW analgesic; Parkinsons disease; asthma;  
 KW chronic obstructive pulmonary disease; bladder disease;  
 KW malnutrition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.  
 XX  
 OS Nocardia sp.  
 XX  
 PN JP2005289890-A.  
 XX  
 PD 20-OCT-2005.  
 XX  
 PF 31-MAR-2004; 2004JP-00107929.  
 XX  
 PR 31-MAR-2004; 2004JP-00107929.  
 XX  
 PA (YOSH ) YOSHITOMI PHARM IND KK.  
 XX  
 PI Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;  
 XX  
 DR WPI; 2005-738172/76.  
 XX  
 PT Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3  
 PT useful for treating diseases e.g. asthma, contains chelate having TPU  
 PT 0052A-F compound derived from Nocardia species TP-A0674 and metal ion.  
 XX  
 PS Disclosure; SEQ ID NO 1; 22pp; Japanese.  
 XX  
 CC The invention relates to a novel binding inhibitor of muscarinic  
 CC acetylcholine receptor subtype 4 or 3, comprising a chelate having a TPU  
 CC 0052A-F compound or its salt and a metal ion. The invention further  
 CC comprises a method and a microorganism for producing the novel binding  
 CC inhibitor. The binding inhibitor and compound are useful as central  
 CC analgesics and memory improving drugs, for treating Parkinson's disease,  
 CC asthma, chronic obstructive pulmonary disease, overactive bladder,  
 CC frequent urination and urinary incontinence. This polynucleotide sequence  
 CC represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674  
 CC microorganism, useful in producing a muscarinic acetylcholine receptor  
 CC binding inhibitor compound of the invention.  
 XX  
 SQ Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;  
 XX  
 Query Match 80.0%; Score 19.2; DB 14; Length 1477;  
 Best Local Similarity 87.5%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 CAAGTCGACCGGTAAGGCCCTTCG 24  
 ||||| ||| ||||| |||||  
 Db 48 CAAGTCGACCGGTAAGGCCCTTCG 71  
 RESULT 63  
 ADS17269  
 ID ADS17269 standard; DNA; 1488 BP.  
 XX  
 AC ADS17269;  
 XX  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Lechevallieria aerocolonigenes strain VK-A9 16S rDNA.  
 XX  
 KW Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;  
 KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.  
 XX



RESULT 68  
AEB98776

PN	WO2003106676-A1.	XX	ds; mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.
XX		KW	
PD	24-DEC-2003.	XX	Unidentified.
XX		OS	
PF	16-JUN-2003; 2003WO-JP007620.	XX	WO2004097369-A2.
XX		PN	
PR	14-JUN-2002; 2002JP-00174564.	XX	11-NOV-2004.
XX		PD	
XX	(HISF ) HITACHI SOFTWARE ENG CO LTD.	XX	22-APR-2004; 2004WO-US012520.
PA	(MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.	PF	
PA		PR	25-APR-2003; 2003US-0466006P.
PI	Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;	XX	(SEQU-) SEQUENOM INC.
PI	Shimadzu M, Kobayashi I, Ishiko H;	XX	(BOEC/) BOECKER S.
XX	WPI; 2004-071565/07.	PA	
XX		XX	Boecker S, Van Den Boom D;
XX		PI	WPI; 2005-012656/01.
PT	20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a	XX	
PT	microorganism for specific detection and identification of the	XX	Obtaining sequence information from target biomolecule, by fragmenting
PT	microorganism in foods and drug compositions.	PT	target biomolecule by partial cleavage, performing mass spectrometry,
XX		PT	extracting information from mass spectra, constructing sequencing graph
PS	Claim 2; SEQ ID NO 146; 150pp; Japanese.	PT	and traversing graphs.
XX		XX	Disclosure; SEQ ID NO 11; 133pp; English.
CC	The present invention relates to probes (ADF93908-ADF94059) for the	XX	
CC	specific detection and identification of harmful microorganisms in	CC	This invention describes a novel method for obtaining sequence
CC	samples of foods and drug compositions. The probe sequences are derived	CC	information from a target biomolecule and involves fragmenting the target
CC	from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,	CC	biomolecule into several fragments by partial cleavage, performing mass
CC	or its complementary sequence. Detection and identification of the	CC	spectrometry on fragments to produce mass spectra, extracting peak
CC	microorganism is by amplification of the complete 16S rRNA gene using	CC	information from the produced mass spectra, constructing sequencing graph
CC	primers ADF94060 and ADF94061, labelling the amplification product (a	CC	using the extracted peak information and traversing the sequencing graphs
CC	fluorescence label is preferred), and hybridising to the probe or probes	CC	to reconstruct sequence information of the target biomolecule. The target
CC	of the invention. The probes may be immobilised on a DNA chip. The	CC	biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein
CC	microorganism is selected from Actinobacillus actinomycetemcomitans,	CC	and the compositions of the two fragments are the base compositions or
CC	Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas	CC	amino acid compositions. This method preferably involves subjecting the
CC	maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas	CC	nucleic acid molecule to partial cleavage reactions with one or more
CC	aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia	CC	specific cleavage reagents, thus generating two or more fragments that
CC	stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Moraxella	CC	are specific cleavage products, determining the molecular weights of the
CC	morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus	CC	two or more fragments, determining the possible base compositions of the
CC	warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter	CC	two or more fragments, ordering the possible base compositions of the two
CC	aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,	CC	or more fragments according to the number of specific cleavage sites that
CC	Serratia marcescens, Streptococcus anginosus, Escherichia coli,	CC	are not cleaved in each fragment, constructing one or more sequencing
CC	Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,	CC	graphs that are a graph theoretical representation of the ordered base
CC	Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,	CC	compositions for the two or more fragments, and traversing the one or
CC	Listeria monocytogenes, Clostridium perfringens, Corynebacterium	CC	more sequencing graph to reconstruct one or more underlying sequence
CC	aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria	CC	candidates, where each sequencing graph corresponds to the ordered base
CC	meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus	CC	compositions derived from a partial cleavage reaction with one base-
CC	caseielliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella	CC	specific cleavage reagent. This method further involves scoring the one
CC	typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella	CC	or more underlying sequence candidates and determining the rank order of
CC	oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella	CC	fitness, where the scoring is done by statistical analysis or maximum
CC	corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella	CC	likelihood statistical analysis. This method determines epigenetic
CC	pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,	CC	changes in a target nucleic acid molecule relative to reference nucleic
CC	Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium	CC	acid molecule and allows the sequencing of large biomolecules. The
XX	gordonae.	CC	invention also describes a method of producing a candidate sequence of a
XX		CC	biomolecule which involves receiving several sequencing graphs having
XX		CC	several vertices and edges, where each vertex represents a compomer of
XX		CC	the biomolecule and each edge represents a cut base of the sequencing
XX		CC	graph and generating the candidate sequence by traversing several
XX		CC	sequencing graphs. This second method further involves traversing several
XX		CC	sequencing graphs by tracing through each sequencing graph, starting at a
XX		CC	source vertex. The results of each method can be read by a program
XX		CC	product for use in a computer that executes program instructions recorded
XX		CC	in a computer-readable media to produce a candidate sequence of a
XX		CC	biomolecule or to obtain sequence information in a target biomolecule.
XX		CC	The target biomolecule contains a sequence variation, which is a mutation
XX		CC	or a polymorphism. The target is a target nucleic acid molecule from an
XX		CC	organism chosen from eukaryotes, prokaryotes and viruses, preferably a
XX		CC	bacterium. The specific cleavage reagent is an RNase chosen from RNase
XX		CC	T1, RNase U2, RNase PhnM, RNase A, chicken liver RNase (RNase CL3) and
XX		CC	cusavitin, or a glycosylase. The sequence variations in the target
XX		CC	biomolecule permit genotyping a subject, forensic analysis, disease

Query Match 79.2%; Score 19; DB 12; Length 50;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCC 19  
|||||  
Db 2 CAACTCGAACGGAAGGCC 20

RESULT 70  
ADU66542  
ID ADU66542 standard; DNA; 80 BP.  
XX  
AC ADU66542;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Cut base A amplicon fragment.

CC diagnosis or disease prognosis. The novel methods are useful for de novo  
 CC sequencing, to identify genetic disease or chromosome abnormality,  
 CC identifying a predisposition to a disease, or condition including  
 CC obesity, atherosclerosis, or cancer, to identify an infection by an  
 CC infectious agent, to identify a pathogen, determine haplotypes, analyze  
 CC microsatellite sequences, and short tandem repeat (STR) loci, determine  
 CC allelic variation and/or frequency, and analyze cellular methylation  
 CC patterns. This sequence represents an amplicon used to illustrate the  
 CC sequencing technique described in the invention.  
 XX

SQ Sequence 80 BP; 18 A; 20 C; 27 G; 15 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 31;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
 Db 51 CAAGTCGAACGGAAGGCC 69

RESULT 71

AE98763  
 ID AEB98763 standard; DNA; 209 BP.

XX

AC AEB98763;

DT 06-OCT-2005 (first entry)

DE Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.

XX microorganism detection; mycobacterium infection; antibacterial; ds.

KW Mycobacterium intracellulare.

OS JP2005204582-A.

PN 04-AUG-2005.

XX 23-JAN-2004; 2004JP-00015195.

PR 23-JAN-2004; 2004JP-00015195.

XX (ASAH ) ASAH KASEI KK.

PA Oda N;

PI WPI; 2005-526965/54.

DR New single-stranded oligonucleotide, useful for amplifying the nucleic

XX acid of Mycobacterium avium, Mycobacterium intracellulare, and

PT Mycobacterium kansasii.

PT Example 1; SEQ ID NO 5; 14pp; Japanese.

XX The invention relates to a novel single-stranded oligonucleotide used in

CC a detection method of an atypical mycobacteria group. The invention

CC further includes: amplifying the nucleic acid of Mycobacterium avium by a

CC loop-mediated isothermal amplification (LAMP) method; amplifying the

CC nucleic acid of M. intracellulare by a LAMP method; amplifying the

CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the

CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of

CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.

CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful

CC in medical applications. This polynucleotide represents a Mycobacterium

CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of

CC the invention.

XX

SQ Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 209;

Best Local Similarity 100.0%; Pred. No. 35;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
 Db 40 CAAGTCGAACGGAAGGCC 58

RESULT 72

ABT23572  
 ID ABT23572 standard; DNA; 560 BP.

XX

AC ABT23572;

XX 22-MAY-2003 (first entry)

DT Stabilising reagent method related oligo SEQ ID No 24.

DE Stabilising reagent method related oligo SEQ ID No 24.

XX Stabilising reagent; PCR; primer; RNaseH; long-term storage;

KW specific amplification; pathogenic microorganism; chimeric;

KW genetic engineering; clinical medicine; ss.

XX Mycobacterium avium.

OS WO2002101042-A1.

PN 19-DEC-2002.

XX 12-JUN-2002; 2002WO-JP005832.

XX 12-JUN-2001; 2001JP-00177737.

PR 20-AUG-2001; 2001JP-00249689.

XX (TAKI ) TAKARA BIO INC.

PA Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi B;

XX Enoki T, Asada K, Kato I;

PI WPI; 2003-148805/14.

DR Method for stabilizing and storing reaction reagents for specific

XX amplification and detection of nucleic acids particularly in e.g.

PT identifying pathogenic microorganisms or viruses in sample.

PT Example 15; Page 110; 177pp; Japanese.

XX The invention relates to a novel stabilising reaction reagent for use in

CC the amplification and/or detection of a target nucleic acid comprising:

CC preparing a reaction mixture with e.g. a nucleic acid as template, at

CC least 1 primer and RNaseH, and incubation of the reaction mixture for a

CC defined period of time to form a reaction product during the

CC amplification of such target nucleic acid. The method is useful for

CC stabilising and long-term storage of reaction reagents for highly

CC sensitive and specific amplification and detection of nucleic acids

CC particularly in identifying pathogenic microorganisms or viruses in a

CC sample using chimeric oligonucleotide primers, which is useful in genetic

CC engineering and clinical medicine. This polynucleotide sequence

CC represents an oligo relating to the novel stabilising reaction reagent

CC method of the invention

XX

SQ Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 10; Length 560;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19

Db 43 CAAGTCGAACGGAAGGCC 61

RESULT 73

AEA22410

ID AEA22410 standard; DNA; 1321 BP.

XX



DE Mycobacterium paraffinicum 16S rRNA sequence SEQ ID NO:14.  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium paraffinicum.  
 XX  
 XX US2005130168-A1.  
 XX 16-JUN-2005.  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 XX (HANX//) HAN X.  
 XX (PHAM//) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 XX  
 XX WPI; 2005-424597/43.  
 XX  
 XX Determining a bacterium species comprises providing oligonucleotide  
 XX primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.  
 XX  
 XX Disclosure; SEQ ID NO 14; 74pp; English.  
 XX  
 XX The invention relates to a method (M1) for determining a bacterium  
 XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 XX extracting a genomic nucleotide from the bacterium to provide a  
 XX nucleotide template; (c) annealing a region of a nucleotide template to a  
 XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 XX complementary fashion, the primer set designed to provide a product  
 XX having a predetermined size dictated by a complementary primer set; (d)  
 XX amplifying the region of the nucleotide template to produce the product;  
 XX and (e) determining a species of a bacterium in a nucleotide sequence of  
 XX the product. Also described is an alternative method (M2) for determining  
 XX a bacterium species comprising: (a) providing a specimen or a sample  
 XX having a template; (b) providing a pair of primers selected from: (i) a  
 XX first forward primer having consecutive bases of an AFB-f comprising any  
 XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 XX or variations; and a first reverse primer having consecutive bases of an  
 XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 XX or their fragments or variations; (ii) a second forward primer having  
 XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 XX bp (AEA22489-AEA22516) or their fragments or variations; and a second  
 XX reverse primer having consecutive bases of an UB-r comprising any of the  
 XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 XX variations; or (iii) a first forward primer having consecutive bases of  
 XX an AFB-f of AEA22417-AEA22452 or their fragments or variations; and a  
 XX second reverse primer having consecutive bases of an UB-r of AEA22517-  
 XX AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 XX comparing the product from the specimen with a nucleotide sequence from a  
 XX database to determine the bacterium species present in the specimen. The  
 XX methods are useful for determining a bacterium species. The present  
 XX sequence represents a Mycobacterium paraffinicum 16S rRNA nucleotide  
 XX sequence, which is used in the exemplification of the present invention.  
 XX  
 XX Sequence 1415 BP; 307 A; 343 C; 480 G; 285 T; 0 U; 0 Other;  
 XX  
 XX Query Match 79.2%; Score 19; DB 14; Length 1415;  
 XX Best Local Similarity 100.0%; Pred. No. 43;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 1 CAAGTCGAACGGAAGGCC 19  
 XX |||||  
 XX Db 16 CAAGTCGAACGGAAGGCC 34  
 XX  
 XX RESULT 76  
 XX AA222765  
 XX ID AA222765 standard; DNA; 1460 BP.  
 XX  
 XX AC AA222765;

XX 15-MAR-2000 (first entry)  
 XX Corynebacterium sp. NK-1 16S rRNA gene.  
 XX  
 XX Seasoning liquor; flavour; vegetable; pickling; salted rice bran paste;  
 XX microorganism; gamma-dodecalactone; gamma-dodecalactone; lactic acid;  
 XX propionic acid; 16S rRNA; pickle; ss.  
 XX  
 XX Corynebacterium sp.  
 XX  
 XX WO9962347-A1.  
 XX 09-DEC-1999.  
 XX 28-MAY-1999; 99WO-JP002854.  
 XX 29-MAY-1998; 98JP-00166226.  
 XX (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Saitoh C, Yashiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;  
 XX Ochiai K, Ando K, Katahira H;  
 XX WPI; 2000-062809/05.  
 XX  
 XX Production of seasoning liquors with the flavor of vegetables pickled in  
 XX salted rice bran.  
 XX  
 XX Disclosure; Page 41-43; 45pp; Japanese.  
 XX  
 XX The invention relates to a method of producing seasoning liquors with the  
 XX flavour of vegetables pickled in salted rice bran paste by culturing a  
 XX microorganism in a rice bran dispersion to produce gamma-dodecalactone  
 XX and/or gamma-dodecalactone. The microorganism produces lactic acid,  
 XX propionic acid, gamma-dodecalactone and/or gamma-dodecalactone. The  
 XX microorganism is especially a novel strain of Corynebacterium (strain NK-  
 XX 1, FERM BP-6329) with properties defined in the specification. This  
 XX sequence represents the 16S rRNA gene from the novel Corynebacterium  
 XX strain. The seasoning liquor is used for preparing a salted rice bran  
 XX pickle bed which provides pickles  
 XX  
 XX Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;  
 XX  
 XX Query Match 79.2%; Score 19; DB 3; Length 1460;  
 XX Best Local Similarity 100.0%; Pred. No. 43;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 1 CAAGTCGAACGGAAGGCC 19  
 XX |||||  
 XX Db 39 CAAGTCGAACGGAAGGCC 57  
 XX  
 XX RESULT 77  
 XX AEA22415  
 XX ID AEA22415 standard; DNA; 1462 BP.  
 XX  
 XX AC AEA22415;  
 XX  
 XX 25-AUG-2005 (first entry)  
 XX  
 XX Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 XX Mycobacterium szulgai.  
 XX  
 XX US2005130168-A1.  
 XX 16-JUN-2005.  
 XX 31-OCT-2003; 2003US-00697802.  
 XX

```

PR 31-OCT-2003; 2003US-00697802.
XX (HANK/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 16; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of 15-21 bp (AEA22517-AEA22544), or their fragments or
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium szulgai 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX Sequence 1462 BP; 314 A; 350 C; 507 G; 291 T; 0 U; 0 Other;
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1462;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAAGTCGACGGAAGGCC 19
XX |||||
XX Db 21 CAAGTCGACGGAAGGCC 39
XX
XX RESULT 78
XX ID AEA22414
XX AC AEA22414;
XX
XX DT 25-AUG-2005 (first entry)
XX
XX DE Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.
XX
XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX OS Mycobacterium simiae.
XX
XX XX US2005130168-A1.
XX
XX PD 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX (HANK/) HAN X.
XX (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 15; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations; (ii) a second forward primer having
XX consecutive bases of 15-21 bp (AEA22517-AEA22544), or their fragments or
XX variations; or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r comprising any of
XX the 28 sequences of 15-22 bp (AEA22489-AEA22516) or their fragments or
XX variations; (c) the specimen; and (d) comparing the product from the
XX specimen with a nucleotide sequence from a database to determine the
XX bacterium species present in the specimen. The present methods are useful
XX for determining a bacterium species. The present sequence represents a
XX Mycobacterium szulgai 16S rRNA nucleotide sequence, which is used in
XX the exemplification of the present invention.
XX
XX Sequence 1484 BP; 320 A; 362 C; 509 G; 293 T; 0 U; 0 Other;
XX
XX Query Match 79.2%; Score 19; DB 14; Length 1484;
XX Best Local Similarity 100.0%; Pred. No. 43;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CAAGTCGACGGAAGGCC 19
XX |||||
XX Db 21 CAAGTCGACGGAAGGCC 39
XX
XX RESULT 79
XX ID ADM92517
XX AC ADM92517 standard; DNA; 1517 BP.
XX
XX DT 03-JUN-2004 (first entry)
XX
XX DE Gordonia genus Actinomycetes DNA sequence SeqID1.
XX
XX KW Gordonia genus; Actinomycetes; ammonia; nitrous acid oxidation;
XX purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;
XX gold fish; ds.
XX

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OS Gordonia.  
 XX JP2004081109-A.  
 XX  
 XX 18-MAR-2004.  
 XX  
 XX 27-AUG-2002; 2002JP-00247166.  
 XX  
 XX 27-AUG-2002; 2002JP-00247166.  
 XX  
 XX (KANM-) KANMONKAI KK.  
 XX  
 XX WPI; 2004-233309/22.  
 XX  
 XX Gordonia genus Actinomyces for purifying fresh water and seawater useful  
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia  
 PT utilizing ability and nitrous acid oxidation ability.  
 XX  
 XX Disclosure; SEQ ID NO 1; 16pp; Japanese.  
 XX  
 XX This invention relates to a novel Gordonia genus Actinomyces which has  
 CC ammonia utilising ability and nitrous acid oxidation ability. The  
 CC invention may be useful for purifying fresh water and seawater, of  
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The  
 CC Gordonia genus actinomyces effectively suppresses concentration of  
 CC ammonia and nitrous acid in fresh water and seawater, and provides  
 CC purified water that is favourable for raising fishes.  
 XX  
 XX Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;  
 SQ  
 Query Match 79.2%; Score 19; DB 12; Length 1517;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCC 19  
 DB 54 CAAGTCGAACGGAAGGCC 72

RESULT 80  
 AD071823  
 ID AD071823 standard; DNA; 1517 BP.  
 XX  
 XX AD071823;  
 AC  
 XX  
 XX 15-JUL-2004 (first entry)  
 DT  
 XX  
 XX DNA of RNA isolated from Gordonia sp. Kanmonkai-1129 SeqID 1.  
 DE  
 XX  
 XX astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;  
 KW ds.  
 XX  
 XX Gordonia sp.  
 OS  
 XX  
 XX JP2004089015-A.  
 XX  
 XX 25-MAR-2004.  
 PD  
 XX  
 XX 29-AUG-2002; 2002JP-00251165.  
 XX  
 XX 29-AUG-2002; 2002JP-00251165.  
 XX  
 XX (KANM-) KANMONKAI KK.  
 PA  
 XX  
 XX WPI; 2004-253025/24.  
 DR  
 XX  
 XX Production of astaxanthin and canthaxanthine useful as fodder and feed  
 PT for livestock, domestic fowl and fish, involves cultivating Actinomyces  
 PT belonging to Gordonia genus.  
 XX  
 XX Disclosure; SEQ ID NO 1; 13pp; Japanese.  
 PS  
 XX  
 XX This invention relates to a novel method for producing astaxanthin and

CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces  
 CC microbial cells belonging to the Gordonia genus using a fresh water or  
 CC sea water mineral nutrition containing culture medium. The present  
 CC invention describes producing astaxanthin and canthaxanthine for use as a  
 CC fodder for livestock and domestic fowl, as well as a feed for fish  
 CC breeding. The production method uses natural products and is efficient at  
 CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated  
 CC from the Gordonia sp. Kanmonkai-1129 microorganism of the invention.  
 XX  
 XX Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;  
 SQ  
 Query Match 79.2%; Score 19; DB 12; Length 1517;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCC 19  
 DB 54 CAAGTCGAACGGAAGGCC 72

RESULT 81  
 AEA22407  
 ID AEA22407 standard; DNA; 1527 BP.  
 XX  
 XX AEA22407;  
 AC  
 XX  
 XX 25-AUG-2005 (first entry)  
 DT  
 XX  
 XX Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.  
 DE  
 XX  
 XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 KW  
 XX  
 XX Mycobacterium heckeshornense.  
 OS  
 XX  
 XX US2005130168-A1.  
 PN  
 XX  
 XX 16-JUN-2005.  
 PD  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 PR  
 XX  
 XX (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 PI  
 XX  
 XX WPI; 2005-424597/43.  
 DR  
 XX  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 8; 74pp; English.  
 PS  
 XX  
 XX The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an AFB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second

CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 14; Length 1527;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCC 19  
 Db 45 CAAGTCGAACGGAAGGCC 63

RESULT 82  
 AAD11264  
 ID AAD11264 standard; DNA; 32 BP.

AC AAD11264;

XX 24-SEP-2001 (first entry)

XX Mycobacterium 16S rRNA amplifying primer #8.

XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;

KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

XX Mycobacterium sp.

PN W0200144510-A2.

XX 21-JUN-2001.

XX 17-DEC-1999; 99WO-US030346.

XX 17-DEC-1999; 99WO-US030346.

XX (GENP-) GEN-PROBE INC.

XX (INMR ) BIOMERIEUX SA.

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

DR WPI; 2001-398170/42.

XX Detecting Mycobacterium species, involves in vitro amplification of 16S  
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
 PT specific primers, and detecting the amplified nucleic acid.

XX Claim 1; Page 35; 44pp; English.

XX The invention relates to a method of detecting Mycobacterium species,  
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
 CC comprising a polymerase, and at least two primers, and then detecting the  
 CC amplified nucleic acid. The method is relatively simple and useful for  
 CC detecting the presence of various Mycobacterium species in a biological  
 CC sample, and thus important for diagnosis of infections resulting from  
 CC them. The method is especially important for screening opportunistic  
 CC infections caused by M. tuberculosis or a Mycobacterium other than  
 CC tuberculosis (MOTT). The present sequence is a PCR primer used for  
 CC amplifying Mycobacterium 16S rRNA

XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 4; Length 32;  
 Best Local Similarity 90.9%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTT 22  
 Db 2 CAAGTCGAACGGAAGGCTCTCT 23

RESULT 83  
 ADG88345  
 ID ADG88345 standard; DNA; 32 BP.

XX AC ADG88345;

XX 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #14.

XX In vitro amplification; PCR; primer; ss.

XX Mycobacterium sp.

XX US2003165824-A1.

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.

XX (JUCK/) JUCKER M T.

XX (DELG/) DELGADO F D.

XX (CLEU/) CLEUZIAZ P.

XX (RODR/) RODRIGUE M.

PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

DR WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 PT in a biological sample comprises performing in vitro nucleic acid  
 PT amplification and detection of amplified products.

XX Claim 1; SEQ ID NO 14; 20pp; English.

XX The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample comprises performing an in vitro  
 CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
 CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
 CC is Mycobacterium amplifying PCR primer.

XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 10; Length 32;  
 Best Local Similarity 90.9%; Pred. No. 36;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTT 22  
 Db 2 CAAGTCGAACGGAAGGCTCTCT 23

RESULT 84  
 AEA08220  
 ID AEA08220 standard; DNA; 32 BP.

XX AC AEA08220;

XX 14-JUL-2005 (first entry)

XX Mycobacterium tuberculosis 16S rRNA amplifying PCR primer, SEQ ID NO: 14.

XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;  
KW PCR; primer; ss.  
XX OS  
XX Mycobacterium tuberculosis; ATCC 27294.  
XX PN  
XX US2005100915-A1.  
XX PD  
XX 12-MAY-2005.  
XX XX  
XX 18-SEP-2003; 2003US-00665708.  
XX PF  
XX 17-DEC-1999; 99US-0172190P.  
XX PR  
XX 15-DEC-2000; 2000US-00738274.  
XX XX  
XX (BREN//) BRENTANO S T.  
XX PA (JUCK//) JUCKER M T.  
XX PA (DELG//) DELGADO F D.  
XX PA (CLEU//) CLEUZAT P.  
XX PA (RODR//) RODRIGUE M.  
XX XX  
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
XX PI  
XX WPI; 2005-345392/35.  
XX DR  
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
XX PT in a biological sample, comprises using in vitro nucleic acid  
XX PT amplification and detection of amplified products.  
XX XX  
XX Example 1; SEQ ID NO 14; 21pp; English.  
XX PS  
XX The present invention relates to a method of detecting Mycobacterium  
XX CC species present in a biological sample. The method involves using in  
XX CC vitro nucleic acid amplification and detection of amplified products. The  
XX CC invention is useful for diagnostic detection of pathogenic bacteria such  
XX CC as Mycobacterium species. The present sequence is the Mycobacterium  
XX CC tuberculosis (ATCC 27294) 16S ribosomal RNA (16SrRNA) amplifying PCR  
XX CC primer.  
XX XX  
XX Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;  
SQ

Query Match 78.3%; Score 18.8; DB 14; Length 32;  
Best Local Similarity 90.9%; Pred. No. 36;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCTTT 22  
Db 2 CAAGTCGAACGGAAGGCTCT 23

RESULT 85  
AAX99199  
ID AAX99199 standard; DNA; 50 BP.  
XX AC AAX99199;  
XX XX  
XX 28-SEP-1999 (first entry)  
XX DE M. kansasii 16S rRNA gene fragment.  
XX XX  
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.  
XX OS  
XX Mycobacterium kansasii.  
XX PN  
XX WO9935284-A1.  
XX PD  
XX 15-JUL-1999.  
XX PF  
XX 30-DEC-1997; 97WO-BR000087.  
XX PR  
XX 30-DEC-1997; 97WO-BR000087.  
XX XX

PA (UYMI-) UNIV FEDERAL MINAS GERAIS.  
XX Peregrino Ferreira PC, Geessien Kroon E;  
PI Bernardes Margutti Pinto ME, Aleixo AW;  
XX WPI; 1999-444201/37.  
DR  
XX Detection of mycobacteria by shift mobility assay.  
XX PT  
XX Disclosure; Fig 7; 20pp; English.  
XX PS  
XX The invention describes a new method for diagnosis, identification and  
XX CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
XX CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
XX CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
XX CC DNA amplification and shift mobility assay. The method is based on  
XX CC divergence in sequences found in 16S rRNA to identify mycobacteria  
XX CC species, since a remarkable shift of heteroduplex bands are obtained  
XX CC between single stranded and homoduplex bands in UPAGE. The method is  
XX CC fast, simple and can produce information not easily obtained when  
XX CC compared with other detection methods. The sensitivity of other assays  
XX CC suffer due to the tendency of the denatured PCR product strands to  
XX CC reassociate and exclude oligonucleotide probes, and stearic interference  
XX CC between the bound oligonucleotides and the solid support which impede  
XX CC hybridization to nucleic acids in solution. Sequences AAX99193-237  
XX CC represent 16S rRNA gene regions of some mycobacterial species  
XX SQ  
XX Sequence 50 BP; 14 A; 12 C; 14 G; 10 T; 0 U; 0 Other;  
SQ

Query Match 78.3%; Score 18.8; DB 2; Length 50;  
Best Local Similarity 90.9%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCTTT 22  
Db 10 CAAGTCGAACGGAAGGCTCT 31

RESULT 86  
AAX99194  
ID AAX99194 standard; DNA; 50 BP.  
XX AC AAX99194;  
XX XX  
XX 28-SEP-1999 (first entry)  
XX DT M. bovis 16S rRNA gene fragment.  
XX DE  
XX Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.  
XX KW  
XX Mycobacterium bovis.  
XX OS  
XX WO9935284-A1.  
XX PN  
XX 15-JUL-1999.  
XX PD  
XX 30-DEC-1997; 97WO-BR000087.  
XX PF  
XX 30-DEC-1997; 97WO-BR000087.  
XX PR  
XX (UYMI-) UNIV FEDERAL MINAS GERAIS.  
XX PA  
XX Peregrino Ferreira PC, Geessien Kroon E;  
PI Bernardes Margutti Pinto ME, Aleixo AW;  
XX WPI; 1999-444201/37.  
DR  
XX Detection of mycobacteria by shift mobility assay.  
XX PT  
XX Disclosure; Fig 7; 20pp; English.  
XX PS  
XX The invention describes a new method for diagnosis, identification and

CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
CC DNA amplification and Shift mobility assay. The method is based on  
CC divergence in sequences found in 16S rRNA to identify mycobacteria  
CC species, since a remarkable shift of heteroduplex bands are obtained  
CC between single stranded and homoduplex bands in UPAGE. The method is  
CC fast, simple and can produce information not easily obtained when  
CC compared with other detection methods. The sensitivity of other assays  
CC suffer due to the tendency of the denatured PCR product strands to  
CC reassociate and exclude oligonucleotide probes, and stearic interference  
CC between the bound oligonucleotides and the solid support which impede  
CC hybridization to nucleic acids in solution. Sequences AAX99193-237  
CC represent 16S rRNA gene regions of some mycobacterial species  
XX  
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
  
Query Match 78.3%; Score 18.8; DB 2; Length 50;  
Best Local Similarity 90.9%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 CAAGTCGAACGGAAGGCTTT 22  
Db 10 CAAGTCGAACGGAAGGCTCT 31  
  
RESULT 87  
AAX99193  
ID AAX99193 standard; DNA; 50 BP.  
XX AC  
XX AAX99193;  
AC  
DT 28-SEP-1999 (first entry)  
XX  
DE M. tuberculosis 16S rRNA gene fragment.  
XX  
KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.  
XX  
OS Mycobacterium tuberculosis.  
XX  
PN WO9935284-A1.  
XX  
XX 15-JUL-1999.  
XX  
XX 30-DEC-1997; 97WO-BR000087.  
XX  
XX 30-DEC-1997; 97WO-BR000087.  
XX  
PA (UYMI-) UNIV FEDERAL MINAS GERAIS.  
XX  
PI Paregrino Ferreira PC, Geessien Kroon E;  
PI Bernardes Margutti Pinto ME, Aleixo AW;  
XX  
XX WPI; 1999-444201/37.  
XX  
PT Detection of mycobacteria by shift mobility assay.  
XX  
PS Disclosure; Fig 7; 20pp; English.  
XX  
CC The invention describes a new method for diagnosis, identification and  
CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
CC DNA amplification and Shift mobility assay. The method is based on  
CC divergence in sequences found in 16S rRNA to identify mycobacteria  
CC species, since a remarkable shift of heteroduplex bands are obtained  
CC between single stranded and homoduplex bands in UPAGE. The method is  
CC fast, simple and can produce information not easily obtained when  
CC compared with other detection methods. The sensitivity of other assays  
CC suffer due to the tendency of the denatured PCR product strands to  
CC reassociate and exclude oligonucleotide probes, and stearic interference  
CC between the bound oligonucleotides and the solid support which impede

CC hybridization to nucleic acids in solution. Sequences AAX99193-237  
CC represent 16S rRNA gene regions of some mycobacterial species  
XX  
SQ Sequence 50 BP; 15 A; 11 C; 14 G; 10 T; 0 U; 0 Other;  
  
Query Match 78.3%; Score 18.8; DB 2; Length 50;  
Best Local Similarity 90.9%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 CAAGTCGAACGGAAGGCTTT 22  
Db 10 CAAGTCGAACGGAAGGCTCT 31  
  
RESULT 88  
ADF94055  
ID ADF94055 standard; DNA; 50 BP.  
XX AC  
XX ADF94055;  
AC  
DT 11-MAR-2004 (first entry)  
XX  
DT Microorganism detection probe, SEQ ID 148.  
XX  
DE Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
KW  
XX Mycobacterium kansasii.  
OS  
PN WO2003106676-A1.  
XX  
XX 24-DEC-2003.  
PD  
XX 16-JUN-2003; 2003WO-JP007620.  
PF  
XX 14-JUN-2002; 2002JP-00174564.  
PR  
XX (HISF ) HITACHI SOFTWARE ENG CO LTD.  
PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
PA  
XX Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimadzu M, Kobayashi I, Ishiko H;  
PI WPI; 2004-071565/07.  
XX  
DR  
XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.  
XX  
XX Claim 2; SEQ ID NO 148; 150pp; Japanese.  
XX  
CC The present invention relates to probes (ADF93908-ADF94059) for the  
CC specific detection and identification of harmful microorganisms in  
CC samples of foods and drug compositions. The probe sequences are derived  
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
CC or its complementary sequence. Detection and identification of the  
CC microorganism is by amplification of the complete 16S rRNA gene using  
CC primers ADF94060 and ADF94061, labelling the amplification product (a  
CC fluorescence label is preferred), and hybridising to the probe or probes  
CC of the invention. The probes may be immobilised on a DNA chip. The  
CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
CC suaralii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria

CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.  
 XX  
 SQ Sequence 50 BP; 13 A; 11 C; 18 G; 8 T; 0 U; 0 Other;  
 Query Match 78.3%; Score 18.8; DB 12; Length 50;  
 Best Local Similarity 90.9%; Pred. No. 37;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 Db 2 CAAGTCGAACGGAAGGTCCT 23  
 RESULT 89  
 ADF94047  
 ID ADF94047 standard; DNA; 50 BP.  
 XX  
 AC ADF94047;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Microorganism detection probe, SEQ ID 140.  
 XX  
 KW Probe; detection; identification; microorganism; food; drug;  
 KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO2003106676-A1.  
 XX  
 PD 24-DEC-2003.  
 XX  
 PF 16-JUN-2003; 2003WO-JP007620.  
 XX  
 PR 14-JUN-2002; 2002JP-00174564.  
 XX  
 PA (HISF) HITACHI SOFTWARE ENG CO LTD.  
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
 XX  
 PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
 PI Shimadzu M, Kobayashi I, Ishiko H;  
 XX  
 DR WPI; 2004-071565/07.  
 XX  
 XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
 PT microorganism for specific detection and identification of the  
 PT microorganism in foods and drug compositions.  
 XX  
 PS Claim 2; SEQ ID NO 140; 150pp; Japanese.  
 XX  
 XX The present invention relates to probes (ADF93908-ADF94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADF94060 and ADF94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter

CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquarium, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Bikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.  
 XX  
 SQ Sequence 50 BP; 13 A; 10 C; 18 G; 9 T; 0 U; 0 Other;  
 Query Match 78.3%; Score 18.8; DB 12; Length 50;  
 Best Local Similarity 90.9%; Pred. No. 37;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CAAGTCGAACGGAAGGCCTTT 22  
 Db 2 CAAGTCGAACGGAAGGTCCT 23  
 RESULT 90  
 AAQ94742  
 ID AAQ94742 standard; DNA; 203 BP.  
 XX  
 AC AAQ94742;  
 XX  
 DT 26-FEB-1996 (first entry)  
 XX  
 DE DNA fragment of 16S rRNA gene of M. tuberculosis.  
 XX  
 KW hybridisation; Mycobacteria; acid-fast; 16S rRNA; ribosomal RNA; probe;  
 KW detection; identification; ss.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_binding complement(1..20)  
 FT /\*tag= a  
 FT /note= "probe binding (see AAQ94743)"  
 FT misc\_binding 41..60  
 FT /\*tag= b  
 FT /note= "probe binding (see AAQ94745)"  
 FT misc\_binding 92..113  
 FT /\*tag= c  
 FT /note= "probe binding (see AAQ94746)"  
 FT misc\_binding 183..203  
 FT /\*tag= d  
 FT /note= "probe binding (see AAQ94744)"  
 XX  
 PN JP07155200-A.  
 XX  
 XX 20-JUN-1995.  
 PD  
 XX 10-DEC-1993; 93JP-00310665.  
 XX  
 PR 10-DEC-1993; 93JP-00310665.  
 XX  
 PA (TOYM) TOYOCO KK.  
 XX  
 XX WPI; 1995-250746/33.  
 DR  
 XX Novel oligo-nucleotide(s) which hybridise with the 16S rRNA gene of  
 XX bacteria - used for detection and identification of acid-fast bacteria,  
 PT eg. Mycobacterium.  
 XX  
 PS Claim 1; Page 10; 13pp; Japanese.  
 XX

CC AQ094743-46 are oligonucleotides used for the detection and  
 CC identification of acid-fast bacteria (pref. Mycobacterium) by hybridising  
 CC with the base sequence of the 16S rRNA gene of the bacteria. The  
 CC oligonucleotides can be represented by all or a part of the 203 base  
 CC sequence shown here. Mycobacteria are gram-positive bacteria which grow  
 CC very slowly and require a lot of time for culture for detection (longer  
 CC than one month). The probes provide a simple, rapid and exact method for  
 CC detection and identification of the bacteria. The method can be applied  
 CC directly to sputum or blood samples and the result obtd. within one day.  
 CC AQ094747-60 are specific probes for different Mycobacteria species  
 XX  
 SQ Sequence 203 BP; 44 A; 42 C; 72 G; 45 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 2; Length 203;  
 Best Local Similarity 90.9%; Pred. No. 43;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22  
 |||||  
 Db 6 CAAGTCGAACGGAAGGCTCT 27

RESULT 91  
 AEB98764  
 ID AEB98764 standard; DNA; 209 BP.  
 XX  
 AC AEB98764;  
 XX  
 DT 06-OCT-2005 (first entry)  
 XX  
 DE Mycobacterium kansasii partial 16S rDNA sequence, SEQ ID 6.  
 XX  
 KW microorganism detection; mycobacterium infection; antibacterial; ds.  
 XX  
 OS Mycobacterium kansasii.  
 XX  
 PN JP2005204582-A.  
 XX  
 PD 04-AUG-2005.  
 XX  
 PF 23-JAN-2004; 2004JP-00015195.  
 XX  
 PR 23-JAN-2004; 2004JP-00015195.  
 XX  
 PA (ASAH ) ASAH KASEI KK.  
 XX  
 PI Oda N;  
 XX  
 DR WPI; 2005-526965/54.  
 XX  
 PT New single-stranded oligonucleotide, useful for amplifying the nucleic  
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and  
 PT Mycobacterium kansasii.  
 XX  
 PS Example 1; SEQ ID NO 6; 14pp; Japanese.

CC The invention relates to a novel single-stranded oligonucleotide used in  
 CC a detection method of an atypical mycobacteria group. The invention  
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a  
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the  
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the  
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the  
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of  
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.  
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful  
 CC in medical applications. This polynucleotide represents a Mycobacterium  
 CC kansasii partial 16S rDNA sequence amplified by the LAMP method of the  
 CC invention.  
 XX  
 SQ Sequence 209 BP; 47 A; 49 C; 72 G; 41 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 209;  
 Best Local Similarity 90.9%; Pred. No. 44;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CAAGTCGAACGGAAGGCTTT 22  
 |||||  
 Db 40 CAAGTCGAACGGAAGGCTCT 61

RESULT 92  
 AEB98761  
 ID AEB98761 standard; DNA; 211 BP.

XX  
 AC AEB98761;  
 XX  
 DT 06-OCT-2005 (first entry)  
 XX  
 DE Mycobacterium tuberculosis partial 16S rDNA sequence, SEQ ID 3.  
 XX  
 KW microorganism detection; mycobacterium infection; antibacterial; ds.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN JP2005204582-A.  
 XX  
 PD 04-AUG-2005.  
 XX  
 PF 23-JAN-2004; 2004JP-00015195.  
 XX  
 PR 23-JAN-2004; 2004JP-00015195.  
 XX  
 PA (ASAH ) ASAH KASEI KK.  
 XX  
 PI Oda N;  
 XX  
 DR WPI; 2005-526965/54.  
 XX  
 PT New single-stranded oligonucleotide, useful for amplifying the nucleic  
 PT acid of Mycobacterium avium, Mycobacterium intracellulare, and  
 PT Mycobacterium kansasii.

XX Example 1; SEQ ID NO 3; 14pp; Japanese.

CC The invention relates to a novel single-stranded oligonucleotide used in  
 CC a detection method of an atypical mycobacteria group. The invention  
 CC further includes: amplifying the nucleic acid of Mycobacterium avium by a  
 CC loop-mediated isothermal amplification (LAMP) method; amplifying the  
 CC nucleic acid of M. intracellulare by a LAMP method; amplifying the  
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the  
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of  
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.  
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful  
 CC in medical applications. This polynucleotide represents a Mycobacterium  
 CC tuberculosis partial 16S rDNA sequence amplified by the LAMP method of  
 CC the invention.

XX Sequence 211 BP; 48 A; 45 C; 74 G; 44 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 211;  
 Best Local Similarity 90.9%; Pred. No. 44;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22  
 |||||  
 Db 40 CAAGTCGAACGGAAGGCTCT 61

RESULT 93  
 ADV99481  
 ID ADV99481 standard; DNA; 349 BP.

XX  
 AC ADV99481;  
 XX  
 DT 24-FEB-2005 (first entry)  
 XX

DE Meningitis causing bacteria DNA fragment #9.  
 KW ds; antibacterial; antiinflammatory; inflammation; neurological disease;  
 KW diagnosis; meningitis; biochip.  
 XX  
 OS Mycobacterium tuberculosis.  
 PN CN1420123-A.  
 XX  
 PD 28-MAY-2003.  
 XX  
 XX 16-NOV-2001; 2001CN-00137478.  
 XX  
 PR 16-NOV-2001; 2001CN-00137478.  
 XX  
 PA (JING-) JINGQI BIO CHEM SCI & TECH CO LTD.  
 XX  
 PI Xu B, Jiang Y, Huang X;  
 XX WPI; 2004-044307/05.  
 XX  
 DR A nucleic acid sequence useful for diagnosing pathogenic bacteria for  
 PT meningitides.  
 PT  
 XX Disclosure; Page 18; 24pp; Chinese.  
 PS  
 XX The invention relates to a nucleic acid sequence group for quickly  
 CC diagnosing 20 kinds of pathogenic bacteria for meningitis. Its method  
 CC includes comparing the DNA sequences of different pathogenic bacteria,  
 CC choosing special fragments, finding out common primer, designing 3  
 CC specific probe fragments for each pathogenic bacterium, dotting them on  
 CC high-molecular polymer to obtain chip, sampling the DNA of pathogenic  
 CC bacterium of patient, labeling, amplification, and reacting with said  
 CC chip for visually recognizing the pathogenic bacterium. Its advantages are  
 CC high speed and low cost. The present sequence represents a meningitis  
 CC causing bacteria DNA fragment.  
 XX  
 SQ Sequence 349 BP; 75 A; 82 C; 125 G; 67 T; 0 U; 0 Other;  
 Query Match 78.3%; Score 18.8; DB 13; Length 349;  
 Best Local Similarity 90.9%; Pred. No. 46;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CAAGTCGAACGGAAGGCTTT 22  
 DB 53 CAAGTCGAACGGAAGGCTCT 74  
 RESULT 94  
 AAV24293  
 ID AAV24293 standard; DNA; 1271 BP.  
 XX  
 AC AAV24293;  
 XX  
 DT 14-SEP-1998 (first entry)  
 XX  
 DE Mycobacterium tuberculosis 16S ribosomal RNA gene.  
 KW Antibacterial; antimycobacterial; oligonucleotide; infection; therapy;  
 KW ribosome binding site; Shine-Dalgarno; ribosomal RNA; cystic fibrosis;  
 KW tuberculosis; ss.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN WO9814567-A2.  
 XX  
 XX 09-APR-1998.  
 PD  
 XX 30-SEP-1997; 97WO-US018094.  
 PF  
 XX 01-OCT-1996; 96US-0027729P.  
 PR  
 XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.  
 PA

Martin WJ, Wisniewski P;  
 WPI; 1998-240079/21.  
 Use of oligonucleotide(s) corresponding to bacterial 16S rRNA - for  
 inhibiting bacterial protein expression and treating bacterial infection.  
 Claim 26; Page 60-61; 73pp; English.  
 This polynucleotide comprises the 16S ribosomal RNA (rRNA) gene of  
 Mycobacterium tuberculosis. The invention relates to methods and  
 compositions for the treatment of Gram-negative bacterial infections  
 employing novel oligonucleotides as antimicrobial agents. The  
 oligonucleotides are targeted to the Shine-Dalgarno (SD) region of  
 prokaryotes to inhibit bacterial expression and hence inhibit bacterial  
 infection. They preferably comprise 10-35 consecutive bases of the 3' end  
 of a bacterial 16S rRNA (see also AAV24291-95). An oligonucleotide may  
 also include a transport moiety and may have DNA phosphate modifications  
 to increase nuclease resistance, or may be formulated in a liposome. A  
 claimed method for treating a bacterial infection of a patient comprises  
 administering a liposomal formulation of such an oligonucleotide. The  
 oligonucleotides can be used particularly for treating bacterial  
 infections in pulmonary diseases such as cystic fibrosis or tuberculosis.  
 Since the SD sequence is not present in eukaryotic cells, the  
 oligonucleotides provide a pathogen-specific therapeutic method  
 Sequence 1271 BP; 260 A; 281 C; 430 G; 300 T; 0 U; 0 Other;  
 Query Match 78.3%; Score 18.8; DB 2; Length 1271;  
 Best Local Similarity 90.9%; Pred. No. 53;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 CAAGTCGAACGGAAGGCTTT 22  
 DB 443 CAAGTCGAACGGAAGGCTCT 464  
 RESULT 95  
 AEA22416  
 ID AEA22416 standard; DNA; 1416 BP.  
 XX  
 AC AEA22416;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Mycobacterium tuberculosis 16S rRNA sequence SEQ ID NO:17.  
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN US2005130168-A1.  
 XX  
 PD 16-JUN-2005.  
 XX  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX 31-OCT-2003; 2003US-00697802.  
 PR  
 XX (HANY/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 PI Han X, Pham AS;  
 XX  
 XX WPI; 2005-424597/43.  
 DR  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 XX Disclosure; SEQ ID NO 17; 74pp; English.  
 PS  
 XX The invention relates to a method (M1) for determining a bacterium  
 CC

species. (M1) comprises: (a) culturing a bacterium from a specimen; (b) extracting a genomic nucleotide from the bacterium to provide a nucleotide template; (c) annealing a region of a nucleotide template to a specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion, the primer set designed to provide a product having a predetermined size dictated by a complementary primer set; (d) amplifying the region of the nucleotide template to produce the product; and (e) determining a species of a bacterium in a nucleotide sequence of the product. Also described is an alternative method (M2) for determining a bacterium species comprising: (a) providing a specimen or a sample having a template; (b) providing a pair of primers selected from: (i) a first forward primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments or variations and a first reverse primer having consecutive bases of an AFB-f comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488) or their fragments or variations, (ii) a second forward primer having consecutive bases of an UB-f comprising any of the 28 sequences of 15-21 bp (AEA22489-AEA22516) or their fragments or variations and a second reverse primer having consecutive bases of an UB-f comprising any of the 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or variations, or (iii) a first forward primer having consecutive bases of an AFB-f of AEA22417-AEA22452 or their fragments or variations and a second reverse primer having consecutive bases of an UB-f of AEA22517-AEA22544 or their fragments or variations; (c) the specimen; and (d) comparing the product from the specimen with a nucleotide sequence from a database to determine the bacterium species present in the specimen. The methods are useful for determining a bacterium species. The present sequence represents a *Mycobacterium tuberculosis* 16S rRNA nucleotide sequence, which is used in the exemplification of the present invention.

Query Match	78.3%	Score 18.8;	DB 14;	Length 1416;
Best Local Similarity	90.9%;	Pred.No.53;		
Matches 20;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	CAAGTCGAACGGAAGGCCCTTT	22	
Db	21	CAAGTCGAACGGAAGGTCCT	42	

RESULT 96  
AEA22402  
ID AEA22402 standard; DNA; 1421 BP.  
XX  
XX  
AC AEA22402;  
XX  
XX  
DT 25-AUG-2005 (first entry)  
XX  
XX  
DE Mycobacterium bovis 16S rRNA sequence SEQ ID NO:3.  
XX  
XX  
KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.

XX	Mycobacterium bovis.	
OS		
XX		
XX	US2005130168-A1.	
PN		
XX		
XX	16-JUN-2005.	
PD		
XX		
XX	31-OCT-2003; 2003US-00697802.	
PF		
XX		
XX	31-OCT-2003; 2003US-00697802.	
PR		
XX	(HANKX/) HAN X.	
PA	(PHAM/) PHAM A S.	
XX		
XX	Han X, Pham AS;	
PI		
XX	WPI; 2005-424597/43.	
XX		
DR		
XX	Determining a bacterium species comprises providing oligonucleotide	
PT	primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.	
XX		
XX		

PS Disclosure; SEQ ID NO 3; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium

CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)

CC extracting a genomic nucleotide from the bacterium to provide a

CC nucleotide template; (c) annealing a region of a nucleotide template to a

CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a

CC complementary fashion, the primer set designed to provide a product

CC having a predetermined size dictated by a complementary primer set; (d)

CC amplifying the region of the nucleotide template to produce the product;

CC and (e) determining a species of a bacterium in a nucleotide sequence of

CC the product. Also described is an alternative method (M2) for determining

CC a bacterium species comprising: (a) providing a specimen or a sample

CC having a template; (b) providing a pair of primers selected from: (i) a

CC first forward primer having consecutive bases of an AFB-f comprising any

CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments

CC or variations and a first reverse primer having consecutive bases of an

CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)

CC or their fragments or variations, (ii) a second forward primer having

CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21

CC bp (AEA22489-AEA22516) or their fragments or variations and a second

CC reverse primer having consecutive bases of an UB-r comprising any of the

CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or

CC variations, or (iii) a first forward primer having consecutive bases of

CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a

CC second reverse primer having consecutive bases of an UB-r of AEA22517-

CC AEA22544 or their fragments or variations; (c) the specimen; and (d)

CC comparing the product from the specimen with a nucleotide sequence from a

CC database to determine the bacterium species present in the specimen. The

CC methods are useful for determining a bacterium species. The present

CC sequence represents a *Mycobacterium bovis* 16S rRNA nucleotide sequence,

CC which is used in the exemplification of the present invention.

XX Sequence 1421 BP: 310 A; 341 C; 484 G; 286 T; 0 U; 0 Other;

Query Match	78.3%	Score 18.8;	DB 14;	Length 1421;
Best Local Similarity	90.9%;	Pred. No. 53;		
Matches 20;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy 1	CAAGTCGAACGGAAGGCCCTTT	22		
Db 21	CAAGTCGAACGGAAGGCTCTCT	42		

RESULT 97	
AEA22409	
ID	AEA22409 standard; DNA; 1463 BP.
XX	
XX	
AC	AEA22409;
XX	
XX	25-AUG-2005 (first entry)
DT	
XX	
DE	Mycobacterium kansasii 16S rRNA sequence SEQ ID NO:10.
XX	
KW	microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX	
OS	Mycobacterium kansasii.
XX	
XX	US2005130168-A1.
PN	
XX	
XX	16-JUN-2005.
PD	
XX	
PF	31-OCT-2003; 2003US-00697802.
XX	
XX	
PR	31-OCT-2003; 2003US-00697802.
XX	
XX	(HANY/) HAN X.
PA	
PA	(PHAM/) PHAM A S.
XX	
XX	Han X, Pham AS;
PI	
XX	
XX	WPI; 2005-424597/43.
XX	
XX	



PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.  
 XX Disclosure; SEQ ID NO 10; 74pp; English.

XX The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations; (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations; or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium kansasii 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.

XX  
 SQ Sequence 1463 BP; 318 A; 354 C; 500 G; 291 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 14; Length 1463;  
 Best Local Similarity 90.9%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 Db 20 CAAGTCGAACGGAAGGCTCT 41  
 |||||

RESULT 98  
 AA235571  
 ID AA235571 standard; DNA; 1464 BP.  
 XX  
 AC AA235571;  
 XX  
 DT 28-JAN-2000 (first entry)  
 XX  
 DE Mycobacterium tuberculosis 16S rRNA gene.  
 XX  
 KW 16S rRNA gene; oligonucleotide primer; amplify; genus specific;  
 KW diagnosis; Mycobacterium; ss.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 PN US5985569-A.  
 XX  
 PD 16-NOV-1999.  
 XX  
 PF 26-SEP-1997; 97US-00938858.  
 XX  
 PR 26-SEP-1997; 97US-00938858.  
 XX  
 PA (BECT ) BECTON DICKINSON & CO.  
 XX  
 PI Foxall PA, Kumar H;

XX WPI; 2000-012779/01.  
 DR  
 XX Oligonucleotide primers useful for detecting microorganisms of the genus  
 PT Mycobacterium.  
 XX  
 XX Example; Fig 3; 2lpp; English.

XX This sequence is the Mycobacterium tuberculosis 16S rRNA gene. This  
 CC sequence is used in an example of a method using oligonucleotide primers  
 CC for amplification of a genus specific sequence of the 16S rRNA gene. The  
 CC method of the invention consists of using primers AA235572-235586 to  
 CC amplify M. tuberculosis DNA and then detecting the amplified nucleic  
 CC acids. The oligonucleotides are useful for the detection of species of  
 CC medical interest of the genus Mycobacterium. In particular the detection  
 CC can be used for human and veterinary diagnosis from samples of biological  
 CC fluids or tissue e.g. sputum, bronchial washings, gastric washings,  
 CC blood, milk, lymph, skin and soft tissues. Identifying the mycobacterium  
 CC using the nucleic acid based diagnostic assay reduces the time required  
 CC for an accurate diagnosis as cultivation of the organisms is not required

XX  
 SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 3; Length 1464;  
 Best Local Similarity 90.9%; Pred. No. 54;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22  
 |||||  
 Db 21 CAAGTCGAACGGAAGGCTCT 42  
 |||||

RESULT 99  
 AAS11027  
 ID AAS11027 standard; DNA; 1464 BP.  
 XX  
 AC AAS11027;  
 XX  
 DT 24-OCT-2001 (first entry)  
 XX  
 DE Mycobacterium tuberculosis 16S ribosomal RNA gene.  
 XX  
 KW Antisense; bacterial 16S ribosomal RNA; rRNA; bacterial infection; human;  
 KW food grain supplement; livestock; poultry; therapeutic; ds.  
 XX  
 OS Mycobacterium tuberculosis.  
 XX  
 FN WO200142457-A2.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 29-NOV-2000; 2000WO-US042391.  
 XX  
 PR 29-NOV-1999; 99US-0168150P.  
 XX  
 PA (AVIB-) AVI BIOPHARMA INC.  
 XX  
 PI Iversen PL;  
 XX  
 DR WPI; 2001-457295/49.  
 XX  
 XX Antibacterial compound, useful for treating bacterial infections and as  
 PT livestock and poultry food supplement, comprises antisense  
 PT oligonucleotides complementary to bacterial 16S and 23S rRNA.  
 XX  
 PS Disclosure; Page: 62pp; English.  
 XX  
 CC AAS11021-AAS11034 represent the coding sequences of bacterial 16S  
 CC ribosomal RNA (rRNA) genes. The sequences were used to design anti-  
 CC bacterial compounds comprising substantially uncharged antisense  
 CC oligomers containing 8-40 nucleotide subunits, including a targeting  
 CC nucleic acid sequence at least 10 nucleotides in length which is  
 CC complementary to a bacterial 16S or 23S rRNA nucleic acid sequence. The

CC antisense oligomers are used for treating a bacterial infection in a  
CC human or a mammalian animal produced by Escherichia coli, Salmonella  
CC typhimurium Pseudomonas aeruginosa, Vibrio cholerae, Neisseria  
CC gonorrhoea, Helicobacter pylori, Bartonella henselae, Haemophilus  
CC influenza, Shigella dysenteriae, Staphylococcus aureus, Mycobacterium  
CC tuberculosis, Streptococcus pneumoniae, Treponema pallidum and Chlamydia  
CC trachomatis. The antibacterial compound may be used as a food grain  
CC supplement in livestock and poultry food composition. Note: The present  
CC sequence is not shown in the specification but has been accessed from  
CC GenBank using the appropriate accession number given in the specification  
XX  
SQ Sequence 1464 BP; 321 A; 349 C; 502 G; 292 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 5; Length 1464;  
Best Local Similarity 90.9%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTCT 22  
|||||  
Db 21 CAAGTCGAACGGAAGGCTTCT 42  
|||||

RESULT 100  
ADR90574  
ID ADR90574 standard; DNA; 1469 BP.  
XX AC ADR90574;  
XX DT 02-DEC-2004 (first entry)  
XX DE M kansasii 16S rRNA gene sequence SeqID3.  
XX KW acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;  
XX KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.  
XX OS Mycobacterium kansasii.  
XX PN JP2004254591-A.  
XX PD 16-SEP-2004.  
XX PF 26-FEB-2003; 2003JP-00048654.  
XX PR 26-FEB-2003; 2003JP-00048654.  
XX PA (MTP ) MITSUBISHI YUKA BCL KK.  
XX DR WPI; 2004-664464/65.  
XX PT Differentiating acid-fast bacterium e.g., Mycobacterium avium complex.  
XX PT useful for detecting mutant of M.avium complex, and for grouping strains  
XX PT of M.kansasii, involves detecting mutation in 16S rRNA gene of acid-fast  
XX PT bacterium.  
XX PS Claim 3; SEQ ID NO 3; 23pp; Japanese.  
XX CC This invention relates to a novel method of differentiating acid-fast  
XX CC bacterium, which involves detecting a mutation in the 16S rRNA gene of  
XX CC the acid-fast bacterium. The method is useful for differentiating acid-  
XX CC fast bacterium such as M avium complex (MAC) or M kansasii, in particular  
XX CC for detecting mutants of MAC, and for grouping strains of M kansasii. The  
XX CC method is also useful for carrying out taxonomic-tree analysis of  
XX CC atypical-mycobacteria and enables detection of MAC accurately and  
XX CC reliably. The present sequence is that of a Mycobacterium 16S rRNA gene  
XX CC which may be used in the method of the invention.  
SQ Sequence 1469 BP; 321 A; 355 C; 502 G; 291 T; 0 U; 0 Other;

Query Match 78.3%; Score 18.8; DB 13; Length 1469;  
Best Local Similarity 90.9%; Pred. No. 54;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTCT 22

Db 31 CAAGTCGAACGGAAGGCTTCT 52  
|||||

Search completed: May 19, 2006, 04:19:09  
Job time : 284.94 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1605.11 Seconds  
(without alignments)  
836.120 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24

Sequence: 1 caagtcgaacggaagcccttccg 24

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_hcc:\*

7: gb\_est2:\*

8: gb\_est7:\*

9: gb\_est8:\*

10: gb\_est9:\*

11: gb\_gss1:\*

12: gb\_gss2:\*

13: gb\_gss3:\*

14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	20.8	86.7	657	8	CN208729 Tor9226 G	
C	2	19.8	82.5	312	7	BB241896 BB241896
C	3	19.8	82.5	356	4	CD122074 ME1-0071G
	4	19.2	80.0	683	14	DU818647 OG_ABA009
	5	19	79.2	650	8	CN204419 Tor4810 G
	6	19	79.2	874	8	C0365133 RTKL_23 G
	7	19	79.2	885	8	CN201712 Tor1780 G
C	8	18.8	78.3	903	12	CC453191 ZMMBBC034
	9	18.8	78.3	910	9	DN561788 92178421
	10	18.4	76.7	735	5	CF882404 trico86xm
	11	18.4	76.7	788	4	CB908942 trico86xm
	12	18.2	75.8	327	10	DY091901 010128BEM
	13	18.2	75.8	421	4	BY457153 BY457153
	14	18.2	75.8	452	11	AQ627316 CITBI-E1-
	15	18.2	75.8	475	9	DN526979 1271790 M
	16	18.2	75.8	540	11	AQ549361 RPCI-11-3
	17	18.2	75.8	630	4	CB378019 rpo6all.Y
	18	18.2	75.8	719	5	CK950118 4075090 B
	19	18.2	75.8	835	9	DN283722 1183944 M

93	17.8	74.2	912	10	DR815819	DR815819 ZM BPB004	C 166	17.6	73.3	452	8	CR470938	CR470938
94	17.8	74.2	918	2	BG247267	BG247267 602360162	C 167	17.6	73.3	462	4	BY599571	BY599571
95	17.8	74.2	945	10	DV062398	DV062398 NEONATAL	C 168	17.6	73.3	465	1	AI235898	AI235898
96	17.8	74.2	995	12	CL029182	CL029182 CH216-28U	C 169	17.6	73.3	466	7	BB833557	BB833557
97	17.8	74.2	1199	9	DR045951	DR045951 FP-11 G06	C 170	17.6	73.3	468	1	AI372548	AI372548
98	17.6	73.3	193	1	AA204210	AA204210 mu60h11.r	C 171	17.6	73.3	473	7	BB283360	BB283360
99	17.6	73.3	233	3	BQ322138	BQ322138 PM3-CT081	C 172	17.6	73.3	478	10	W54232	W54232
100	17.6	73.3	239	1	AV366949	AV366949 AV266949	C 173	17.6	73.3	485	1	AA832954	AA832954
101	17.6	73.3	242	3	EUB99169	EUB99169 mai46911.	C 174	17.6	73.3	490	4	CB434145	CB434145
102	17.6	73.3	247	1	AV314699	AV314699 AV314699	C 175	17.6	73.3	490	4	CB437180	CB437180
103	17.6	73.3	247	7	BB015618	BB015618 BB015618	C 176	17.6	73.3	490	4	CB438188	CB438188
104	17.6	73.3	256	1	AV264774	AV264774 AV264774	C 177	17.6	73.3	496	3	BU579473	BU579473
105	17.6	73.3	257	1	AV140604	AV140604 AV140604	C 178	17.6	73.3	496	3	BU548707	BU548707
106	17.6	73.3	266	1	AV268640	AV268640 AV268640	C 179	17.6	73.3	499	2	BM121724	BM121724
107	17.6	73.3	270	1	AV074580	AV074580 AV074580	C 180	17.6	73.3	502	9	CX598149	CX598149
108	17.6	73.3	277	1	AV015856	AV015856 AV015856	C 181	17.6	73.3	504	7	AW361919	AW361919
109	17.6	73.3	279	1	AV078336	AV078336 AV078336	C 182	17.6	73.3	504	9	DN363141	DN363141
110	17.6	73.3	282	1	AV351905	AV351905 AV351905	C 183	17.6	73.3	504	9	BM232039	BM232039
111	17.6	73.3	290	3	BQ840493	BQ840493 mah68h07.	C 184	17.6	73.3	509	1	AA000190	AA000190
112	17.6	73.3	291	1	AV066368	AV066368 AV066368	C 185	17.6	73.3	509	5	DR790755	DR790755
113	17.6	73.3	293	1	AV144872	AV144872 AV144872	C 186	17.6	73.3	513	4	CA282280	CA282280
114	17.6	73.3	293	7	BB516293	BB516293 BB516293	C 187	17.6	73.3	517	4	BM283328	BM283328
115	17.6	73.3	295	7	BB028015	BB028015 BB028015	C 188	17.6	73.3	517	4	BM283328	BM283328
116	17.6	73.3	295	7	BB511052	BB511052 BB511052	C 189	17.6	73.3	517	5	CK840680	CK840680
117	17.6	73.3	297	7	BB031763	BB031763 BB031763	C 190	17.6	73.3	524	7	AW435159	AW435159
118	17.6	73.3	300	1	AV147017	AV147017 AV147017	C 191	17.6	73.3	526	2	BM131991	BM131991
119	17.6	73.3	305	1	AV088825	AV088825 AV088825	C 192	17.6	73.3	529	1	AI838320	AI838320
120	17.6	73.3	305	1	AV258314	AV258314 AV258314	C 193	17.6	73.3	532	2	BG012793	BG012793
121	17.6	73.3	305	4	BY432536	BY432536 BY432536	C 194	17.6	73.3	532	7	BF017987	BF017987
122	17.6	73.3	305	8	CK213854	CK213854 MNS20950	C 195	17.6	73.3	539	1	BE989007	BE989007
123	17.6	73.3	311	1	AV310522	AV310522 AV310522	C 196	17.6	73.3	539	7	AA542056	AA542056
124	17.6	73.3	312	7	BB361078	BB361078 BB361078	C 197	17.6	73.3	569	5	CK902574	CK902574
125	17.6	73.3	319	1	AA374314	AA374314 EST86475	C 198	17.6	73.3	574	2	BM383870	BM383870
126	17.6	73.3	324	1	AV216218	AV216218 AV216218	C 199	17.6	73.3	580	5	CF968672	CF968672
127	17.6	73.3	334	8	CO939094	CO939094 UMC-pd20f	C 200	17.6	73.3	600	2	BG806032	BG806032
128	17.6	73.3	336	7	AW014662	AW014662 UI-H-B10P	C 201	17.6	73.3	601	3	BM735102	BM735102
129	17.6	73.3	336	7	AW524972	AW524972 UI-R-B10P	C 202	17.6	73.3	620	4	CB337903	CB337903
130	17.6	73.3	353	4	CB779991	CB779991 AMGNNUC:S	C 203	17.6	73.3	660	11	BH794488	BH794488
131	17.6	73.3	353	10	DR409871	DR409871 EST00056	C 204	17.6	73.3	674	9	DN120598	DN120598
132	17.6	73.3	359	4	BY445959	BY445959 BY445959	C 205	17.6	73.3	674	9	DN120950	DN120950
133	17.6	73.3	361	7	BE991892	BE991892 UI-M-B21-	C 206	17.6	73.3	675	5	CJ746041	CJ746041
134	17.6	73.3	362	4	BY426276	BY426276 BY426276	C 207	17.6	73.3	676	4	BY755829	BY755829
135	17.6	73.3	369	4	BY663759	BY663759 BY663759	C 208	17.6	73.3	680	9	DN116917	DN116917
136	17.6	73.3	371	1	AA967999	AA967999 V931C07.r	C 209	17.6	73.3	681	7	AW967239	AW967239
137	17.6	73.3	377	7	BB791326	BB791326 BB791326	C 210	17.6	73.3	684	2	BI184236	BI184236
138	17.6	73.3	380	2	BB803041	BB803041 BB803041	C 211	17.6	73.3	697	2	BG477861	BG477861
139	17.6	73.3	392	4	BY625882	BY625882 mad91b09.	C 212	17.6	73.3	713	2	BG478164	BG478164
140	17.6	73.3	392	4	BY625882	BY625882 mad91b09.	C 213	17.6	73.3	721	7	BE384503	BE384503
141	17.6	73.3	394	4	CA976745	CA976745 AGENCOURT	C 214	17.6	73.3	725	14	CR921765	CR921765
142	17.6	73.3	395	4	BY626963	BY626963 BY626963	C 215	17.6	73.3	744	9	CX605206	CX605206
143	17.6	73.3	398	4	BY434099	BY434099 BY434099	C 216	17.6	73.3	755	4	EX667075	EX667075
144	17.6	73.3	399	3	EQ104075	EQ104075 g91205.e	C 217	17.6	73.3	755	2	BG764347	BG764347
145	17.6	73.3	400	4	BY420961	BY420961 BY420961	C 218	17.6	73.3	772	3	BQ716203	BQ716203
146	17.6	73.3	401	1	AI372546	AI372546 EST175437	C 219	17.6	73.3	788	5	CJ457834	CJ457834
147	17.6	73.3	401	1	BY625353	BY625353 BY625353	C 220	17.6	73.3	790	2	BG767613	BG767613
148	17.6	73.3	405	8	CO059683	CO059683 est_k_bre	C 221	17.6	73.3	792	8	CX242558	CX242558
149	17.6	73.3	409	5	CJ199163	CJ199163 CJ199163	C 222	17.6	73.3	794	3	BU962186	BU962186
150	17.6	73.3	409	5	BE173992	BE173992 QV1-HF0057	C 223	17.6	73.3	798	2	BI224442	BI224442
151	17.6	73.3	410	2	BE175046	BE175046 UI-R-CX0-	C 224	17.6	73.3	801	14	AY410663	AY410663
152	17.6	73.3	421	1	AA655960	AA655960 v94f08.r	C 225	17.6	73.3	806	2	BI157204	BI157204
153	17.6	73.3	421	1	AI043633	AI043633 UI-R-CO-J	C 230	17.6	73.3	851	5	DR790756	DR790756
154	17.6	73.3	425	5	CJ317470	CJ317470 CJ317470	C 231	17.6	73.3	855	3	BU239599	BU239599
155	17.6	73.3	425	1	AV011735	AV011735 AV011735	C 232	17.6	73.3	859	5	CD789655	CD789655
156	17.6	73.3	426	1	AV011735	AV011735 AV011735	C 233	17.6	73.3	879	3	BU853415	BU853415
157	17.6	73.3	434	5	CJ228806	CJ228806 CJ228806	C 234	17.6	73.3	882	5	CD793487	CD793487
158	17.6	73.3	435	3	BU961211	BU961211 AGENCOURT	C 235	17.6	73.3	882	5	BI265517	BI265517
159	17.6	73.3	443	4	BY452887	BY452887 BY452887	C 236	17.6	73.3	907	2	CD782407	CD782407
160	17.6	73.3	444	4	BY432547	BY432547 BY432547	C 237	17.6	73.3	916	5	CD782407	CD782407
161	17.6	73.3	444	4	CA563760	CA563760 K0317F10-	C 238	17.6	73.3	918	10	CV043823	CV043823
162	17.6	73.3	447	4	CA563760	CA563760 K0317F10-	C 239	17.6	73.3	940	12	CC597932	CC597932

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239 17.6 73.3 942 10 DV043460
240 17.6 73.3 943 2 BG761740
241 17.6 73.3 949 6 AK009715 Mus muscu
242 17.6 73.3 951 7 BF688762
243 17.6 73.3 952 6 AK160217 Mus muscu
244 17.6 73.3 952 12 CL065269
245 17.6 73.3 953 6 AK166410 Mus muscu
246 17.6 73.3 955 2 BI903760
247 17.6 73.3 957 6 AK011011 Mus muscu
248 17.6 73.3 967 3 BU509953
249 17.6 73.3 986 12 CC934245
250 17.6 73.3 1085 3 BH803090
251 17.6 73.3 1535 6 CR596731 full-leng
252 17.6 73.3 1610 6 CR591390
253 17.6 73.3 1634 6 CR599521 full-leng
254 17.6 73.3 1641 6 CR620180 full-leng
255 17.6 73.3 1649 6 CR619642 full-leng
256 17.6 73.3 1673 6 CR614333 full-leng
257 17.6 73.3 1699 6 CR623628 full-leng
258 17.6 73.3 1715 6 CR605450 full-leng
259 17.6 73.3 1722 6 CR621364 full-leng
260 17.6 73.3 1723 6 CR594015 full-leng
261 17.6 73.3 1723 6 CR603520 full-leng
262 17.6 73.3 1728 6 CR603258 full-leng
263 17.6 73.3 1740 6 CR613057 full-leng
264 17.6 73.3 1741 6 CR622122 full-leng
265 17.6 73.3 1765 6 CR592980 full-leng
266 17.6 73.3 1772 6 CR620296 full-leng
267 17.6 73.3 1807 6 CR859228 Pongo pyg
268 17.6 73.3 1822 6 A1609775 Sus scrof
269 17.6 73.3 1832 6 CR592602 full-leng
270 17.6 73.3 1886 6 CR605577 full-leng
271 17.4 72.5 316 4 CB603496 L843 Late
272 17.4 72.5 476 11 AZ737267 RPCI-24-1
273 17.4 72.5 492 7 BF6223830 HVSME000
274 17.4 72.5 493 7 BF257478 HVSMEF001
275 17.4 72.5 544 7 BF253911 HVSMEF000
276 17.4 72.5 591 8 CN207299 Tor7720 G
277 17.4 72.5 639 7 BF622550 HVSME001
278 17.4 72.5 698 7 BF622265 HVSME000
279 17.4 72.5 799 7 BE195630 HVSME008
280 17.4 72.5 817 8 CN207539 Tor7952 G
281 17.4 72.5 866 1 AL516191 AL516191
282 17.4 72.5 907 10 DR421359 CHSSE05
283 17.4 72.5 1173 9 DR139870 49349140
284 17.4 72.5 1242 11 BZ559026 pacs2-164
285 17.2 71.7 228 14 CNS03YNO AL266541 Tetradon
286 17.2 71.7 315 2 B1166846 REU7072.5
287 17.2 71.7 325 7 BF560949 UI-R-EI-f
288 17.2 71.7 384 9 DN971154 A02 ISUFM
289 17.2 71.7 396 5 CJI187723 CJI187723
290 17.2 71.7 425 3 BM862819 mgcm004xE
291 17.2 71.7 425 7 AW638562 B148b2.w
292 17.2 71.7 446 5 CK234849 SB010090
293 17.2 71.7 472 2 BG019725 dc67ell.x
294 17.2 71.7 510 3 BP741473 BP741473
295 17.2 71.7 532 2 BM261043 dag33b10.
296 17.2 71.7 538 11 AQ519367 HS 5162.A
297 17.2 71.7 570 3 BQ397715 NISC mc01
298 17.2 71.7 573 2 BG021806.x
299 17.2 71.7 586 11 AQ267094 RPCI11-72
300 17.2 71.7 622 2 BM327318 PIC1_12_A
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## ALIGNMENTS

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RESULT 1
CN208729 657 bp mRNA linear EST 30-APR-2004
LOCUS Tor9226 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
DEFINITION sequence.
ACCESSION CN208729
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VERSION CN208729.1 GI:46905460
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Tortula.
REFERENCE 1 (bases 1 to 657)
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15546486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbk.ars.usda.gov
PCR Primers
FORWARD: GTTTTCCCAAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.
FEATURES
source Location/Qualifiers
1..657
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration Library"
/notes="Organ: Green Gametophyte; Vector: pSport1; Site_1:
SalI; Site_2: NotI"
ORIGIN
Query Match 86.7%; Score 20.8; DB 8; Length 657;
Best Local Similarity 91.7%; Pred. No. 55;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CAAGTCGAACGGAAAGCCCTTTCG 24
|||||
Db 240 CAAGTCGAACGGAAAGCCCTTTCG 263
RESULT 2
BB241896/c
LOCUS BB241896 RIKEN full-length enriched, 3 days neonate thymus Mus
DEFINITION musculus cDNA clone A630089H08 3', mRNA sequence.
ACCESSION BB241896
VERSION BB241896.1 GI:8934642
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 312)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
Hirozane,T., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Iizawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,
Okazaki,K., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K.,
Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
Takagishi,F., Tominaga,N., Toya,T., Tsunoda,Y., Tagawa,A.,
Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A.,
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Konno,H., et al.)
JOURNAL Unpublished (2000)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
```

The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@isc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoaka, S.,  
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermostabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
 Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)  
 Please visit our web site (http://genome.rtc.riken.go.jp) for  
 further details.

#### FEATURES

source  
 Location/Qualifiers  
 1. 312  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="A630089H08"  
 /tissue\_types="thymus"  
 /dev\_stage="3 days neonate"  
 /lab\_host="DH10B"  
 /clone\_lib="RIKEN full-length enriched, 3 days neonate  
 thymus"  
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 20.0 and subtraction to Rot = 459.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGAGATTCGAGTTAATAATTAATCCCCCCCCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLC I."

#### ORIGIN

Query Match 82.5%; Score 19.8; DB 7; Length 312;  
 Best Local Similarity 91.3%; Pred. No. 1.5e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTCG 24

Db 73 AAGTCGAACGGAAGGCTTACG 51

#### RESULT 3

CD122074/c  
 LOCUS  
 DEFINITION  
 ME1-0071G-A160-E04-1.B ME1-0071 Schistosoma mansoni cDNA clone  
 ME1-0071G-A160-E04.B, mRNA sequence.

CD122074 356 bp mRNA linear EST 14-SEP-2003

CD122074 1 GI:34660126

EST.

Schistosoma mansoni

Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 356)

Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,

Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,  
 Kitajima, J.P., Adanson, R.B., Ashton, P.D., Bonaldo, M.F.,  
 Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,  
 Leite, R.A., Malaquias, L.C., Marques, R.C.P., Miyasato, P.A.,  
 Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, M.A.,  
 Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,  
 Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,  
 Stubal, J.C., Leite, L.C.C. and Dias-Neto, E.  
 Transcriptome analysis of the acelomate human parasite Schistosoma  
 mansoni

Nat. Genet. 35 (2), 148-157 (2003)

12973350

Other ESTs: ME1-0071G-A160-E04-2.B

Contact: Dr. Sergio Verjovski-Almeida

Departamento de Bioquímica

Instituto de Química - Universidade de Sao Paulo

Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,

Brasil

Tel: +55-11-3091-2173

Fax: +55-11-3091-2186

Email: verjo@iq.usp.br

This sequence was derived from the FAPESP Schistosoma mansoni EST  
 Genome Project. All sequences in the project were assembled and  
 annotated. This entry and all the assembled sequences can be seen  
 in the following URL: http://bioinfo.iq.usp.br/schisto/

Plate: ME1-0071G-A160 row: 4 column: E.

#### FEATURES

source  
 Location/Qualifiers  
 1. 356  
 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6183"  
 /clone="ME1-0071G-A160-E04.B"  
 /sex="mixed pool"  
 /dev\_stage="egg"  
 /lab\_host="Mus musculus"  
 /clone\_lib="ME1-0071"  
 /note="Vector: pGEM T-easy"

#### ORIGIN

Query Match 82.5%; Score 19.8; DB 4; Length 356;  
 Best Local Similarity 91.3%; Pred. No. 1.5e+02;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTC 23

Db 294 CAAGTCGAACGGAAGGCTTGC 272

#### RESULT 4

DU818647

LOCUS

DEFINITION  
 DU818647 683 bp DNA linear GSS 13-DEC-2005  
 OQ\_Aba0092L10.r OG\_Aba Oryza granulata genomic clone OG\_Aba0092L10  
 3', genomic survey sequence.

ACCESSION  
 DU818647

VERSION  
 DU818647.1 GI:83614306

KEYWORDS  
 GSS.

SOURCE  
 Oryza granulata

ORGANISM  
 Oryza granulata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 683)

SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,

Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,

Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.

OMAP (Oryza Map Alignment Project) - Purdue University

Unpublished (2004)

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 7654963621

Fax: 7654967255

Email: sjackson@purdue.edu  
 Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with lucy version 1.19s. Bases 111-793 of the raw sequence (length 1048) were retained after clipping.  
 Plate: 0092 row: L column: 10  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.

FEATURES source  
 Location/Qualifiers  
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 /organism="Oryza granulatata"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:110450"  
 /clone="OG\_ABA0092L10"  
 /tissue\_type="young leaves"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="OG\_ABA"  
 /note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 80.0%; Score 19.2; DB 14; Length 683;  
 Best Local Similarity 87.5%; Pred. No. 3.2e+02;  
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24  
 ||||| ||||| ||||| ||||| |||||  
 Db 238 CAAGTCGAGCGTAAGGCCCTTCG 261

RESULT 5  
 CN204419  
 LOCUS Tor4810 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA  
 DEFINITION  
 sequence.  
 ACCESSION CN204419  
 VERSION CN204419.1 GI:46901150  
 KEYWORDS EST.  
 SOURCE Tortula ruralis  
 ORGANISM Tortula ruralis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.  
 1 (bases 1 to 650)  
 Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauget, S.A. and Payton, P.R.  
 The rehydration transcriptome of the desiccation-tolerant bryophyte  
 Tortula ruralis: transcript classification and analysis  
 BMC Genomics 5 (1), 89 (2004)  
 15546486  
 Contact: Oliver Melvin J  
 Plant Stress Lab  
 USDA-ARS  
 3810 4th St, Lubbock, TX 79415, USA  
 Tel: 806-749-5560  
 Fax: 806-723-5272  
 Email: moliver@lbrk.ars.usda.gov  
 PCR Primers  
 FORWARD: GTTTTCCAGTCACGAC  
 BACKWARD: CAGGAACAGCTATGAC.

FEATURES source  
 Location/Qualifiers  
 1..650  
 /organism="Tortula ruralis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:38588"  
 /clone\_lib="Gametophyte rehydration Library"  
 /note="Organ: Green Gametophyte; Vector: pSport1; Site\_1: SalI; Site\_2: NotI"

## ORIGIN

Query Match 79.2%; Score 19; DB 8; Length 650;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
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Db 34 CAAGTCGAACGGAAGGCC 52  
 RESULT 6  
 CO365133  
 LOCUS RTK1\_23\_G09\_g1\_A029 Roots minus potassium Pinus taeda cDNA clone  
 DEFINITION  
 ACCESSION CO365133  
 VERSION CO365133.1 GI:49446450  
 KEYWORDS EST.  
 SOURCE Pinus taeda (loblolly pine)  
 ORGANISM Pinus taeda  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.  
 1 (bases 1 to 874)  
 Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and  
 Dean, J.F.D.  
 An EST database from potassium-deficient loblolly pine (Pinus taeda) roots  
 Unpublished (2004)  
 Other ESTs: RTK1\_23\_G09\_bi\_A029  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.  
 Seq primer: JENREV (CAGGAACAGCTATGACC).

## FEATURES

source  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /strain="3 CCLONES"  
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 /clone="RTK1\_23\_G09\_A029"  
 /lab\_host="DH10B-T1 phage-resistant E. coli"  
 /clone\_lib="Roots minus potassium"  
 /note="Organ: Root; Vector: pSL1180; Site\_1: EcoRI; Site\_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. The rooted cuttings were maintained for 117 days (July 2003 harvest) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. For twenty-eight days (28 d) prior to harvesting roots for mRNA preparation, the trees received Hoagland's solution lacking potassium (K) to induce a potassium-deficiency. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

## ORIGIN

Query Match 79.2%; Score 19; DB 8; Length 874;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
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 Db 24 CAAGTCGAACGGAAGGCC 42

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RESULT 7
LOCUS      CN201712
DEFINITION Tor1780 Gametophyte rehydration Library Tortula ruralis EST 30-APR-2004
            sequence.
ACCESSION  CN201712
VERSION    CN201712.1 GI:46898443
KEYWORDS   EST.
SOURCE     Tortula ruralis
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
            Bryopsida; Dictyodiales; Pottiaceae; Tortula.
REFERENCE  1 (bases 1 to 885)
AUTHORS   Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE     The rehydration transcriptome of the desiccation-tolerant bryophyte
            Tortula ruralis: transcript classification and analysis
JOURNAL   BMC Genomics 5 (1), 89 (2004)
PUBMED    15546486
COMMENT   Contact: Oliver Melvin J
            Plant Stress Lab
            USDA-ARS
            3810 4th St, Lubbock, TX 79415, USA .
            Tel: 806-749-5560
            Fax: 806-723-5272
            Email: moliver@lbrk.ars.usda.gov
PCR PRIMERS
FORWARD: GTTTCCTCCAGTCAGCAG
BACKWARD: CAGGAACAGCTATGAC.
            Location/Qualifiers
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            /organism="Tortula ruralis"
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            /clone_lib="Gametophyte rehydration Library"
            /note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
            SalI; Site_2: NotI"

ORIGIN
Query Match      79.2%; Score 19; DB 8; Length 885;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CAACTCGAACGGAAGGCC 19
        |||||||
Db      54  CAACTCGAACGGAAGGCC 72

RESULT 8
LOCUS      CC453191/c
DEFINITION ZMMBBC0347A07f ZMMBBC Zea mays genomic clone ZMMBBC0347A07 5',
            genomic survey sequence.
ACCESSION  CC453191
VERSION    CC453191.1 GI:31000754
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 903)
AUTHORS   Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
            Rouzard,K., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE     Sequencing of the maize genome at PCR (2003b)
JOURNAL   Unpublished (2003)
COMMENT   Contact: Bharti,A.K.
            Dr. Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
```

```
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 398.
            Location/Qualifiers
            1..903
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /cultivar="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBBC0347A07"
            /lab_host="E. coli DH10B"
            /clone_lib="ZMMBBC"
            /note="Vector: pTARBAC1.3; Site_1: BamHI; Site_2: BamHI"

ORIGIN
Query Match      78.3%; Score 18.8; DB 12; Length 903;
Best Local Similarity 90.9%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CAACTCGAACGGAAGGCCTTT 22
        |||||
Db      75  CAAATTGATCGGAAGGCCTTT 54

RESULT 9
LOCUS      DN561788
DEFINITION DN561788.1 GI:61120827
            Strongylocentrotus purpuratus
            Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoidea;
            Strongylocentrotidae; Strongylocentrotus.
            1 (bases 1 to 910)
            Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
            Ettensohn,C.A.
            A large scale analysis of mRNAs expressed by primary mesenchyme
            cells of the sea urchin embryo
            Development 128 (13), 2615-2627 (2001)
            11493577
            Contact: Erica Sodergren
            Human Genome Sequencing Center
            Baylor College of Medicine
            One Baylor Plaza, Houston, TX 77030, USA
            Tel: 713-798-7676
            Fax: 713-798-6977
            Email: ericas@bcm.tmc.edu
            NCBI Trace Archive: 48682679
            Insert Length: 1750 Std Error: 0.25
            Plate: 102 row: A column: 16.
            Location/Qualifiers
            1..910
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            /clone="PMCSPP2-102A16"
            /tissue_type="embryo"
            /cell_type="primary mesenchyme cells"
            /lab_host="E.coli"
            /clone_lib="Sea Urchin primary mesenchyme cell cDNA
            library"
            /note="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
            dt priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match      78.3%; Score 18.8; DB 9; Length 910;
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Best Local Similarity 90.9%; Pred. No. 5.2e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 AGTCGAACGGAAGGCGCTTTCG 24
|||
Db 790 AGGCGACGGAAGGCGCTTTCG 811

RESULT 10
CF882404 735 bp mRNA linear EST 31-OCT-2003
LOCUS
DEFINITION trico86xm16.b1 T.reesei mycelial culture, Version 6 October 2003
ACCESSION Hypocrea jecorina cDNA clone trico86xm16, mRNA sequence.
VERSION CF882404
KEYWORDS EST.
SOURCE CF882404.1 GI:38137086
ORGANISM Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
REFERENCE 1 (bases 1 to 735)
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
1. 735
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico86xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="vector: PREP3Y; Site_1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 76.7%; Score 18.4; DB 5; Length 735;
Best Local Similarity 95.0%; Pred. No. 7.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCGCTTTC 23
|||
Db 58 GTCGACGGAAGGCGCTTTC 77

RESULT 11
CB908942 788 bp mRNA linear EST 02-JUL-2003
LOCUS
DEFINITION trico86xm16 T.reesei mycelial culture, Version 3 april Hypocrea
jecorina cDNA clone trico86xm16, mRNA sequence.
ACCESSION CB908942
VERSION CB908942.1 GI:30123600
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.

```

```

REFERENCE 1 (bases 1 to 788)
AUTHORS Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
TITLE Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
JOURNAL J. Biol. Chem. 278 (34), 31988-31997 (2003)
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: Pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
1. 788
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="trico86xm16"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 3 april"
/note="vector: PREP3Y; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN
Query Match 76.7%; Score 18.4; DB 4; Length 788;
Best Local Similarity 95.0%; Pred. No. 8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCGCTTTC 23
|||
Db 111 GTCGACGGAAGGCGCTTTC 130

RESULT 12
DY091901 327 bp mRNA linear EST 31-JAN-2006
LOCUS
DEFINITION 010128BENMN062222HT BENM Bos taurus CDNA, mRNA sequence.
ACCESSION DY091901
VERSION DY091901.1 GI:86238488
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 327)
AUTHORS McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S.,
Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T.,
Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C.,
McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J.,
Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J.,
Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and
Atkinson,P.
TITLE AgResearch, Genesis and Primary Industry Victoria Bovine EST
project
JOURNAL Unpublished (2006)
COMMENT Contact: Maqbool N
AgResearch Ltd.
Invermay Agricultural Centre, Puddle Alley, Private Bag 50034,
Mosgiel, New Zealand
Email: nauman.maqbool@agresearch.co.nz.
Location/Qualifiers
1. 327
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Life Tech Normalised library"

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/clone lib="BEMN" /note="Vector: pCMV-Sport6; Life Tech Normalised library"	
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Query Match	75.8%; Score 18.2; DB 10; Length 327;
Best Local Similarity	87.0%; Pred. No. 9e+02;
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 CAAGTCGAACGGAAGGCCCTTTC 23 
Db	106 CAAGTCGAACGGAAGGACTGTC 128 
RESULT 13	
LOCUS	BY457153 421 bp mRNA linear EST 13-DEC-2002
DEFINITION	BY457153 RIKEN full-length enriched, 15 days pregnant adult female
VERSION	BY457153
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus. 1 (bases 1 to 421)
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusica, V., Chotia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragan, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Analysis of the mouse transcriptome based on functional annotation
JOURNAL	of 60, 770 full-length cDNAs
PUBMED	Nature 420, 563-573 (2002)
COMMENT	1246851 Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site (http://genome.gsc.riken.go.jp) for further details. Location/Qualifiers 1. .421 /organism="Mus musculus" /mol_type="mRNA" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="K630096B19" /sex="female" /tissue_type="amnion" /dev_stage="15 days pregnant adult" /clone_lib="RIKEN full-length enriched, 15 days pregnant adult female amnion"	
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Query Match	75.8%; Score 18.2; DB 4; Length 421;
Best Local Similarity	87.0%; Pred. No. 9.2e+02;
Matches	20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy	1 CAAGTCGAACGGAAGGCCCTTTC 23 
Db	272 CAAGTCGAGCAGAAAGCTCTTC 294 
RESULT 14	
LOCUS	AQ627316 452 bp DNA linear GSS 16-JUN-1999
DEFINITION	CITBI-E1-2650113.TR CITBI-E1 Homo sapiens genomic clone 2650113, genomic survey sequence.
ACCESSION	AQ627316
VERSION	AQ627316.1 GI:5089708
KEYWORDS	GSS.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 452)
AUTHORS	Zhao, S., Adams, M. D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J. C.
TITLE	Use of BAC End Sequences from CalTech Libraries for Sequence-Ready Map Building
JOURNAL	Unpublished (1997)
COMMENT	Other GSSs: CITBI-E1-2650113.TF Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbe@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html. Seq primer: M13 Reverse Class: BAC ends. Location/Qualifiers

RESULT 16



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/tissue_type="pooled"
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/clone_lib="MARC 7BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."

ORIGIN
Query Match      75.8%; Score 18.2; DB 9; Length 835;
Best Local Similarity 87.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
    |||||
Db 552 CAAGTCGAACGGAAGGACTGTC 574

RESULT 20
CR077081
LOCUS      835 bp      DNA      linear      GSS 05-JUL-2004
DEFINITION Reverse strand read from insert in 3'HPRT insertion targeting and
chromosome engineering clone MHP284c21, genomic survey sequence.
ACCESSION  CR077081
VERSION     CR077081.1 GI:49810669
KEYWORDS   GSS; genome survey sequence; MICRR.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 835)
AUTHORS   Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
            Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
            Rogers,J. and Bradley,A.
TITLE     Direct Submission
JOURNAL   Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICRR
FEATURES
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            /db_xref="taxon:10090"
            /clone_lib="MHP284c21"
            /clone_lib="MHPP"

ORIGIN
Query Match      75.8%; Score 18.2; DB 14; Length 835;
Best Local Similarity 87.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24
    |||||
Db 519 AATTAGAAGGAAGGCGCTTTCG 541

RESULT 21
DN282351/c
LOCUS      843 bp      mRNA      linear      EST 02-MAR-2005
DEFINITION DN282351
ACCESSION  DN282351
VERSION     DN282351.1 GI:60450961
KEYWORDS   EST.
SOURCE     Bos taurus (cattle)
ORGANISM   Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE  1 (bases 1 to 843)
AUTHORS   Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keefe,J.W.
TITLE     A second set of bovine ESTs from pooled-tissue normalized libraries
            Unpublished (2003)

Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8014 row: J column: 12
Seq primer: TAGAAGGCACAGTCGAGG.
FEATURES
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            /tissue_type="pooled"
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            /clone_lib="MARC 7BOV"
            /notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
            Library made with RNA pooled from multiple tissues
            including ovary, hindbrain, uterus, and day-30 whole
            embryos."

ORIGIN
Query Match      75.8%; Score 18.2; DB 9; Length 843;
Best Local Similarity 87.0%; Pred. No. 1e+03;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
    |||||
Db 284 CAAGTCGAACGGAAGGACTGTC 262

RESULT 22
DU746898/c
LOCUS      906 bp      DNA      linear      GSS 27-JAN-2006
DEFINITION ANSC3551.b2 HF10_10-07-02 uncultured marine microorganism
            HF10_10-07-02 genomic clone HF0010_049G12, genomic survey sequence.
ACCESSION  DU746898
VERSION     DU746898.1 GI:85756734
KEYWORDS   GSS.
SOURCE     uncultured marine microorganism HF10_10-07-02
            uncultured marine microorganism HF10_10-07-02
            unclassified sequences; environmental samples.
ORGANISM   1 (bases 1 to 906)
            DeLong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,
            Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.
            and Karl,D.M.
REFERENCE  1
AUTHORS   Comparative genomics reveals ecological trends in stratified
            microbial communities in the ocean's interior
            Science (2006) In press
TITLE     Contact: Susan Lucas, Alex Copeland, Sam Bitluck, Alla Lapidus,
            Kerrie Barry, Rijana Glavinadelrio, David Bruce, Paul Richardson
            and Edward DeLong
JOURNAL   US DOE Joint Genome Institute
            US DOE Joint Genome Institute
            2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
            Tel: 617-253-5271
            Fax: 617-253-2679
            Email: PMRichardson@lbl.gov; delong@mit.edu
            North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid
            DNA library prepared from marine picoplankton in the less than 1.6
            um, greater than 0.22 um fraction. Sample Date: 10/7/2002
            Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C
            Salinity 35.08 psu Oxygen: 204.6 umol/kg
            Class: fosmid ends.
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            /mol_type="genomic DNA"
            /db_xref="taxon:361145"
            /clone="HF0010_049G12"

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/cell type="marine picoplankton, less than 1.8 um, greater than 0.22 um fraction"  
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/notes="vector: pCIRFOS; North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid DNA library prepared from marine picoplankton in the less than 1.6 um, greater than 0.22 um fraction. Picoplankton collected at 10 m depth on 10/7/2002. Coordinates: 22.45 N, 158 W. Sample Date: 10/7/2002 Coordinates: 22.45 N, 158 W Depth: 10 m Temperature: 26.4 C Salinity 35.08 psu Oxygen: 204.6 umol/kg"

ORIGIN

Query Match 75.8%; Score 18.2; DB 14; Length 906;  
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 3;  
  
Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24  
||||||| | |||||  
Db 421 AAGTCGAACGCGAGGCGCTTTCG 399  
||||||| | |||||

RESULT 23

DQ213078 1052 bp mRNA linear HTC 25-OCT-2005  
LOCUS Taeniopygia guttata clone 0058P0007D03 gephyrin-like mRNA, complete sequence.  
DEFINITION  
ACCESSION DQ213078  
VERSION DQ213078.1 GI:76152437  
KEYWORDS  
SOURCE  
ORGANISM Taeniopygia guttata (Poepphia guttata)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Estrilidae; Estrilidae; Taeniopygia.  
1 (bases 1 to 1052)  
Wada,K., Howard,J.T., McConnell,P., Lints,T., Rivas,R.V., Whitney,O.B., Horita,H., Patterson,M., White,S., Zhao,S., Sakaguchi,H., Hagiwara,M., Toshiyuki,S., Hirozane-Kishikawa,T., Skene,P., Hayashizaki,Y., Carninci,P. and Jarvis,E.D.  
A molecular neuroethological approach for identifying and characterizing a melody of behaviorally regulated genes Unpublished

JOURNAL

2 (bases 1 to 1052)  
Wada,K. and Jarvis,E.D.  
Direct Submission  
TITLE Submitted (21-SEP-2005) Neurobiology, Duke University Medical Center, Box 3209, Durham, NC 27710, USA  
JOURNAL Location/Qualifiers

FEATURES

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1..1052  
/organism="Taeniopygia guttata"  
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/db\_xref="taxon:59729"  
/clone="0058P0007D03"  
/sex="female"  
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/clone\_lib="normalized (50 mix pooled juveniles + adults)"  
/dev\_stage="PH88"  
/notes="common: zebra finch; authority: Taeniopygia guttata Vieillot (1817); synonym: Poepphia guttata"  
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/note="similar to gephyrin"

ORIGIN

Query Match 75.8%; Score 18.2; DB 6; Length 1052;  
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 3;  
  
Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23  
||||||| | |||||  
Db 193 CAAGTCGAACGCAAGGCGCTTTC 215  
||||||| | |||||

RESULT 24

CL645653/c 1242 bp DNA linear GSS 06-JUL-2004  
LOCUS CH213-99C02.SP6 CH213 Gasterosteus aculeatus genomic clone  
DEFINITION CH213-99C02 3', genomic survey sequence.  
ACCESSION CL645653  
VERSION CL645653.1 GI:49665077  
KEYWORDS GSS.  
SOURCE Gasterosteus aculeatus (three spined stickleback)  
ORGANISM Gasterosteus aculeatus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.  
1 (bases 1 to 1242)  
Kingsley,D., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.  
Expressed sequence tags from Gasterosteus aculeatus Unpublished (2004)  
JOURNAL  
COMMENT Contact: Grimwood, Jane  
Stanford Human Genome Center  
Stanford University School of Medicine  
975 S California Avenue, Palo Alto, CA 94304, USA  
Tel: 650 320 5917  
Fax: 650 320 5801  
Email: jane@hgsc.stanford.edu  
Plate: 99  
Class: BAC ends  
High quality sequence start: 18  
High quality sequence stop: 933.  
Location/Qualifiers

FEATURES

source  
1..1242  
/organism="Gasterosteus aculeatus"  
/mol\_type="genomic DNA"  
/strain="Salmon River"  
/db\_xref="taxon:69293"  
/clone="CH213-99C02"  
/sex="Mixed"  
/cell\_type="Blood"  
/clone\_lib="CH213"  
/notes="Vector: pIARBAC2.1; Site\_1: EcoRI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (http://cegs.stanford.edu). The clone was isolated from the BAC library CHORI-213 built by Pieter deJong in collaboration with the Stanford Genome Evolution Center (http://www.chori.org/bacpac/). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering\_information.html)."

ORIGIN

Query Match 75.8%; Score 18.2; DB 13; Length 1242;  
Best Local Similarity 87.0%; Pred. No. 1e+03; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 3;  
  
Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24  
||||||| | |||||  
Db 517 AAGTCGAACGGAAGGCGCTTTCG 495  
||||||| | |||||

RESULT 25

BX342644 994 bp mRNA linear EST 07-APR-2004  
LOCUS BX342644 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED  
DEFINITION Homo sapiens cDNA clone CS0DL004YB13 5-PRIME, mRNA sequence.  
ACCESSION BX342644  
VERSION BX342644.2 GI:46275066  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS      1 (bases 1 to 994)
TITLE        Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
JOURNAL      Full-length cDNA libraries and normalization
COMMENT      Unpublished (2001)
              On May 2, 2003 this sequence version replaced gi:30342105.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              6269.r
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CS0DL004CA07QP1&c=6269.r.

FEATURES
source
1. .994
   Location/Qualifiers
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /clone="CS0DL004VB13"
   /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
   /cell_lines="RAMOS CELL LINE"
   /note="1st strand cDNA was primed with a NotI-oligo(dT)
   primer. Five prime end enriched, double-strand cDNA was
   digested with Not I and cloned into the Not I and EcoR V
   sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      75.0%; Score 18; DB 4; Length 994;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Oy 1 CAAGTCGAACGGAAGGCCCTTCG 24
    |||:|||||:|||||:|||||
Db 928 CAARTCGAATTKAAAGGMCCTGCG 951

RESULT 26
W10183
LOCUS      W10183
DEFINITION ma3f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:313469 5', mRNA sequence.
W10183
ACCESSION W10183
VERSION   W10183.1 GI:1284500
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 223)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
           Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
           Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
           Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
           Waterston,R.
           The WashU-HHMI Mouse EST Project
           Unpublished (1996)
JOURNAL   Contact: Marra M/Mouse EST Project
COMMENT   WashU-HHMI Mouse EST Project
           Washington University School of MedicineP
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI: 204085

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Seq primer: mob.REGA+ET
High quality sequence stop: 213.
Location/Qualifiers
1. .223
   /organism="Mus musculus"
   /mol_type="mRNA"
   /db_xref="taxon:10090"
   /clone="IMAGE:313469"
   /dev_stage="19.5 dpc total fetus"
   /lab_host="DH10B (ampicillin resistant)"
   /clone_lib="Soares mouse p3NMF19.5"
   /note="Vector: p7T73D (Pharmacia) with a modified
   polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
   was primed with a Not I - oligo(dT) primer [5',
   TGTTACCAATCTGAAGTGGAGGCGCGCATTTTTTTTTTTTTTTT 3'],
   double-stranded cDNA was size selected, ligated to Eco RI
   adapters (Pharmacia), digested with Not I and cloned into
   the Not I and Eco RI sites of a modified p7T73 vector
   (Pharmacia). Library went through one round of
   normalization to a Cot = 5. Library constructed by Bento
   Soares and M.Patima Bonaldo. RNA was kindly provided by
   Dr. Minoru Ko (Wayne State University).".

ORIGIN
Query Match      74.2%; Score 17.8; DB 10; Length 223;
Best Local Similarity 90.5%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CNACTCGAACGGAAGGCCCTT 21
    |||:|||||:|||||:|||||
Db 42 CAAGTCGAACGTGAAGGACTT 62

RESULT 27
AA815626
LOCUS      AA815626
DEFINITION vt03c06.r1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone
IMAGE:1161994 5', mRNA sequence.
AA815626
ACCESSION AA815626
VERSION   AA815626.1 GI:2885222
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muroidae; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 273)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
           Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
           Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
           Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
           Waterston,R.
           The WashU-HHMI Mouse EST Project
           Unpublished (1996)
JOURNAL   Contact: Marra M/Mouse EST Project
COMMENT   WashU-HHMI Mouse EST Project
           Washington University School of MedicineP
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:627906
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 259.
Location/Qualifiers
1. .273
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="C3H"
   /db_xref="taxon:10090"
   /clone="IMAGE:1161994"

```

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/cell_line="C2C12"
/lab_host="DH10B"
/clone_lib="Barstead mouse myotubes MPLRB5"
/notes="vector: p773D-PacI; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACGAATCTGAAGTGGGAGCGCGCCGCTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGGATCCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified p773 vector.
Library constructed by Bob Barstead. The C2C12 cell line
(available from ATCC, catalog # CRL-1772) differentiates
rapidly, forming contractile myotubes and producing
characteristic muscle proteins."

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ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 273;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGGCCTT 21  
|||||  
Db 216 CAAGTCGAACCTGAAGGACTT 236  
|||||

RESULT 28  
LOCUS BG147420 337 bp mRNA linear EST 01-FEB-2001  
DEFINITION mac03g07.y1 Soares mouse 3NbMS Mus musculus cDNA clone  
IMAGE:3998796 5' similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT  
7A. i. mRNA sequence.

ACCESSION BG147420.1 GI:12650828  
VERSION BG147420.1  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 337)  
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapsb-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:1496524  
Seq primer: -40RP from Gibco  
High quality sequence stop: 326.  
FEATURES  
source Location/Qualifiers  
1..337  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3998796"  
/sex="male"  
/tissue\_type="Spleen"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse 3NbMS"  
/notes="vector: p773D-PacI; Site\_1: Not I; Site 2: Eco RI;  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5',  
TGTTACGAATCTGAAGTGGGAGCGCGCCGCTTTTTTTTTTTTTTTTTTTTTTT  
3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p773 vector. RNA  
provided by Dr. Bertrand Jordan. Library went through  
three rounds of normalization, and was constructed by  
Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 337;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGGCCTT 21  
|||||  
Db 207 CAAGTCGAACCTGAAGGACTT 227  
|||||

RESULT 29  
LOCUS CB705072 347 bp mRNA linear EST 10-APR-2003

DEFINITION AMNNUC.SRPB2-00218-D5-A srpb2 (10220) Rattus norvegicus cDNA clone  
CB705072 srpb2-00218-d5 5', mRNA sequence.

ACCESSION CB705072  
VERSION CB705072.1 GI:29762220  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 347)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished (2003)  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00218 row: d column: 5.

FEATURES  
source Location/Qualifiers  
1..347  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="srpb2-00218-d5"  
/tissue\_type="prostate tissue"  
/clone\_lib="srpb2 (10220)"  
/notes="Vector: pSPOR1; Site\_1: SalI; Site\_2: NotI; rat  
prostate normalized double selected poly(A+) mRNA size  
fraction > 1 kb"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 347;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGGCCTT 21  
|||||  
Db 95 CAAGTCGAACCTGAAGGACTT 115  
|||||

RESULT 30  
LOCUS W65078 357 bp mRNA linear EST 10-JUN-1996

DEFINITION me01d06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA  
clone IMAGE:386219 5', mRNA sequence.

ACCESSION W65078  
VERSION W65078.1 GI:1372728  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 357)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisai, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and



Waterston, R.  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Marta M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:238051  
Seq primer: mob.REGA+ET  
High quality sequence stop: 327.  
FEATURES  
source  
1..357  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:386219"  
/sex="unknown"  
/tissue\_type="embryo"  
/dev\_stage="13.5-14.5dpc total fetus"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse embryo NME13.5 14.5"  
/note="Vector: p7T73D-PacI; Site 1: Not 1; Site 2: Eco RI;  
1st strand cDNA was primed with a Not I - oligo(dT) primer  
[5',  
TGTTACCAATCTGAAGTGGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTT  
T 3'] , on equal amounts of mRNA from 2 13.5dpc and 2  
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne  
State Univ., from 2 ]; double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pT773 vector. Library went through one round of  
normalization, and was constructed by Bento Soares and  
M.Fatima Bonaldo. "

ORIGIN  
Query Match 74.2%; Score 17.8; DB 10; Length 357;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 183 CAAGTCGAACGGAAGGCCTT 203  
|||||

RESULT 31  
CF425395/c  
LOCUS  
DEFINITION  
CF425395 384 bp mRNA linear EST 03-SEP-2003  
lad5je02.y1 Gastric Epithelial Progenitor Mus musculus cDNA 5'  
similar to TR:088546 O88546 COP9 COMPLEX SUBUNIT 7A. ;, mRNA  
sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CF425395.1 GI:34438096  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 384)  
Tidwell, R., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J.,  
Wylie, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennet, J.,  
Ronko, I., Tsagarisvili, R., Belaygorod, L., Grow, A., Maguire, L.,  
Waterston, R. and Wilson, R.  
WashU Stem cell EST Project  
Unpublished (2002)  
Contact: Jeff Gordon and Mike Lovett  
WashU, Human Genetics Division

Washington University School of Medicine  
1st strand of cDNA was synthesized with reverse transcriptase and  
oligo(dT) beads, then cDNA was amplified by PCR using modified  
SMART primers. The final cDNA was cloned in pAMP1 vector in  
annealing reaction with Uracil DNA Glycosylase (UDG). Library  
constructed by Y.Korshunova and M. Lovett. Library materials  
provided by Mills JC & Gordon JI.  
Putative full length read  
vector to vector length is  
Possible reversed clone: similarity on wrong strand  
Seq primer: -40RP from Gibco.  
FEATURES  
source  
1..384  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="Gastric Epithelial Progenitor"  
/dev\_stage="adult"  
/lab\_host="DH5alpha"  
/clone\_lib="Gastric Epithelial Progenitor"  
/note="Vector: pAMP1; This library was created from  
laser-captured isthmal cells from tox176 transgenic mice.  
1st strand of cDNA was synthesized with reverse  
transcriptase and oligo(dT) beads, then cDNA was amplified  
by PCR using modified SMART primers. The final cDNA was  
cloned in pAMP1 vector in annealing reaction with Uracil  
DNA Glycosylase (UDG). Library constructed by Y.Korshunova  
and M. Lovett. Library materials provided by Mills JC &  
Gordon JI."

ORIGIN  
Query Match 74.2%; Score 17.8; DB 5; Length 384;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 90 CAAGTCGAACGGAAGGCCTT 70  
|||||

RESULT 32  
AL363886  
LOCUS  
DEFINITION  
AL363886 ICRFP 522 and 523 Mus musculus cDNA clone V9719B01 5',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AL363886.1 GI:9695157  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 400)  
Eickhoff, H., Schuchhardt, J., Ivanov, I., Meier-Ewert, S., O'Brien, J.,  
Malik, A., Tandon, N., Wolski, E., Rohlf, E., Nyarsik, L.,  
Reinhardt, R., Nietfeld, W. and Lehrach, H.  
Tissue gene expression analysis using arrayed normalized cDNA  
libraries  
Genome Res. (2000) In press  
Contact: MPING  
Abt. Lehrach  
Max Planck Institut Fuer Molekulare Genetik  
Innesstrasse 73, Berlin, 14195 Germany  
The cDNA libraries ICRFP 522 and 523 were normalized with  
oligonucleotide fingerprinting, resulting in a unique subset of  
5376 cDNA clones.  
FEATURES  
source  
1..400  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"

```

/clones="V9719B01"
/tissue_type="embryo"
/dev_stage="9 and 12 pc embryo"
/clone_lib="ICRFp 522 and 523"

ORIGIN
Query Match          74.2%; Score 17.8; DB 1; Length 400;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 350 CAAGTCGAACGGAAGGACTT 370

RESULT 33
AI050353
LOCUS
DEFINITION
  ub29f09.r1 Soares thymus 2NBMT Mus musculus cDNA clone
  IMAGE:1379177 5', mRNA sequence.
ACCESSION
  AI050353
VERSION
  AI050353.1 GI:3299470
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 419)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:901645
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 418.
  Location/Qualifiers
    1..419
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="IMAGE:1379177"
      /sex="male"
      /tissue_type="Thymus"
      /dev_stage="4 weeks"
      /lab_host="DH10B"
      /clone_lib="Soares thymus 2NBMT"
      /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match          74.2%; Score 17.8; DB 1; Length 419;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 350 CAAGTCGAACGGAAGGACTT 370

RESULT 34
AI050353
LOCUS
DEFINITION
  ub29f09.r1 Soares thymus 2NBMT Mus musculus cDNA clone
  IMAGE:1379177 5', mRNA sequence.
ACCESSION
  AI050353
VERSION
  AI050353.1 GI:3299470
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 419)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:901645
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 418.
  Location/Qualifiers
    1..419
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="IMAGE:1379177"
      /sex="male"
      /tissue_type="Thymus"
      /dev_stage="4 weeks"
      /lab_host="DH10B"
      /clone_lib="Soares thymus 2NBMT"
      /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match          74.2%; Score 17.8; DB 1; Length 420;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 367 CAAGTCGAACGGAAGGACTT 387

RESULT 35
AI050353
LOCUS
DEFINITION
  ub29f09.r1 Soares thymus 2NBMT Mus musculus cDNA clone
  IMAGE:1379177 5', mRNA sequence.
ACCESSION
  AI050353
VERSION
  AI050353.1 GI:3299470
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 420)
  Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
  Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
  Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
  Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
  Waterston,R.
  The WashU-HMI Mouse EST Project
  Unpublished (1996)
  Contact: Marra M/Mouse EST Project
  WashU-HMI Mouse EST Project
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: mouseest@watson.wustl.edu
  This clone is available royalty-free through LLNL; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  MGI:901645
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 418.
  Location/Qualifiers
    1..420
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="IMAGE:1379177"
      /sex="male"
      /tissue_type="Thymus"
      /dev_stage="4 weeks"
      /lab_host="DH10B"
      /clone_lib="Soares thymus 2NBMT"
      /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through two
rounds of normalization, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match          74.2%; Score 17.8; DB 1; Length 420;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 143 CAAGTCGAACGGAAGGACTT 163

```

```

Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 367 CAAGTCGAACGGAAGGACTT 387

RESULT 34
AI050353
LOCUS
DEFINITION
  ub29f09.r1 Soares thymus 2NBMT Mus musculus cDNA clone
  IMAGE:1379177 5', mRNA sequence.
ACCESSION
  AI050353
VERSION
  AI050353.1 GI:5017507
KEYWORDS
  EST.
SOURCE
  Rattus norvegicus (Norway rat)
ORGANISM
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE
  1 (bases 1 to 420)
  Bonaldo,M.F., Lennon,G. and Soares,M.B.
  Normalization and subtraction: two approaches to facilitate gene
  discovery
  Genome Res. 6 (9), 791-806 (1996)
  8889548
  Contact: Soares, MB
  Coordinated Laboratory for Computational Genomics
  University of Iowa
  375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
  Tel: 319 335 8250
  Fax: 319 335 9565
  Email: Bento-soares@uiowa.edu
  Oligo-dT track not found, Not I site shown in beginning of sequence
  is likely internal to the message. cDNA Library Preparation: M.B.
  Soares Lab Clone distribution: clones will be available through
  Research Genetics (www.resgen.com)
  Seq primer: M13 Forward
  POLYA=No.
  Location/Qualifiers
    1..420
      /organism="Rattus norvegicus"
      /mol_type="mRNA"
      /strain="Sprague-Dawley"
      /db_xref="taxon:10116"
      /clone="UI-R-AGI-aso-b-08-0-UI"
      /dev_stage="adult"
      /lab_host="DH10B (Life Technologies)"
      /clone_lib="UI-R-AGI"
      /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;
The UI-R-AGI library is a normalized library constructed
from 13 dpc rat ventricle. The tag is a string of 6
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Jim Lin, Department of
Biology, University of Iowa.
TAG TISSUE=atrium at 16.5 dpc
TAG LIB=UI-R-AGI
TAG_SEQ=GATTC"

ORIGIN
Query Match          74.2%; Score 17.8; DB 1; Length 420;
Best Local Similarity 90.5%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    |||||
Db 143 CAAGTCGAACGGAAGGACTT 163

```

AA818546  
LOCUS  
DEFINITION UI-R-A0-aw-f-05-0-UI.s1 424 bp mRNA linear EST 03-JUL-1999  
UI-R-A0-aw-f-05-0-UI 3' similar to gb|L02529|RATPRZRH Rattus  
norvegicus Drosophila polarity gene (frizzled) homologue mRNA,  
complete cds, mRNA sequence.  
ACCESSION AA818546 GI:4228339  
VERSION AA818546.1  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
1 (bases 1 to 424)  
TITLE Bernaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
PUBMED 889548  
COMMENT On Feb 17, 1998 this sequence version replaced gi:2889285.  
Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu  
Oligo-dT track not found, Not 1 site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.  
Fatima Bernaldo, Ph.D. Clone distribution: clones will be available  
through Research Genetics This clone is also available through the  
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE  
ID=1776549  
Seq primer: M13 Forward  
POLYA=No.

FEATURES  
source  
1..424  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clones="UI-R-A0-aw-f-05-0-UI"  
/dev\_stages="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_libs="UI-R-A0"  
/notes="Vector: pT73D-PacI; Site 1: Not 1; Site 2: Eco RI;  
This library consists of a mixture of individually tagged  
normalized libraries constructed from rat placenta, adult  
lung, brain, liver, kidney, heart, spleen, ovary, and  
muscle. The tag is a string of 3-5 nucleotides present  
between the Not I site and the oligo-dT track which allows  
identification of the library of origin of a clone within  
the mixture."

ORIGIN  
Query Match 74.2%; Score 17.8; DB 1; Length 424;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 143 CAAGTCGAACGGAAGGCCTT 163  
|||||

RESULT 36  
BU743860  
LOCUS  
DEFINITION mai49f01.y1 McCarrey Eddy round spermatid Mus musculus cDNA clone  
IMAGE:6449520 5', mRNA sequence.  
ACCESSION BU743860  
VERSION BU743860.1 GI:23691980  
KEYWORDS EST.

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 444)  
McCarrey, J., Eddy, M., Marra, M., Hillier, L., Clifton, S., Pape, D.,  
Martin, J., Wylie, T., Dante, M., Bowers, Y., Theising, B., Gibbons, M.,  
Ritter, E., Tsagareishvili, R., Ronko, I., Maguire, L., Kennedy, S.,  
Bennett, J., Waterston, R. and Wilson, R.  
NIEHS Mouse  
Unpublished (2002)  
Contact: McCarrey/Eddy NIEHS Mouse  
NIEHS Mouse  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:2093832  
Seq primer: -40RP from Gibco  
High quality sequence stop: 422.  
Location/Qualifiers  
1..444  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="CD-1"  
/db\_xref="taxon:10090"  
/clones="IMAGE:6449520"  
/sex="male"  
/tissue\_type="round spermatids, pooled from multiple mice"  
/dev\_stage="60 day"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_libs="McCarrey Eddy round spermatid"  
/notes="Organ: testis; Vector: pBluescript SK+  
(Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo  
dT-primed [5'-(GA)10-ACTAGTCGAGTTTTTTTTTT-3'] and  
directionally cloned using 5' linkers 5'-AATTCGACGAG-3'  
and 5'-CTCGTCCG-3'. Size selection of 400bp material  
gives average insert size ranging from 1-2 kb. Library was  
mass excised (from lambda-UnizAP-XR) and resulting  
single-stranded phagemids were prepped and transformed  
into DH10B. Library contains 98.5% recombinants.  
References: J. Androl. 20:635-639 and Gene 25:263-269.  
Library constructed and donated by J. McCarrey, Ph.D.  
(Southwest Foundation for Biomedical Research, Dept. of  
Genetics); excision done by E.M. Eddy, Ph.D. (National  
Institutes of Health, National Institute of Environmental  
Health Sciences). Original lambda-based library is  
available through ATCC, catalog #63423."

ORIGIN  
Query Match 74.2%; Score 17.8; DB 3; Length 444;  
Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 12 CAAGTCGAACGGAAGGCCTT 32  
|||||

RESULT 37  
W47680  
LOCUS  
DEFINITION mc89h02.r1 Soares mouse embryo NM0E13.5 14.5 Mus musculus cDNA  
clone IMAGE:355731 5', mRNA sequence.  
ACCESSION W47680  
VERSION W47680.1 GI:1537643  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 446)

**REFERENCE**  
**AUTHORS**  
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 The WashU-HMI Mouse EST Project  
 Unpublished (1996)  
 On Sep 12, 1996 this sequence version replaced gi:1332776.  
**COMMENT**  
 Contact: Marra M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:227531  
 Seq primer: -28M13 rev2 from Amersham  
 High quality sequence stop: 400.  
**FEATURES**  
 source  
 1..446  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:355731"  
 /sex="unknown"  
 /tissue\_type="embryo"  
 /dev\_stage="13.5-14.5dpc total fetus"  
 /lab\_host="DH10B"  
 /clone\_lib="Soares mouse embryo NbME13.5 14.5"  
 /note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACCAATCTGAAGTGGAGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

**ORIGIN**  
 Query Match 74.2%; Score 17.8; DB 10; Length 446;  
 Best Local Similarity 90.5%; Pred. No. 1.4e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1 CAAGTCGACGGAAGGCCTT 21  
 |||||  
**Db** 80 CAAGTCGACGGAAGGACTT 100  
 |||||

**RESULT 38**  
**AI593186**  
**LOCUS**  
**DEFINITION**  
 vt03c06.y1 Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone  
**ACCESSION**  
**AI593186**  
**VERSION**  
**AI593186.1** GI:4602234  
**KEYWORDS**  
**SOURCE**  
 Mus musculus (house mouse)  
**ORGANISM**  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 473)

**AUTHORS**

**TITLE**  
**JOURNAL**  
**COMMENT**  
 Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:627906  
 This read is a RESEQUENCE of a previously sequenced mouse clone  
 This read has been verified (found to hit its original self in the correct orientation)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 466.  
**FEATURES**  
 source  
 1..473  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C3H"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:1161994"  
 /cell\_line="C2C12"  
 /lab\_host="DH10B"  
 /clone\_lib="Barstead mouse myotubes MPLRB5"  
 /note="Vector: pT7T3D-PacI; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTACGAATCTGAAGTGGAGCGCGGCCTTTTTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins. "

**ORIGIN**  
 Query Match 74.2%; Score 17.8; DB 1; Length 473;  
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 1 CAAGTCGACGGAAGGCCTT 21  
 |||||  
**Db** 293 CAAGTCGACGGAAGGACTT 313  
 |||||

**RESULT 39**  
**CN692701**  
**LOCUS**  
**DEFINITION**  
 E0326F01-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus musculus cDNA clone NIA:E0326F01 IMAGE:30861468 5', mRNA sequence.  
**ACCESSION**  
**CN692701**  
**VERSION**  
**CN692701.1** GI:47461449  
**KEYWORDS**  
**SOURCE**  
 Mus musculus (house mouse)  
**ORGANISM**  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus. 1 (bases 1 to 492)  
 Sharov,A.A., Piao,Y., Matoba,R., Dudekula,D.B., Qian,Y., VanBuren,V., Falco,G., Martin,P.R., Staggs,C.A., Bassey,U.C., Wang,Y., Carter,M.G., Hamatani,T., Aiba,K., Akutsu,H., Sharova,L., Tanaka,T.S., Kimber,W.L., Yoshikawa,T., Jaradat,S.A., Pantano,S., Nagaraja,R., Boheler,K.R., Taub,D., Hodess,R.J., Longo,D.L., Schlessinger,D., Keller,J., Klotz,E., Kelsee,G., Umezawa,A.,

Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.  
Transcriptome analysis of mouse stem cells and early embryos  
PLoS Biol. 1 (3), 410-419 (2003)  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: E0326 row: F column: 01  
Seq primer: M13 Reverse  
High quality sequence stop: 492  
POLYA=No.

FEATURES  
source  
1. .492  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="niaEST:E0326F01-5"  
/clone="NTA:E0326F01 IMAGE:30861468"  
/tissue\_type="whole embryo including extraembryonic tissues at 10 5-days postcoitum"  
/dev\_stage="E10.5"  
/lab\_host="DH10B"  
/clone\_lib="NTA Mouse E10.5 whole embryo cDNA library (Long)"  
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 8 embryos at 10.5-days postcoitum. Double-stranded cDNAs were synthesized with an oligo(dT) primer (Invitrogen):  
5'-pGACTAGTCTAGACGCGAGCGCCCTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker Li-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4Kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 8; Length 492;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||

Db 107 CAAGTCGAACGGAAGGACTT 127  
|||||

## RESULT 40

AA014214/c  
LOCUS  
DEFINITION  
mhl8910.r1 Soares mouse placenta 4NBMP13.5 14.5 Mus musculus cDNA  
clone IMAGE:442914 5', mRNA sequence.

AA014214

ACCESSION  
VERSION  
AA014214.1 GI:1476046  
EST.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (Bases 1 to 500)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HHMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HHMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MG1:268250

Seq primer: mob.REGA+ET

High quality sequence stop: 477.

## FEATURES

## source

1. .500  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:442914"  
/sex="unknown"  
/tissue\_type="placenta"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Soares mouse placenta 4NBMP13.5 14.5"  
/note="Organ: placenta; Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGGCGCGCGGAAATTTTTTTTTTTTTTTTTTTT  
T 3']; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 500;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||

Db 122 CAAGTCGAACGGAAGGACTT 102  
|||||

## RESULT 41

## LOCUS

## DEFINITION

AA509546  
vh50c08.r1 Soares mammary gland\_NbMNG Mus musculus cDNA clone  
IMAGE:890414 5', mRNA sequence.

AA509546

VERSION  
AA509546.1 GI:2247400  
EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

1 (Bases 1 to 502)  
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wyllie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.  
The WashU-HHMI Mouse EST Project

## TITLE

JOURNAL  
COMMENT

Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of MedicineP  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:518374

Seq primer: -28m13 rev2 ET from Amersham  
High quality sequence stop: 469.

FEATURES  
source

1..502  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="IMAGE:890414"  
/sex="male"  
/tissue\_type="mammary gland"  
/dev\_stage="4 weeks"  
/lab\_host="DH10B"  
/clone\_lib="Soares mammary gland NbMMG"

/note="Organ: mammary gland; Vector: pT7T3D-PacI; Site:1:  
Not I; Site 2: Eco RI; 1st strand cDNA was primed with a  
Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGCGCCGCGAATGGTTTTTTTTTTTTTTTT  
T 3'] ; double-stranded cDNA was ligated to Eco RI  
adaptors (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of the modified pT7T3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima  
Bonaldo."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 502;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAAGGCCTT 21  
|||||  
Db 58 CAAAGTCGAACGAAAGGACTT 78  
|||||

RESULT 42  
CG036380/c

LOCUS  
DEFINITION CG036380 502 bp DNA linear GSS 19-AUG-2003  
PUILV37TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0612H02,  
genomic survey sequence.

ACCESSION CG036380  
VERSION CG036380.1 GI:33908536  
KEYWORDS GSS.

SOURCE  
Zea mays

ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 502)  
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
Reenick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
Bennetzen,J.

TITLE Maize Genomics Consortium  
JOURNAL Unpublished (2003)  
COMMENT Other GSSes: PUILV37TB  
Contact: Cathy Whitelaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TF

FEATURES  
source

Class: sheared ends.  
Location/Qualifiers  
1..502  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBTa0612H02"  
/clone\_lib="ZM\_0.6 1.0 KB"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
Cot selected genomic DNA library"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 12; Length 502;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAAGGCCTT 21  
|||||  
Db 431 CAAAGTCGAACGAAAGGCCTT 411  
|||||

RESULT 43  
BE863637

LOCUS  
DEFINITION BE863637 527 bp mRNA linear EST 29-SEP-2000  
UI-M-BH0-ake-d-02-0-UI.r1 NIH BMAP\_M\_S1 Mus musculus cDNA clone  
UI-M-BH0-ake-d-02-0-UI 5', mRNA sequence.

ACCESSION BE863637.1 GI:10383879  
VERSION BE863637  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Murioidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 527)  
Bonaldo,M.F., Lennon,G. and Soares,M.B.

AUTHORS  
TITLE Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
PUBMED 8889548

COMMENT  
Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643 USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov

cDNA Library Preparation: M.B. Soares Lab Clone distribution:  
CDNA Libraries may obtain BMAP cDNA clones from RESEARCH GENETICS. It  
should be noted that Bento Soares is generating a small number of  
additional specialized non-redundant arrays of BMAP cDNAs whose  
availability will be considered under appropriate and limited  
collaborative arrangements  
Seq primer: M13 Reverse.

FEATURES  
source

Location/Qualifiers  
1..527  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UI-M-BH0-ake-d-02-0-UI"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH\_BMAP\_M\_S1"

/note="Vector: pT7T3D-PacI; Site 1: Not I; Site 2: Eco RI;  
The NIH BMAP M\_S1 library is a subtracted library derived  
from a mixture of normalized libraries from ten regions of  
the mouse brain (cerebellum, brain stems, olfactory bulbs,  
hypothalamus, cortex, amygdala, basal ganglia, pineal  
gland, striatum, hippocampus). The driver used for  
subtraction consisted of a pool of 20,000 cDNA clones  
obtained from non-normalized and normalized libraries of

these ten regions of the mouse brain."

Query Match 74.2%; Score 17.8; DB 7; Length 527;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 83 CAAGTCGAACGGAAGGCCTT 103  
|||||

RESULT 44  
BQ569727 532 bp mRNA linear EST 19-JUN-2002  
LOCUS gll35c11.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
DEFINITION clone gll35c11 5', mRNA sequence.

BQ569727

BQ569727.1 GI:21473044

ACCESSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished (2002)

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 135 row: c column: 11

Seq primer: M13RP1 reverse primer (ABI).

#### FEATURES

source

1. 532  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/clone="gll35c11"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

#### ORIGIN

Query Match 74.2%; Score 17.8; DB 3; Length 532;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||

Db 334 CAAGTCGAACGGAAGGCCTT 354  
|||||

#### RESULT 45

BQ569727/c

LOCUS

DEFINITION

BF022607

BF022607.1 GI:10753940

EST.

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 542)

NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: gqabs-1@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

Cloning by: Washington University Genome Sequencing Center

Cloning by: NCI-CCGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LMNL at:

image.llnl.gov/image/html/iresources.shtml

MGI:1423861

Possible reversed clone: similarity on wrong strand

Seq primer: -40RP from Gibco  
High quality sequence stop: 461.

## FEATURES

source  
Location/Qualifiers  
1. .542  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3663093"  
/tissue\_type="tumor, metastatic to mammary"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu30"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; transgenic model WNT-1, expression driven by  
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo  
dT. Library constructed by Life Technologies.  
Investigator providing samples: Gilbert Smith, NIH"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 542;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 135 CAAGTCGACTGAAGGACTT 115  
|||||

## RESULT 46

LOCUS AI603423 543 bp mRNA linear EST 21-APR-1999  
DEFINITION UI-R-AC1-xu-b-09-0-UI.s1 UI-R-AC1 Rattus norvegicus cDNA clone  
AI603423  
ACCESSION AI603423.1 GI:4612584  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Rattus norvegicus (Norway rat)

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

## REFERENCE

1 (bases 1 to 543)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)

## JOURNAL

PUBMED 8889548  
COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
Oligo-dT track not found, Not I site shown in beginning of sequence  
is likely internal to the message. cDNA Library Preparation: M.B.  
Soares Lab Clone distribution: clones will be available through  
Research Genetics (www.resgen.com)

## Seq primer: M13 Forward.

Location/Qualifiers

## FEATURES

source  
1. .543  
Location/Qualifiers  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clones="UI-R-AC1-xu-b-09-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-AC1"

/note="vector: p773D-PacI; Site\_1: Not I; Site\_2: Eco RI;  
The UI-R-AC1 library is a normalized library constructed  
from 16.5 dpc rat atrioventricular (AV) canal. The tag

## ORIGIN

Query Match 74.2%; Score 17.8; DB 1; Length 543;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 143 CAAGTCGACTGAAGGACTT 163  
|||||

## RESULT 47

LOCUS AZ024985/c 566 bp DNA linear GSS 25-FEB-2000  
DEFINITION RPCI-23-386J13.TJ RPCI-23 Mus musculus genomic clone  
AZ024985  
ACCESSION AZ024985  
VERSION  
KEYWORDS  
SOURCE GSS.  
ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 566)  
Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,  
Akinret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de  
Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)

## TITLE

JOURNAL RPCI-23-386J13.TV

## COMMENT

Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pieterdejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)  
or from Resea ch Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end page:  
[http://www.tigr.org/tdb/bac\\_ends/mouse/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/mouse/bac_end_intro.html)  
Plate: 386 row: J column: 13  
Seq primer: SP6  
Class: BAC ends.

## FEATURES

source  
1. .566  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-23-386J13"  
/sex="Female"  
/lab\_host="DH10B"  
/clone\_lib="RPCI-23"  
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:  
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested  
with a combination of EcoRI and EcoRI Methyase. Size  
selected DNA was cloned into the pBACe3.6 vector at the  
EcoRI sites. The ligation products were transformed into  
DH10B electrocompetent cells (BRL Life Technologies)."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 11; Length 566;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;

is a string of 5 nucleotides present between the Not I  
site and the oligo-dT track. The library was constructed  
as described by Bonaldo, Lennon and Soares, Genome  
Research 6: 791-806, 1996. Tissue provided by Jim Lin,  
Department of Biology, University of Iowa."



Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
||||||| ||||| |||||  
Db 417 CAAGTCGAGCGAAGGCCTT 397

## RESULT 48

CN692527

LOCUS

DEFINITION E0324C02-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus EST 18-MAY-2004

musculus cDNA clone NIA:E0324C02 IMAGE:30861241 5', mRNA sequence.

ACCESSION

CN692527

VERSION

CN692527.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@igsun.grc.nia.nih.gov

Plate: E0324 row: C column: 02

Seq primer: M13 Reverse

High quality sequence stop: 571

POLYA-No.

Location/Qualifiers

1..571

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="niaEST:E0324C02-5"

/db\_xref="taxon:10090"

/clone="NIA:E0324C02 IMAGE:30861241"

/tissue\_type="whole embryo including extraembryonic

tissues at 10.5-days postcoitum"

/dev\_stages="E10.5"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse E10.5 whole embryo cDNA library

(Long)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;

Site 2: NotI; Mouse cDNA project by the laboratory of

Genetics, National Institute on Aging (NIA), Intramural

Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).

This is a long-transcript enriched cDNA library (Ref.

Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total

RNAs were extracted from a pool of 8 embryos at 10.5-days

postcoitum. Double-stranded cDNAs were synthesized with an

Oligo(dT) primer [Invitrogen:

5'-TGACTAGTCTAGATCGGAGCGCCCTTTTCTTTT-3'] from

2ug of total RNA, treated with T4 DNA polymerase, and

purified by ethanol-precipitation. The cDNAs were ligated

to lona-linker LL-Sal4, purified by phenol/chloroform, and

separated from free linkers by Centricon 100. Then, the

cDNAs were amplified by long-range high fidelity PCR using

Ex Taq polymerase (Takara) with a primer Sal4-S. The

products were purified by phenol/chloroform and Centricon

100. The cDNAs were digested with SalI and NotI enzymes

and cloned into SalI/NotI site of pCMV-SPORT6 plasmid

## ORIGIN

Query Match 74.2%; Score 17.8; DB 8; Length 571;

Best Local Similarity 90.5%; Pred. No. 1.5e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

||||||| ||||| ||||| |||||

Db 107 CAAGTCGAACGGAAGGCCTT 127

## RESULT 49

BE288370/C

LOCUS

DEFINITION

601094841F1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3489299 5',

mRNA sequence.

ACCESSION

BE288370

VERSION

BE288370.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 577)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8530 row: a column: 12

High quality sequence stop: 577.

Location/Qualifiers

1..577

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db\_xref="taxon:10090"

/clone="IMAGE:3489299"

/tissue\_type="tumor, gross tissue"

/dev\_stages="7 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam5"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators

providing samples: Lothar Hennighausen/Robin Humphreys,

NIH"

## ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 577;

Best Local Similarity 90.5%; Pred. No. 1.5e+03;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21

||||||| ||||| ||||| |||||

Db 202 CAAGTCGAACGGAAGGCCTT 182

## RESULT 50

DN215604/C

LOCUS

DN215604

600 bp

mRNA

linear

EST 28-FEB-2005

DEFINITION MEST971\_D01.T7-1 UGA-ZmSAM-XZ2 Zea mays cDNA, mRNA sequence.  
 ACCESSION DN215604  
 VERSION DN215604.1 GI:60348631  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 600)  
 AUTHORS Chen,H.D., Zhang,X., Zhou,R.L., Arias L.A.C., Shendeiman,J.M.,  
 Zazubovits,N., Borsuk,L.A., Emrich,S.J., Ashlock,D.A., Scanlon,M.J.  
 and Schnable,P.S.  
 TITLE Expressed Sequence Tags from B73 Maize Shoot Apical Meristems  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Patrick S. Schnable  
 Schnable Laboratory  
 Iowa State University  
 2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA  
 Tel: 515-294-0975  
 Fax: 515-294-5256  
 Email: schnable@iastate.edu.

FEATURES

source

Location/Qualifiers

1. 600

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="inbred B73"

/db\_xref="taxon:4577"

/tissue\_type="vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4"

/lab\_host="XL1-Blue"

/clone\_lib="UGA-2mSAM-X22"

/note="Organ: Shoot apex; Vector: Uni-Zap XR; Site 1: EcoRI; Site 2: XhoI; This library was constructed by Xiaolan Zhang. Vegetative Shoot Apical Meristem (SAM) and leaf primordia staged P1-P4 from 14-17 day-after germination seedlings were quickly dissected into dry ice under a light microscope. Total RNA was isolated using Trizol and mRNA was purified with Dynal Oligo-DT25. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with an XhoI oligo-dT primer (5'-GAGAGAGAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol-I-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with XhoI and size-selected to be >600 bp. The resulting molecules were directionally cloned into the EcoRI and XhoI sites of the Uni-Zap XR vector. The lambda library was packaged with Gigapack III Gold packaging extract and was mass excised by XL1-Blue cells and ExAssist helper phage. Excised phagemids were titered in SOLR cells and plated onto LB-ampicillin agar plates. Base calling was conducted using Phred. Trimming was performed using Lucy with the following criteria: (-minimum 200 -error 0.01 0.01 -bracket 10 0.01). A low complexity filter was applied and additional trimming was conducted to remove E. coli, vector, and organelle contamination. After processing ~30% of the sequences contained a minimum of 10 ts at the beginning of the sequence. For reasons that are not understood many of the clones in this library lack an XhoI site at their 3' ends."

## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 9; Length 600;
Best Local Similarity 90.5%; Pred.No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAAGGCCTT 21
    |||||
Db 550 CAAGTGGAAAGAAAGGCCTT 530
    |||||

```

[illegible]

FEATURES  
source

/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/notes="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 10; Length 602;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAGGCCTT 21
    ||||| ||||| |||||
Db 583 CAAGTGGACGAAAAGCCTT 563

```

```

RESULT 52
CA934753/c
LOCUS
DEFINITION MTU5TS.P23.C06 Aspen stem cDNA Library Populus tremuloides cDNA,
              609 bp mRNA linear EST 30-DEC-2002
              mRNA sequence.
ACCESSION CA934753
VERSION CA934753.1 GI:27423233
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
REFERENCE 1 (bases 1 to 609)
AUTHORS Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
          Tsai,C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished (2003)
COMMENT Contact: Tsai C-J
          Michigan Technological University, School of Forest Resources &
          Environmental Science
          1400 Townsend Drive, Houghton, MI 49931-1295, USA
          Tel: 906 487 2914
          Fax: 906 487 2915
          Email: chtsai@mtu.edu.

FEATURES             Location/Qualifiers
     source            1..609
                     /organism="Populus tremuloides"
                     /mol_type="mRNA"
                     /db_xref="taxon:3693"
                     /clone_lib="Aspen stem cDNA Library"
                     /note="Organ: stem"

ORIGIN
Query Match          74.2%; Score 17.8; DB 4; Length 609;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 274 AAGTCGTTCCGGAAGGCCTTT 254

RESULT 53
AW914801
LOCUS
DEFINITION EST346105 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone
              RG1BH48 5' end, mRNA sequence.
ACCESSION AW914801
VERSION AW914801.1 GI:8080481
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 613)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
          Kerlavage,A.R. and Adams,M.D.
TITLE Rat Genome Project: Generation of a Rat EST (RST) Catalog & Rat
JOURNAL Unpublished (1998)
COMMENT Contact: Lee, NH
          The Institute for Genomic Research
          9712, Medical Center Drive, Rockville, MD 20850, USA
          Tel: (301)-838-3529
          Fax: (301)-838-0208
          Email: nhlee@tigr.org
          This clone is available through the ATCC, contact the ATCC
          tel#703-365-2700 for further information
          Seq primer: M13 Reverse.

FEATURES             Location/Qualifiers
     source            1..613
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strains="129,C57BL/6J,FVB/N"
                     /db_xref="taxon:10090"
                     /clone_lib="IMAGE:5318818"
                     /tissue_type="tumor, gross tissue"
                     /dev_stage="10 months"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Mam3"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sali;
                     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigators
                     providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
                     Reference for transgenic model: Xu et al., Nature Genetics
                     22, 37-43 (1999)."
```

```

Db      433 CAAGTCGAAGTGAAGGACTT 453

RESULT 55
CX734384/c
LOCUS
DEFINITION j01e11.y1 Mouse whole eye, equalized: ja/jb/jc Mus musculus cDNA
Clone j01e11 5', mRNA sequence.
ACCESSION CX734384
VERSION j01e11
KEYWORDS EST.
SOURCE CX734384.1 GI:58061220
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 635)
AUTHORS Wistow,G. and Tomarev,S.
TITLE Expressed sequence tag analysis of mouse whole eye
JOURNAL Unpublished (2004)
COMMENT Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 01 row: e column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1. .635
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl6J"
/db_xref="taxon:10090"
/clone="j01e11"
/tissue_type="Whole eye"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Mouse Whole eye, equalized: ja/jb/jc"
/notes="Organ: Eye; Vector: pSport1; Approximately 1mg
total RNA was extracted from 100 adult mouse whole eyes. A
directionally cloned cDNA library in the pSPORT1 vector
(Invitrogen) was constructed at Bioserve Biotechnology
(Laurel MD) essentially following the protocols of the
SuperScript Plasmid System full details of which are
contained in the manufacturer's instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adaptor
[5'-pGACTAGTTCTAGATCGAGCGCGGCC(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed on
the unamplified library at the NIH Intramural Sequencing
Center (NISC)."
```

ORGANISM

Query Match 74.2%; Score 17.8; DB 9; Length 635;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAAGTGAAGGACTT 21  
|||||  
Db 403 CAAGTCGAAGTGAAGGACTT 383

RESULT 56  
BI331633  
LOCUS  
DEFINITION BI331633  
mRNA sequence.  
ACCESSION BI331633  
VERSION BI331633.1 GI:15016290  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM

Query Match 74.2%; Score 17.8; DB 9; Length 635;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAAGTGAAGGACTT 21  
|||||  
Db 403 CAAGTCGAAGTGAAGGACTT 383

RESULT 57  
CF897511  
LOCUS  
DEFINITION CF897511  
641 bp mRNA linear EST 04-NOV-2003  
A0226B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (long,  
subtracted) Mus musculus cDNA clone NIA:A0226B05 IMAGE:30730864 5',  
mRNA sequence.  
ACCESSION CF897511  
VERSION CF897511.1 GI:38164560  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 641)  
AUTHORS Pao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
TITLE Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
PUBMED 11544199  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: A0226 row: B column: 05  
Seq primer: M13 Reverse  
High quality sequence stop: 641  
POLYA=No.

```

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-i@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11334 row: 9 column: 17
High quality sequence stop: 640.
Location/Qualifiers
1. .641
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5136040"
/lab_host="DHI0B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Li9"
/notes="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1-9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
```

ORGANISM

Query Match 74.2%; Score 17.8; DB 2; Length 641;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAAGTGAAGGACTT 21  
|||||  
Db 206 CAAGTCGAAGTGAAGGACTT 226

RESULT 57  
CF897511  
LOCUS  
DEFINITION CF897511  
641 bp mRNA linear EST 04-NOV-2003  
A0226B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (long,  
subtracted) Mus musculus cDNA clone NIA:A0226B05 IMAGE:30730864 5',  
mRNA sequence.  
ACCESSION CF897511  
VERSION CF897511.1 GI:38164560  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 641)  
AUTHORS Pao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.  
TITLE Construction of long-transcript enriched cDNA libraries from  
submicrogram amounts of total RNAs by a universal PCR amplification  
method  
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)  
PUBMED 11544199  
COMMENT Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@lgsun.grc.nia.nih.gov  
Plate: A0226 row: B column: 05  
Seq primer: M13 Reverse  
High quality sequence stop: 641  
POLYA=No.

## FEATURES

Location/Qualifiers

```

1. .641
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL6"
/db_xref="niaEST:A0226B05-5"
/db_xref="taxon:10090"
/clones="NIA:A0226B05 IMAGE:30730864"
/sex="male"
/dev_stage="embryonic day 8"
/lab_host="DH10B"
/clone_lib="NIA Mouse Embryonic Germ Cell cDNA Library
(Long, subtraced)"
/notes="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;
Site 2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun-grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). EG
cells were obtained from Dr. Brigid L.M. Hogan and RNA was
prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells
were cultured at 37. C. 5% CO2 in DMEM supplemented with
15% ES cell-qualified FBS, 0.1mM non-essential amino
acids, 2 mM glutamine, penicillin/streptomycin, 1 mM
sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7
units of LIF per liter. Double-stranded cDNAs were
synthesized with an Oligo(dT) primer [Invitrogen:
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTTTTT-3'] from
2.5 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lona-linker Li-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were double digested with NotI and SalI enzymes,
then purified by phenol/chloroform and centrifuged 100. The
cDNA mixture was subjected to a special subtraction
procedure by Dr. Kazuhiro Kondo at AIGIN Cosmos. Then the
subtracted cDNAs were cloned into SalI/NotI site of
pCMV-SPORT6 plasmid vector. The DH10B E. coli host was
transformed with the ligation mixture by the standard
chemical method. The average insert size is about 2.2kb.
The library was constructed by Yulan Piao and Kazuhiro
Kondo."

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## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 5; Length 641;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1  CAAGTCGAACGGAAGGCCTT 21
        ||||| ||||| ||||| ||||| |||||
Db      468 CAAGTCGAACGGAAGGACTT 498

```

## RESULT 58

```

DVI69729/c
LOCUS      DVI69729      643 bp      mRNA      linear      EST 04-OCT-2005
DEFINITION ZM_BFN0168P08.f_ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION  DVI69729
VERSION     DVI69729.1 GI:76923942
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 643)
Kim,H., Collura,K., Wisotsaki,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
TITLE      Zea Full-length cDNA Project
JOURNAL    Unpublished (2005)
COMMENT    Contact: Yeisoo Yu

```

Arizona Genomics Institute

The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0168 row: P column: 08.

Location/Qualifiers

source

```

1. .643
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot
tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
/notes="Vector: pCMV-SPORT 6.1; Site_1: EcoRV; Site_2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector.
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 day aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 day whole seed; 11. 12 day endosperm and
embryo; 12. 7 day endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA Project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."
```

## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 10; Length 643;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      1  CAAGTCGAACGGAAGGCCTT 21
        ||||| ||||| ||||| ||||| |||||
Db      535 CAAGTCGAACGGAAGGCCTT 515

```

## RESULT 59

```

BF237353
LOCUS      BF237353      647 bp      mRNA      linear      EST 14-NOV-2000
DEFINITION 602035026F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4160215 5',
mRNA sequence.
ACCESSION  BF237353
VERSION     BF237353.1 GI:11151271
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Murinae; Mus.
1 (bases 1 to 647)
NTH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL    Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.

```

Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LHAM9439 row: d column: 08  
 High quality sequence stop: 647.  
 Location/Qualifiers  
 1. 647  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:4160215"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NCI CGAP L19"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 Kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

## FEATURES

source

## ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 647;  
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAAGGCCTT 21

Db 530 CAACTCGAACGTAAGGACTT 550

## RESULT 60

CF898433

LOCUS CF898433 651 bp mRNA linear EST 04-NOV-2003  
 DEFINITION A0239B05-5 NIA Mouse Embryonic Germ Cell cDNA Library (long, subtracted) Mus musculus CDNA clone NIA:A0239B05 IMAGE:30732112 5', mRNA sequence.

ACCESSION CF898433.1 GI:38165482

VERSION EST.

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 651)

AUTHORS Pao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.  
 TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL Genome Res. 11 (9), 1553-1558 (2001)

PUBMED 11544199

COMMENT Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cDNA@gsun.grc.nia.nih.gov

Plate: A0239 row: B column: 05

Seq primer: M13 Reverse

High quality sequence stop: 651

POLYA-No.

Location/Qualifiers

1. 651

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="niaEST:A0239B05-5"

/db\_xref="taxon:10090"

/clone="NIA:A0239B05 IMAGE:30732112"

/sex="male"

## FEATURES

source

/dev\_stage="embryonic day 8"  
 /lab\_host="DH10B"  
 /clone\_lib="NIA Mouse Embryonic Germ Cell cDNA Library (long, subtracted)"  
 /note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://lgsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001)). [PMID: 11544199]. EG cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). EG cells were cultured at 37. C. 5% CO2 in DMEM supplemented with 15% ES cell-qualified FBS, 0.1mM non-essential amino acids, 2 mM glutamine, penicillin/streptomycin, 1 mM sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^-7 units of LIF per liter. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGAGCGCGCCCTTTT-TTTT-3'] from 2.5 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were double digested with NotI and SalI enzymes, then purified by phenol/chloroform and Centricon 100. The cDNA mixture was subjected to a special subtraction procedure by Dr. Kazuhiro Kondo at Aisin Cosmos. Then the subtracted cDNAs were cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.2kb. The library was constructed by Yulan Piao and Kazuhiro Kondo."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 5; Length 651;  
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAAGGCCTT 21

Db 468 CAACTCGAACGTAAGGACTT 488

## RESULT 61

DV023955/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DV023955 680 bp mRNA linear EST 26-SEP-2005  
 ZM\_BFB0143008.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.

DV023955

DV023955.1 GI:76284387

EST.

Ze mays

Ze mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 680)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project

Unpublished (2005)

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0143 row: O column: 08.

Location/Qualifiers

1. 680

## FEATURES

source

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/organism="Zea mays"
/mol_type="mRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM BFB"
/notes="Vector: pCWV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."

```

## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 10; Length 680;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| ||||| |||||
Db 513 CAAGTCGAACGGAAGGCCTT 493

```

```

RESULT 62
CN525338
LOCUS      CN525338      682 bp      mRNA      linear      EST 29-APR-2004
DEFINITION UI-M-HKO-cmw-p-08-0-UI.r1 NIH_BMAP_HKO Mus musculus cDNA clone
IMAGE:30623887 5', mRNA sequence.
ACCESSION  CN525338
VERSION     CN525338.1 GI:46852991
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 682)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. Jim Lin University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
Mammalia Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

```

## FEATURES source

```

Seq primer: pYX-5.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:30623887"
/tissue_type="Upper Head"
/dev_stage="9.5 and 10.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HKO"
/notes="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTCGAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
```

## ORIGIN

```

Query Match      74.2%; Score 17.8; DB 8; Length 682;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
||||| ||||| ||||| ||||| |||||
Db 148 CAAGTCGAACGGAAGGCCTT 168

```

## RESULT 63 DT945027/c

```

LOCUS      DT945027      685 bp      mRNA      linear      EST 21-SEP-2005
DEFINITION ZM_BFB0132B03.f ZM_BFB Zea mays cDNA 3', mRNA sequence.
ACCESSION  DT945027
VERSION     DT945027.1 GI:76017857
KEYWORDS   EST.
SOURCE     Zea mays

```

## ORGANISM

```

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```

## REFERENCE

```

AUTHORS    Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Wallbot,V. and Yu,Y.

```

## TITLE

```

JOURNAL     Maize Full-length cDNA Project
COMMENT     Unpublished (2005)
Contact: Yeisoo Yu

```

## COMMENT

```

Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
Plate: 0132 row: B column: 03.
Location/Qualifiers
1..685
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
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/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"

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## FEATURES

## source





(http://www.genome.arizona.edu/orders/)."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 700;  
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21  
 ||||| ||||| ||||| ||||| |||||  
 Db 363 CAAAGTCGAACGGAAGGCCTT 383

## RESULT 66

DV541234/c

LOCUS DV541234 710 bp mRNA linear EST 25-OCT-2005  
 DEFINITION ZM\_BFB0235018.f\_ZM\_BFB\_Zea mays cDNA 3', mRNA sequence.

ACCESSION DV541234

VERSION DV541234.1 GI:78122850

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

AUTHORS

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,

Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

Maize Full-length cDNA Project

Unpublished (2005)

JOURNAL

COMMENT

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0235 row: O column: 18.

## FEATURES

source

1..710  
 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="mixed (silks, husks, ears, pollen, shoot  
 tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFB"  
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:  
 NotI; Maize Full length cDNA library (3530 library)  
 created by Invitrogen from multiple tissues; Organ: silks,  
 husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector,  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A) + mRNA was  
 prepared by Invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Maize Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona

## ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 710;  
 Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAAGTCGAACGGAAGGCCTT 21  
 ||||| ||||| ||||| ||||| |||||  
 Db 565 CAAAGTCGAACGGAAGGCCTT 545

## RESULT 67

DT654257/c

LOCUS DT654257 711 bp mRNA linear EST 07-SEP-2005  
 DEFINITION ZM\_BFB0127110.f\_ZM\_BFB\_Zea mays cDNA 3', mRNA sequence.

ACCESSION DT654257

VERSION DT654257.1 GI:74246343

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## REFERENCE

AUTHORS

Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,

Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.

Maize Full-length cDNA Project

Unpublished (2005)

JOURNAL

COMMENT

Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: yeisoo@genome.arizona.edu

Plate: 0127 row: I column: 10.

## FEATURES

source

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 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
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 /tissue\_type="mixed (silks, husks, ears, pollen, shoot  
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 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"

/clone\_lib="ZM\_BFB"  
 /note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:  
 NotI; Maize Full length cDNA library (3530 library)  
 created by Invitrogen from multiple tissues; Organ: silks,  
 husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector,  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A) + mRNA was  
 prepared by Invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Maize Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona

(<http://www.genome.arizona.edu/orders/>)

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Query Match          74.2%; Score 17.8; DB 10; Length 714;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CAAGTCGAACGGAAAGGCCTT 21  
|||||  
db 513 CAAGTGGAAACGAAAAGGCCTT 493

RESULT	69
BF099995	
LOCUS	
BF099995	
DEFINITION	601752156F1 NCI CGAP Mam1 Mus musculus cDNA clone IMAGE:3980005 5'
LOCUS	716 bp mRNA linear EST 19-Oct-2000

ACCESSION	BF0999995	1	GT:10882521
VERSION	BF0999995	1	

KEYWORDS	EST.	SOURCE	ORGANISM
	Mus musculus	(house mouse)	
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		

## REFERENCE

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>  
**EDITOR** National Institutes of Health

JOURNAL Unpublished (1999)

CONTACT: ROBERT SCIAUSBERY, FR.  
Email: [cgapps-r@mail.nih.gov](mailto:cgapps-r@mail.nih.gov)

Tissue Procurement: Gilbert Smith

cdna Library Arrayed by: The I

DNA sequencing by: Incyte Genomics  
clone distribution: MGC clone only

found through the I.M.A.G.E. Conference: <http://image111.com>

Plate: LLaM9174 row: 0 column

**FEATURES**

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1. .716  
/organism-11Mus muscu]

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/clone="IMAGE:3980005"
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/dev_stage="3 months, v
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/clone lib="NCI CGAP Ma
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/note="Organ: mammary;
site 3. NotI: cloned "

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Library constructed by

ORIGIN

Quercus Monticola 74 28. 000000 17 0

Best Local Similarity 90.5%; Pred. No.

RECEIVED  
JAN 10 1964  
U.S. DEPARTMENT OF AGRICULTURE  
WASHINGTON, D.C.

QY  
1 CAAGTCGAACGGAAAGGCCTT 21

D<sub>b</sub> 513 CAAGTCGAAGTGAAGGACTT 533

RESULT 70  
PC145033

LOCUS BQ445033 729 bp

IMAGE:5711460 5', mRNA sequence

ACCESSION	BQ445033	
VERSION	BQ445033	1
		CT: 31248145

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KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS
TITLE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15342 row: f column: 19
            High quality sequence stop: 612.

FEATURES
source
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        /strain="C57BL/6"
        /db_xref="taxon:10090"
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        /tissue_type="whole brain"
        /dev_stages="embryo 15.5 dpc"
        /lab_host="DH10B (T1 phage resistant)"
        /clone_lib="NIH BMAP ERO"
        /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTCGCTGAAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN
Query Match      74.2%; Score 17.8; DB 3; Length 729;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACCGAAGGCCTT 21
    |||||
Db 142 CAAGTCGAACCGAAGGCCTT 162

RESULT 71
CO383984
LOCUS      AGNCOURT_26623469 NIH_MGC_253 Rattus norvegicus cDNA clone
DEFINITION IMAGE:7307949 5', mRNA sequence.
ACCESSION CO383984
VERSION    CO383984.1 GI:49489807
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
            1 (bases 1 to 738)

REFERENCE
AUTHORS    Robert Strausberg, Ph.D.
TITLE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

AUTHORS
TITLE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics / NIH
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
            cDNA Library Preparation: Express Genomics
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15342 row: f column: 19
            High quality sequence stop: 612.

FEATURES
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        /db_xref="taxon:10116"
        /clone="IMAGE:7304949"
        /tissue_type="Ovary - Brown Norway Line 3 Age 8 weeks. Tissues were snap-frozen and transferred in -70C. RNase free the entire procedure."
        /lab_host="DH10B Tona"
        /clone_lib="NIH_MGC_253"
        /note="Organ: ovary; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer: 5'-pGACTACTTTCAGTCGCGAGCGCCGCCCTT 25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.5 kb. This primary library is normalized (non-normalized primary library is NIH MGC 252) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN
Query Match      74.2%; Score 17.8; DB 8; Length 738;
Best Local Similarity 90.5%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACCGAAGGCCTT 21
    |||||
Db 202 CAAGTCGAACCGAAGGCCTT 222

RESULT 72
BI414831/c
LOCUS      BI414831
DEFINITION 602990771F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5146936 5', mRNA sequence.
ACCESSION BI414831
VERSION    BI414831.1 GI:15175754
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
            1 (bases 1 to 739)

REFERENCE
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/.
TITLE      NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL    National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11362 row: m column: 17  
High quality sequence start: 23  
High quality sequence stop: 739.

FEATURES  
source

1. 739  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
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/clone="IMAGE:5146936"  
/tissue\_types="pooled lung tumors"  
/lab\_hosts="DH10B (phage-resistant)"  
/clone\_lib="NCI\_CGAP Lu33"  
/notes="Organ: lung; Vector: pT7T3D-PacI; Site 1: NotI;  
Site 2: EcoRI; 1st strand cDNA was prepared from mRNA  
obtained from pooled lung tumors with a Not I - oligo(dT)  
primer [5'-  
TGTACCAATCTGAAGTGGAGCGCGCTCTGTTTTTTTTTTTTTTT 3'].  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization, and was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 74.2%; Score 17.8; DB 2; Length 739;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 708 CAAGTCGAACGGAAGGACT 688  
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RESULT 73  
BX855983/c

LOCUS  
DEFINITION BX855983 tcay Oncorhynchus mykiss cDNA clone tcay0040b.g.16 5prim.  
mRNA sequence.  
BX855983  
BX855983 2 GI:42752904  
EST.

ORGANISM

Oncorhynchus mykiss (rainbow trout)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

1 (bases 1 to 740)  
Govoroun,M., Guiguen,Y. and Le Gac,F.  
Construction and primary characterization of normalized cDNA  
libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
On Dec 16, 2003 this sequence version replaced gi:39952993.

COMMENT

Contact: Guiguen Y  
INRA - SCRIBE  
Campus de Beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20

Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us  
at [sigenasupport@jouy.inra.fr](mailto:sigenasupport@jouy.inra.fr) to obtain the chromatogram of this  
sequence.

Seq primer: M13R. Location/Qualifiers

FEATURES  
source

1. 740  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"

/db\_xref="taxon:8022"  
/clone="tcay0040b.g.16"  
/tissue\_type="adipose tissue, blood, brain,  
differentiating gonads, gills, interrenal, intestine,  
kidney, liver, muscle, ovary, pituitary, testis"  
/dev\_stage="from embryos to adults"  
/lab\_host="DH10B"  
/clone\_lib="tcay"  
/note="Vector: pT7T3D-PacI; Rainbow trout multi-tissues -  
normalized + 1 subtraction (tcay); Clone distribution:  
AGENAE Resource centre. Francois PIUMI,  
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et  
Etude du genome (LREG), Domaine de Vilvert, 78352,  
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33  
(0) 1.34.65.22.73"

ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 740;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 552 CACGTCGACAGAAAGGCCTT 532  
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RESULT 74

BY732037

LOCUS

DEFINITION BY732037 RIKEN full-length enriched, 8 cells embryo Mus musculus  
cDNA clone E860117P18 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AUTHORS

REFERENCE

1 (bases 1 to 745)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusci,V.,

Chothia,C., Corbani,L.E., Cousins,S., Dalia,E., Dragani,I.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gough,J., Grimmond,S.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Jarvis,E.D., Kanai,A.,

Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,

Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,

Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,

Uvarov,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y.,

Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,

Yell,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,

Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y.,

Itoh,M., Kigawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,

Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,

Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

JOURNAL

PUBLISHED

COMMENT

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Tel: 81-45-503-9222  
Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
Fukuda, S., Hashizume, W., Hayaashida, K., Hirozane, T., Hori, F.,  
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
Nomura, K., Numazaki, R., Onno, M., Oheato, N., Saito, R., Sakazume, N.,  
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

#### FEATURES

source  
1. .745  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="E860117P18"  
/cell\_type="8 cells"  
/dev\_stage="8 cells embryo"  
/clone\_lib="RIKEN full-length enriched, 3 cells embryo"

#### ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 745;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 368 CAAGTCGAACGGAAGGACTT 388

#### RESULT 75

DV942547/c 746 bp mRNA linear EST 05-DEC-2005  
LOCUS  
DEFINITION  
ACCESSION DV942547  
VERSION DV942547.1 GI:83278539  
KEYWORDS EST.

source  
Zea mays  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 746)

Zhou, R.L., Shendelman, J.M., Borsuk, L.A., Chen, H.D., Chen, Y.R. and  
Schnable, P.S.

Resequencing Unigene I EST set  
JOURNAL  
Unpublished (2005)  
Contact: Patrick S. Schnable  
Schnable Laboratory  
Iowa State University

2035B R.J. Carver Co-Lab, Ames, IA 50011-3650, USA  
Tel: 515-294-0975  
Fax: 515-294-5256  
Email: schnable@iastate.edu

Insert Length: 746 Std Error: 0.00.  
Location/Qualifiers  
1. .746

/organism="Zea mays"  
/mol\_type="mRNA"  
/db\_xref="taxon:4577"  
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#### ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 746;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 613 CAAGTCGAACGGAAGGCCTT 593

#### RESULT 76

DR794419/c 752 bp mRNA linear EST 27-JUL-2005  
LOCUS  
DEFINITION ZM BF50015C05.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DR794419

VERSION DR794419.1 GI:71315610  
KEYWORDS EST.

source  
Zea mays  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 752)

Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C.,  
Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Veisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: veisoo@genome.arizona.edu  
Plate: 0015 row: C column: 05.

#### FEATURES

source  
1. .752  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot  
tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BPB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:  
NotI; Maize Full length cDNA library (3530 library)  
created by invitrogen from multiple tissues; Organ: silks,  
husks, ears, pollen, shoot tips, leaf, root tips, whole  
seed, embryo. This is a Gateway compatible vector,  
permitting clone movement to new vector backbones for  
expression in diverse host cells using recombination  
rather than restriction enzymes. poly(A) + mRNA was  
prepared by invitrogen, and equimolar amounts of RNA from  
each of the 12 tissue samples were mixed together for  
a normalization step was conducted against the mixture of  
RNA sources. Tissues prepared: 1. just emerging silks; 2.  
inner husks from ears of sample #1; 3. 20 day aleurone; 4.  
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to



2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/).

## ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 777;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
||||| ||||| ||||| ||||| |||||  
Db 535 CAAGTGAACGGAAGGCCTT 515

## RESULT 79

DR954333/c  
LOCUS DR954333 777 bp mRNA linear EST 03-AUG-2005  
DEFINITION ZM\_BFD0046F03.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DR954333  
VERSION DR954333.1 GI:71756396  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 777)  
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
Plate: 0046 row: F column: 03.

## FEATURES

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/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV, Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/).

## ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 777;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
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Db 535 CAAGTGAACGGAAGGCCTT 515

## RESULT 80

DV164117/c  
LOCUS DV164117 780 bp mRNA linear EST 04-OCT-2005  
DEFINITION ZM\_BFD0160H01.f ZM\_BFB Zea mays cDNA 3', mRNA sequence.  
ACCESSION DV164117  
VERSION DV164117.1 GI:76910962  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 780)  
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
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## FEATURES

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/mol\_type="mRNA"  
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/db\_xref="taxon:4577"  
/tissue\_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"  
/dev\_stage="varies by tissue"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM BFB"  
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV, Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to

2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

## ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 780;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
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Db 510 CAAGTCGAACGGAAGGCCTT 490

RESULT 81  
CB953248  
LOCUS  
DEFINITION  
AGENCOURT 13687210 NIH\_MGC\_176 Mus musculus cDNA clone  
IMAGE:30304304 5', mRNA sequence.

ACCESSION  
CB953248  
VERSION  
CB953248.1 GI:30209366  
KEYWORDS  
EST.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 808)  
NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgabs@mail.nih.gov](mailto:cgabs@mail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Michael Brownstein Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

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High quality sequence stop: 477.

## FEATURES

## source

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/clone="IMAGE:30304304"  
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/clone\_lib="NIH\_MGC\_176"

/notes="Organ: kidney; Vector: pDNR-LIB; Site:1: Sfii (ggccattggcc); Site:2: Sfii (ggccgctcgcc); cDNA made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:

5'-AACGAGTGGTATCAACGACAGTGGCCATTACGCGCGG-3' and  
5'-ATCTAGAGCCGAGCGGCGGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 74.2%; Score 17.8; DB 4; Length 808;  
Best Local Similarity 90.5%; Pred. No. 1.5e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
||||| ||||| ||||| ||||| |||||  
Db 394 CAAGTCGAACGGAAGGCCTT 414

## RESULT 82

## DR794420

## LOCUS

## DEFINITION

## ACCESSION

## DR794420

## VERSION

## DR794420.1 GI:71315611

## KEYWORDS

## EST.

## SOURCE

## Zea mays

## ORGANISM

## Zea mays

## Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

## 1 (bases 1 to 816)

## Kim, H., Collura, K., Wissotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

## Maize Full-length cDNA Project

## Unpublished (2005)

## Contact: Yeisoo Yu

## Arizona Genomics Institute

## The University of Arizona

## Forbes Building Room 303, Tucson, AZ 85721-0036, USA

## Tel: 520 626 9585

## Fax: 520 621 1259

Email: [yeisoo@genome.arizona.edu](mailto:yeisoo@genome.arizona.edu)

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## FEATURES

## source

Location/Qualifiers  
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/organism="Zea mays"  
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/notes="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>).

## ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 816;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;



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Qy 1 CAAAGTCGAACGGAAGGCCTT 21
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Db 776 CAAAGTCGAACGGAAGGCCTT 796

RESULT 83
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DEFINITION ZM_BF00160P07.r_ZM_BFb Zea mays cDNA 5', mRNA sequence.
ACCESSION DV164477
VERSION DV164477.1 GI:76911880
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 820)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)
Contact: Yeisoo Yu
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9585
Fax: 520 621 1259
Email: yeisoo@genome.arizona.edu
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/clone_lib="ZM_BFb"
/note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2:
NotI; Maize Full length cDNA library (3530 library)
created by Invitrogen from multiple tissues; Organ: silks,
husks, ears, pollen, shoot tips, leaf, root tips, whole
seed, embryo. This is a Gateway compatible vector.
permitting clone movement to new vector backbones for
expression in diverse host cells using recombination
rather than restriction enzymes. poly(A)+ mRNA was
prepared by Invitrogen, and equimolar amounts of RNA from
each of the 12 tissue samples were mixed together for
a selection of mRNA with a 5' cap. After synthesis of cDNA,
a normalization step was conducted against the mixture of
RNA sources. Tissues prepared: 1. just emerging silks; 2.
inner husks from ears of sample #1; 3. 20 dap aleurone; 4.
immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to
2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from
15 day old seedlings; all leaves with an expanded or
partially expanded sheath were removed; 8. mature leaf
tissue; 9. 0.5 cm long root tips from 15 day old
seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and
embryo; 12. 17 dap endosperm and embryo. All of the
sequenced clones in Maize Full-length cDNA project will be
archived at the University of Arizona. Clones, high
density filters and amplified library can be ordered from
the University of Arizona
(http://www.genome.arizona.edu/orders/)."

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 820;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


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Qy 1 CAAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 776 CAAAGTCGAACGGAAGGCCTT 796

RESULT 84
LOCUS DY361640 824 bp mRNA linear EST 09-FEB-2005
DEFINITION ZO_Ed0007M16.r_ZO_Ed Zingiber officinale cDNA clone ZO_Ed0007M16
3' mRNA sequence.
ACCESSION DY361640
VERSION DY361640.1 GI:87094856
KEYWORDS EST.
SOURCE Zingiber officinale
ORGANISM Zingiber officinale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
Zingiberaceae; Zingiber.
1 (bases 1 to 824)
Ma,X.Q., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
Comparative Analysis of Expressed Sequence Tags from Different
Organs of Ginger and Turmeric. Insights into Specialized Metabolism
in Traditional Medicinal Plants
Unpublished (2006)
Contact: David R. Gang
Department of Plant Sciences
The University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 621 7154
Fax: 520 621 7186
Email: gang@ag.arizona.edu
Plate: 0007 row: M column: 16.
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1..824
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Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTTTC 23
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Db 337 AGACGAACGGAAGGCCTTTC 357

RESULT 85
LOCUS DR786718 827 bp mRNA linear EST 27-JUL-2005
DEFINITION ZM_BF0003M18.r_ZM_BFb Zea mays cDNA 5', mRNA sequence.
ACCESSION DR786718
VERSION DR786718.1 GI:71301367
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 827)
Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C.,
Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.
Maize Full-length cDNA Project
Unpublished (2005)

ORIGIN
Query Match 74.2%; Score 17.8; DB 10; Length 820;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
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Location/Qualifiers

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/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="ZM\_BFB"  
/notes="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (<http://www.genome.arizona.edu/orders/>)."

FEATURES

source

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ORIGIN
Query Match          74.2%; Score 17.8; DB 10; Length 848;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  CAAGTCGAACGGAAAGGCCTT 21
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Db      777  CAAAGTGAACGAAAGGCCTT 797

RESULT 87
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LOCUS   B03290184F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5324391 5';
DEFINITION linear
EST 12-SEP-2001
BI664538 856 bp mRNA
BI664538.1 GI:15578771
ACCESSION BI664538
VERSION   BI664538
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 856)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
REFERENCE
AUTHORS
TITLE
JOURNAL

```

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COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: Jeffrey Green M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Inyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
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                Library constructed by Life Technologies. Investigator
                providing samples: Jeffrey Green, M.D., NIH"

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    Library constructed by Life Technologies. Investigator
    providing samples: Jeffrey Green, M.D., NIH"

ORIGIN
Query Match      74.2%; Score 17.8; DB 2; Length 856;
Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTT 21
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Db      331 CAAGTCGAACGGAAGGCCTT 351
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RESULT 89
BU522312
LOCUS      BU522312      862 bp      mRNA      linear      EST 25-SEP-2003
DEFINITION AGNCOURT_15585358 NIH_MGC_222 Mus musculus cDNA clone
IMAGE:30526004 5', mRNA sequence.
ACCESSION  CF551692
VERSION     CF551692
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE   1 (bases 1 to 862)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Daniela S. Gerhard, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Naryan Bhat
            cDNA Library Preparation: Express Genomics
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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    Library constructed by Life Technologies. Investigator
    providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match      74.2%; Score 17.8; DB 5; Length 862;
Best Local Similarity 90.5%; Pred. NO. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTT 21
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Db      331 CAAGTCGAACGGAAGGCCTT 351
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RESULT 89
BU522312
LOCUS      BU522312      874 bp      mRNA      linear      EST 13-SEP-2002
DEFINITION AGNCOURT_10152472 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6528688 5', mRNA sequence.
ACCESSION  BU522312
VERSION     BU522312
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE   1 (bases 1 to 874)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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              Library constructed by Life Technologies. Investigator
              providing samples: Gilbert Smith, NIH"

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    Library constructed by Life Technologies. Investigator
    providing samples: Gilbert Smith, NIH"

ORIGIN

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Query Match 74.2%; Score 17.8; DB 3; Length 874;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21  
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Db 550 CAAGTCGAACGGAAGGACTT 570

RESULT 90  
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DEFINITION  
ACCESSION DT942318  
VERSION DT942318.1 GI:76015148  
KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Kim,H., Collura,K., Wissotski,M., Smart,D., Kudrna,D., Muller,C., Rao,K., Haller,K., Wing,R., Soderlund,C., Walbot,V. and Yu,Y.  
TITLE Maize Full-length cDNA Project  
JOURNAL Unpublished (2005)  
COMMENT Contact: Yeisoo Yu  
Arizona Genomics Institute  
The University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9585  
Fax: 520 621 1259  
Email: yeisoo@genome.arizona.edu  
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/note="Vector: pCMV-SPORT 6.1; Site\_1: EcoRV; Site\_2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues; Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A)+ mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona  
(http://www.genome.arizona.edu/orders/)."

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ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 891;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 794 CAAGTCGAACGGAAGGCCTT 814

RESULT 91  
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DEFINITION  
ACCESSION BE367787  
VERSION BE367787.1 GI:9313059  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 894)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapps-f@mail.nih.gov  
Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLAM8748 row: 0 column: 01  
High quality sequence stop: 679.  
Location/Qualifiers  
1 .894  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3586776"  
/tissue\_type="spontaneous tumor, metastatic to mammary. Stem cell origin."  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Lu29"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

FEATURES  
source  
1 .894  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="Czech II"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3586776"  
/tissue\_type="spontaneous tumor, metastatic to mammary. Stem cell origin."  
/lab\_host="DH10B"  
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/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 74.2%; Score 17.8; DB 7; Length 894;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 507 CAAGTCGAACGGAAGGACTT 527

RESULT 92  
BQ944677  
LOCUS AGENCOURT\_8933003 NCI CGAP\_Mam2 Mus musculus cDNA clone IMAGE:6488886 5', mRNA sequence.  
DEFINITION  
ACCESSION BQ944677  
VERSION BQ944677.1 GI:22360155  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 906)  
AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LHAM14036 row: d column: 07  
High quality sequence stop: 639.  
Location/Qualifiers

#### FEATURES

source

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1..906
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
/db_xref="taxon:10090"
/clone="IMAGE:648886"
/tissue_type="tumor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam2"
note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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#### ORIGIN

Query Match 74.2%; Score 17.8; DB 3; Length 906;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21  
|||||  
Db 92 CAAGTCGAACGGAAGGCGCTT 112

#### RESULT 93

DR815819  
LOCUS  
ZM\_BF00046F03.r ZM\_BFB Zea mays cDNA 5', mRNA linear EST 28-JUL-2005  
DEFINITION  
DR815819  
VERSION  
DR815819.1 GI:71434769  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
1 (bases 1 to 912)  
AUTHORS  
Kim, H., Collura, K., Wisotski, M., Smart, D., Kudrna, D., Muller, C., Rao, K., Haller, K., Wang, R., Soderlund, C., Walbot, V. and Yu, Y.

Maize Full-length cDNA Project  
Unpublished (2005)  
Contact: Yeisoo Yu

Arizona Genomics Institute

The University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9585

Fax: 520 621 1259

Email: [yeisoo@genome.arizona.edu](mailto:yeisoo@genome.arizona.edu)

Plate: 0046 row: F column: 03.

#### FEATURES

source

```
1..912
/organism="Zea mays"
/mol_type="mRNA"
```

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/cultivar="B73"
/db_xref="taxon:4577"
/tissue_type="mixed (silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo)"
/dev_stage="varies by tissue"
/lab_hosts="DH10B T1 phage resistant"
/clone_lib="ZM_BFB"
note="Vector: pCMV-SPORT 6.1; Site 1: EcoRV; Site 2: NotI; Maize Full length cDNA library (3530 library) created by Invitrogen from multiple tissues: Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of cDNA, a normalization step was conducted against the mixture of RNA sources. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in Maize Full-length cDNA Project will be archived at the University of Arizona. Clones, high density filters and amplified library can be ordered from the University of Arizona (http://www.genome.arizona.edu/orders/)."
```

#### ORIGIN

Query Match 74.2%; Score 17.8; DB 10; Length 912;  
Best Local Similarity 90.5%; Pred. No. 1.6e+03;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21  
|||||  
Db 775 CAAGTCGAACGGAAGGCGCTT 795

#### RESULT 94

BG247267  
LOCUS  
602360162F1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:4488711 5', mRNA sequence.  
DEFINITION  
BG247267  
VERSION  
BG247267.1 GI:12757082  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 918)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHAM10335 row: k column: 16

High quality sequence stop: 667.

Location/Qualifiers

#### FEATURES

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source
1. .918
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4488711"
/tissue_types="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mam1"
/notes="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN
Query Match 74.2%; Score 17.8; DB 2; Length 918;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 531 CAAGTCGAACGGAAGGACTT 551

RESULT 95
LOCUS DV062398 945 bp mRNA linear EST 27-SEP-2005
DEFINITION NEONATAL_12_F04.x1 FH NEONATAL Mus musculus cDNA clone
NEONATAL_12_F04 similar to COP9 (constitutive photomorphogenic)
homolog subunit 7a (Arabidopsis thaliana), mRNA sequence.
ACCESSION DV062398
VERSION DV062398.1 GI:76389696
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 945)
Nelson,P.S., Pritchard,C., Abbott,D.E. and Clegg,N.
The human (PEDB) and mouse (mPEDB) Prostate Expression Databases
Nucleic Acids Res. 30 (1), 218-220 (2002)
11752298
PUBMED
COMMENT Contact: Nelson PS
Peter Nelson Lab, Department of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Ave N D4-100, Seattle, WA 98109, USA
Fax: 206 667 2917
Email: pnelson@fhcrc.org
Insert Length: 945 Std Error: 0.00
High quality sequence start: 23
High quality sequence stop: 663.
Location/Qualifiers
1. .945
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="NEONATAL_12_F04"
/sex="Male"
/tissue_types="Equal amounts of pooled ventral prostate, dorsolateral prostate, and coagulating gland (anterior prostate)"
/lab_host="BM25.8"
/clone_lib="FH NEONATAL"
/notes="Organ: prostate; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; Library was constructed using Clontechs SMART cDNA library construction kit. 0.1ug of total RNA from pooled 2-day dorsolateral prostate, 0.1ug of total RNA from pooled 2-day ventral prostate, and 0.1ug of total RNA from pooled 2-day coagulating gland (anterior prostate) was combined and used in 1st strand cDNA synthesis. 2nd strand cDNA was generated by 23 cycles of PCR, digested with SfiI and ligated into the lambdaTriplex2 phagemid. Phagemids were converted to pTriplex2 plasmids in the BM25.8 e-coli strain. Created from pooled prostate from five two day old male C57BL/6 mice by Colin Pritchard."

source
1. .995
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-28J13"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis BAC library"

ORIGIN
Query Match 74.2%; Score 17.8; DB 12; Length 995;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCCTT 22
|||||
Db 773 AAGTGAACAGAAAGGCCTT 793

RESULT 97
LOCUS DR045951/c 1199 bp mRNA linear EST 02-JUN-2005
DEFINITION FP-11_G06.SFQ cDNA library of Phaeosphaeria nodorum grown on wheat cell walls Phaeosphaeria nodorum cDNA, mRNA sequence.
ACCESSION DR045951
```

```

VERSION DR045951.1 GI:66909787
SOURCE EST.
ORGANISM Phaeosphaeria nodorum
Phaeosphaeria nodorum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Phaeosphaeriaceae; Phaeosphaeria.
REFERENCE 1 (bases 1 to 1199)
AUTHORS Bindeshdler,L.V., Cooper,R.M., Thomas,S.W., Madrid,M.P. and
Oliver,R.P.
TITLE cDNA library of Phaeosphaeria nodorum grown on wheat cell walls
JOURNAL Unpublished (2005)
COMMENT Contact: Richard Oliver
Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)
Murdoch University
South Street, Murdoch, W.A 6150, Australia
Tel: +0893607404
Email: roliver@murdoch.edu.au.
FEATURES source
1..1199
/organism="Phaeosphaeria nodorum"
/mol_type="mRNA"
/db_xref="taxon:13684"
/clone_lib="cDNA library of Phaeosphaeria nodorum grown on
wheat cell walls"

ORIGIN
Query Match 74.2%; Score 17.8; DB 9; Length 1199;
Best Local Similarity 90.5%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
|||||
Db 489 CAAGTCGAACGGAAGGCCTT 469

RESULT 98
AA204210 193 bp mRNA linear EST 27-JAN-1997
DEFINITION mu60h11.r1 Soares mouse lymph node NbMLN Mus musculus cDNA clone
IMAGE:643845 5', mRNA sequence.
ACCESSION AA204210
VERSION AA204210.1 GI:1800807
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
REFERENCE 1 (bases 1 to 193)
AUTHORS Maizra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HHMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LInL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MG1:395837
Purative full length read
vector to vector length is 242
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 133.
FEATURES source
1..193
/organism="Mus musculus"

/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:643845"
/sex="male"
/tissue_type="lymph node"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares mouse lymph node NbMLN"
I; Site 2; Eco RI; 1st strand cDNA was primed with a Not I
oligo(dnt) primer [5',
TGTACCAATCTGAAGTGGGAGCGCGCGATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTZ19 vector. RNA
provided by Dr. Bertrand Jordan. Library constructed and
normalized by Bento Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 73.3%; Score 17.6; DB 1; Length 193;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
|||||
Db 85 CAAGTCGAGCAGAAAGTCCTTACG 108

RESULT 99
BQ322138 233 bp mRNA linear EST 17-MAY-2002
DEFINITION PM3-CT0817-240501-007-d02 CT0817 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ322138
VERSION BQ322138.1 GI:20931368
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 233)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-CT0817-
240501-007-d02&t3=2001-05-24&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 232.
FEATURES source
1..233
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

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/clone lib="CT0817"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match      73.3%; Score 17.6; DB 3; Length 233;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTCG 24
        ||||| ||||| ||||| ||||| |||||
Db      154 CAAGTCGAATGAAGGACTGTCG 177

RESULT 100
LOCUS      AV366949          239 bp      mRNA      linear      EST 14-NOV-1999
DEFINITION AV366949 RIKEN full-length enriched, 16 days embryo lung Mus
            musculus cDNA clone 8430426E07 3', mRNA sequence.
ACCESSION   AV366949
VERSION     AV366949.1 GI:6414596
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Mus.
            1 (bases 1 to 239)
            Konno.H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F.,
            Iehii,Y., Iehikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tomihaga,N.,
            Tanoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Konno,H., et al. 1999)
            Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
FEATURES             Location/Qualifiers
     source           1..239
                     /Organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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GenCore version 5.1.8  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 73.4458 Seconds  
 (without alignments)  
 611.425 Million cell updates/sec

Title: US-10-665-708-22

Perfect score: 24

Sequence: 1 caagtcgaacggaagccttcg 24

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 300 summaries

Database : Issued Patents NA.\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PTUS\_COMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	US-09-738-274-22	Sequence 22, Appl
2	24	100.0	25	US-09-738-274-21	Sequence 21, Appl
3	21	87.5	22	US-09-738-274-23	Sequence 23, Appl
4	20.8	86.7	1584	US-09-949-230A-1	Sequence 1, Appl
5	20.4	85.0	32	US-09-738-972-7	Sequence 7, Appl
6	20.4	85.0	32	US-09-738-972-7	Sequence 14, Appl
7	20	83.3	1475	US-08-641-291A-92	Sequence 92, Appl
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9	19.2	80.0	1471	US-10-085-871C-2	Sequence 2, Appl
10	19.2	80.0	1488	US-10-756-683B-1	Sequence 1, Appl
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c 136	15.2	63.3	601	3	US-09-949-016-169844	Sequence 169844, A	c 209	15	62.5	1131	3	US-09-420-211-1	Sequence 1, Appl
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c 139	15.2	63.3	1017	3	US-08-957-351-5	Sequence 5, Appl	c 212	15	62.5	1532	3	US-09-118-324-1	Sequence 1, Appl
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c 142	15.2	63.3	1223	3	US-08-957-351-29	Sequence 29, Appl	c 215	15	62.5	1710	3	US-09-533-559-5520	Sequence 5520, Ap
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c 146	15.2	63.3	2340	3	US-09-495-050A-215	Sequence 215, App	c 219	15	62.5	2260	3	US-09-976-594-91	Sequence 91, Appl
c 147	15.2	63.3	3405	4	US-10-184-419-35	Sequence 35, Appl	c 220	15	62.5	2969	3	US-09-976-594-739	Sequence 739, App
c 148	15.2	63.3	4064	3	US-10-209-792-1	Sequence 1, Appl	c 221	15	62.5	3152	3	US-09-221-017B-931	Sequence 931, App
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c 150	15.2	63.3	4614	3	US-09-912-165-17	Sequence 17, Appl	c 223	15	62.5	37615	3	US-09-620-312D-330	Sequence 330, App
c 151	15.2	63.3	4657	3	US-09-364-707A-18	Sequence 18, Appl	c 224	15	62.5	7657	3	US-09-620-312D-353	Sequence 353, App
c 152	15.2	63.3	4657	3	US-09-912-165-18	Sequence 18, Appl	c 225	15	62.5	8461	3	US-09-949-016-13428	Sequence 13428, A
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c 162	15.2	63.3	46819	3	US-10-114-170-72	Sequence 72, Appl	c 235	15	62.5	110403	3	US-09-949-016-12741	Sequence 12741, A
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c 280 14.6 60.8 197 3 US-09-621-976-16001
c 281 14.6 60.8 198 3 US-09-621-976-16000
c 282 14.6 60.8 203 3 US-09-621-976-15993
c 283 14.6 60.8 204 5 US-09-974-300-4209
c 284 14.6 60.8 269 3 US-09-513-999C-24178
c 285 14.6 60.8 306 3 US-09-199-637A-2
c 286 14.6 60.8 315 3 US-09-710-279-1777
c 287 14.6 60.8 331 3 US-10-004-115B-18
c 288 14.6 60.8 362 3 US-09-513-999C-710
c 289 14.6 60.8 369 3 US-09-199-637A-4
c 290 14.6 60.8 417 3 US-09-252-991A-3429
c 291 14.6 60.8 428 5 US-09-974-300-3023
c 292 14.6 60.8 439 3 US-09-585-173B-27
c 293 14.6 60.8 474 3 US-09-513-999C-715
c 294 14.6 60.8 476 3 US-09-513-999C-714
c 295 14.6 60.8 561 3 US-09-199-637A-6
c 296 14.6 60.8 566 3 US-09-735-271-1284
c 297 14.6 60.8 576 3 US-09-710-279-1339
c 298 14.6 60.8 579 3 US-09-199-637A-8
c 299 14.6 60.8 579 3 US-09-252-991A-9991
300 14.6 60.8 601 3 US-09-949-016-58488
```

## ALIGNMENTS

## RESULT 1

```
US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
```

```
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22
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Query Match 100.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
| | | | | | | | | | | | | | | |
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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## RESULT 2

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US-09-738-274-21
; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-21
```

```
Query Match 100.0%; Score 24; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
| | | | | | | | | | | | | | | |
Db 2 CAAGTCGAACGGAAGGCGCTTTCG 25
```

## RESULT 3

```
US-09-738-274-23
; Sequence 23, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
```

; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-23

Query Match 87.5%; Score 21; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GTCGACGGAAGGCCTTTCG 24  
|||||  
DB 1 GTCGACGGAAGGCCTTTCG 21

RESULT 4  
US-09-949-230A-1  
; Sequence 1, Application US/09949230A  
; Patent No. 6551591  
; GENERAL INFORMATION:  
; APPLICANT: Essential Therapeutics, Inc.  
; TITLE OF INVENTION: New Antibiotics for Microbispora  
; FILE REFERENCE: 262/095  
; CURRENT APPLICATION NUMBER: US/09/949,230A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1584  
; TYPE: DNA  
; ORGANISM: Microbispora corallina  
; FEATURE:  
; NAME/KEY: n  
; LOCATION: (1350)..(1584)  
; OTHER INFORMATION: Unsure  
; NAME/KEY: misc feature  
; LOCATION: (1350)..(1584)  
; OTHER INFORMATION: Unsure  
US-09-949-230A-1

Query Match 86.7%; Score 20.8; DB 3; Length 1584;  
Best Local Similarity 91.7%; Pred. No. 0.96; Indels 2; Gaps 0;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTTCG 24  
|||||  
DB 125 CAAGTCGAGCGGAAGGCCTTTCG 148

RESULT 5  
US-09-738-972-7  
; Sequence 7, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972

; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: primer  
US-09-738-972-7

Query Match 85.0%; Score 20.4; DB 3; Length 32;  
Best Local Similarity 95.5%; Pred. No. 0.67; Indels 1; Gaps 0;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
|||||  
DB 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 6  
US-09-738-972-14/c  
; Sequence 14, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: probe  
US-09-738-972-14

Query Match 85.0%; Score 20.4; DB 3; Length 32;  
Best Local Similarity 95.5%; Pred. No. 0.67; Indels 1; Gaps 0;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
|||||  
DB 31 CAAGTCGAACGGAAGGCCTCT 10

RESULT 7  
US-08-641-291A-92  
; Sequence 92, Application US/08641291A  
; Patent No. 6037122  
; GENERAL INFORMATION:  
; APPLICANT: MABILAT Claude  
; APPLICANT: RUMY Raymond  
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERIUM  
; NUMBER OF SEQUENCES: 92  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oliff & Berridge  
; STREET: 700 South Washington Street, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22314

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release # 1.0, version # 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,291A
; FILING DATE: 30-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38273
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1475 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; US-08-641-291A-92

Query Match      83.3%; Score 20; DB 3; Length 1475;
Best Local Similarity 90.0%; Pred. No. 2.4;
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20
Db 25 CAAGUCGAACGGAAGGCCU 44

RESULT 8
US-10-085-871C-1
; Sequence 1, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin u
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442
US-10-085-871C-1

Query Match      80.0%; Score 19.2; DB 3; Length 1437;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 31 CAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 9
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
```

```
; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin u
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-085-871C-2

Query Match      80.0%; Score 19.2; DB 3; Length 1471;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 31 CAAGTCGAGCGGTAAGGCCCTTCG 54

RESULT 10
US-10-756-683B-1
; Sequence 1, Application US/10756683B
; Patent No. 7022875
; GENERAL INFORMATION:
; APPLICANT: Hwang, Byung Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: THIIBUTACIN AND ANTIFUNGAL AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756,683B
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KR 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683B-1

Query Match      80.0%; Score 19.2; DB 5; Length 1488;
Best Local Similarity 87.5%; Pred. No. 6.1;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
Db 43 CAAGTCGAGCGGTAAGGCCCTTCG 66

RESULT 11
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
```

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; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match          79.2%; Score 19; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 12
US-09-463-618A-1
; Sequence 1, Application US/09463618A
; Patent No. 6368835
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/09/463.618A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-09-463-618A-1

Query Match          79.2%; Score 19; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 39 CAAGTCGAACGGAAGGCC 57

RESULT 13
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062.777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; NAME/KEY: unsure
; FEATURE:
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          79.2%; Score 19; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
Db 39 CAAGTCGAACGGAAGGCC 57

RESULT 14
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          78.3%; Score 18.8; DB 3; Length 32;
Best Local Similarity 90.9%; Pred. No. 4.3;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCCTTT 22
Db 2 CAAGTCGAACGGAAGGCTCTCT 23

RESULT 15
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; TITLE OF INVENTION: Specific Sequence of the Mycobacterium 16S rRNA Gene
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-938-858-1

Query Match 78.3%; Score 18.8; DB 2; Length 1464;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTT 22
| | | | | | | | | | | | | | | | | |
Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 16
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match 78.3%; Score 18.8; DB 3; Length 1464;
Best Local Similarity 90.9%; Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTT 22
| | | | | | | | | | | | | | | | | |
Db 21 CAAGTCGAACGGAAGGCTCT 42

RESULT 17
US-08-311-731A-134/c
; Sequence 134, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
```

```
;
; ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36241 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
US-08-311-731A-134

Query Match 78.3%; Score 18.8; DB 3; Length 36241;
Best Local Similarity 90.9%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTT 22
| | | | | | | | | | | | | | | | | |
Db 3940 CAAGTCGAACGGAAGGCTCT 3919

RESULT 18
US-08-311-731A-123/c
; Sequence 123, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESS: WOLF, GREENFIELD & SACKS, P.C.
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
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; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36470 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
;
US-08-311-731A-123

Query Match 78.3%; Score 18.8; DB 3; Length 36470;
Best Local Similarity 90.9%; Pred. No. 19;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 36187 CAAGTCGAACGGAAGGCTCT 36166

RESULT 19
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 78.3%; Score 18.8; DB 3; Length 4403765;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 1471428 CAAGTCGAACGGAAGGCTCT 1471449

RESULT 20
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 78.3%; Score 18.8; DB 3; Length 4411529;
Best Local Similarity 90.9%; Pred. No. 50;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
Db 1471904 CAAGTCGAACGGAAGGCTCT 1471925

RESULT 21
US-09-738-274-24
; Sequence 24, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match 75.0%; Score 18; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GAACGGAAGGCCTTTCG 24
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 22
US-09-149-476-59
; Sequence 59, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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1	EARLIER	FILING DATE:	1997-03-07
2	EARLIER	APPLICATION NUMBER:	60/038,621
3	EARLIER	FILING DATE:	1997-03-07
4	EARLIER	APPLICATION NUMBER:	60/040,626
5	EARLIER	FILING DATE:	1997-03-07
6	EARLIER	APPLICATION NUMBER:	60/040,334
7	EARLIER	FILING DATE:	1997-03-07
8	EARLIER	APPLICATION NUMBER:	60/040,336
9	EARLIER	FILING DATE:	1997-03-07
10	EARLIER	APPLICATION NUMBER:	60/040,163
11	EARLIER	FILING DATE:	1997-03-07
12	EARLIER	APPLICATION NUMBER:	60/047,600
13	EARLIER	FILING DATE:	1997-05-23
14	EARLIER	APPLICATION NUMBER:	60/047,615
15	EARLIER	FILING DATE:	1997-05-23
16	EARLIER	APPLICATION NUMBER:	60/047,597
17	EARLIER	FILING DATE:	1997-05-23
18	EARLIER	APPLICATION NUMBER:	60/047,502
19	EARLIER	FILING DATE:	1997-05-23
20	EARLIER	APPLICATION NUMBER:	60/047,633
21	EARLIER	FILING DATE:	1997-05-23
22	EARLIER	APPLICATION NUMBER:	60/047,583
23	EARLIER	FILING DATE:	1997-05-23
24	EARLIER	APPLICATION NUMBER:	60/047,617
25	EARLIER	FILING DATE:	1997-05-23
26	EARLIER	APPLICATION NUMBER:	60/047,618
27	EARLIER	FILING DATE:	1997-05-23
28	EARLIER	APPLICATION NUMBER:	60/047,503
29	EARLIER	FILING DATE:	1997-05-23
30	EARLIER	APPLICATION NUMBER:	60/047,592
31	EARLIER	FILING DATE:	1997-05-23
32	EARLIER	APPLICATION NUMBER:	60/047,500
33	EARLIER	FILING DATE:	1997-05-23
34	EARLIER	APPLICATION NUMBER:	60/047,587
35	EARLIER	FILING DATE:	1997-05-23
36	EARLIER	APPLICATION NUMBER:	60/047,492
37	EARLIER	FILING DATE:	1997-05-23
38	EARLIER	APPLICATION NUMBER:	60/047,598
39	EARLIER	FILING DATE:	1997-05-23
40	EARLIER	APPLICATION NUMBER:	60/047,613
41	EARLIER	FILING DATE:	1997-05-23
42	EARLIER	APPLICATION NUMBER:	60/047,582
43	EARLIER	FILING DATE:	1997-05-23
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50	EARLIER	APPLICATION NUMBER:	60/047,601
51	EARLIER	FILING DATE:	1997-05-23
52	EARLIER	APPLICATION NUMBER:	60/043,580
53	EARLIER	FILING DATE:	1997-04-11
54	EARLIER	APPLICATION NUMBER:	60/043,568
55	EARLIER	FILING DATE:	1997-04-11
56	EARLIER	APPLICATION NUMBER:	60/043,314
57	EARLIER	FILING DATE:	1997-04-11
58	EARLIER	APPLICATION NUMBER:	60/043,569
59	EARLIER	FILING DATE:	1997-04-11
60	EARLIER	APPLICATION NUMBER:	60/043,311
61	EARLIER	FILING DATE:	1997-04-11
62	EARLIER	APPLICATION NUMBER:	60/043,671
63	EARLIER	FILING DATE:	1997-04-11
64	EARLIER	APPLICATION NUMBER:	60/043,674
65	EARLIER	FILING DATE:	1997-04-11
66	EARLIER	APPLICATION NUMBER:	60/043,669
67	EARLIER	FILING DATE:	1997-04-11
68	EARLIER	APPLICATION NUMBER:	60/043,312
69	EARLIER	FILING DATE:	1997-04-11

1	EARLIER APPLICATION NUMBER: 60/043,313
2	EARLIER FILING DATE: 1997-04-11
3	EARLIER APPLICATION NUMBER: 60/043,672
4	EARLIER FILING DATE: 1997-04-11
5	EARLIER APPLICATION NUMBER: 60/043,315
6	EARLIER FILING DATE: 1997-04-11
7	EARLIER APPLICATION NUMBER: 60/048,974
8	EARLIER FILING DATE: 1997-06-06
9	EARLIER APPLICATION NUMBER: 60/056,886
10	EARLIER FILING DATE: 1997-08-22
11	EARLIER APPLICATION NUMBER: 60/056,877
12	EARLIER FILING DATE: 1997-08-22
13	EARLIER APPLICATION NUMBER: 60/056,889
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15	EARLIER APPLICATION NUMBER: 60/056,893
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17	EARLIER APPLICATION NUMBER: 60/056,630
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19	EARLIER APPLICATION NUMBER: 60/056,878
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21	EARLIER APPLICATION NUMBER: 60/056,662
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23	EARLIER APPLICATION NUMBER: 60/056,872
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25	EARLIER APPLICATION NUMBER: 60/056,882
26	EARLIER FILING DATE: 1997-08-22
27	EARLIER APPLICATION NUMBER: 60/056,637
28	EARLIER FILING DATE: 1997-08-22
29	EARLIER APPLICATION NUMBER: 60/056,903
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31	EARLIER APPLICATION NUMBER: 60/056,888
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38	EARLIER FILING DATE: 1997-08-22
39	EARLIER APPLICATION NUMBER: 60/056,911
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41	EARLIER APPLICATION NUMBER: 60/056,636
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47	EARLIER APPLICATION NUMBER: 60/056,864
48	EARLIER FILING DATE: 1997-08-22
49	EARLIER APPLICATION NUMBER: 60/056,892
50	EARLIER FILING DATE: 1997-08-22
51	EARLIER APPLICATION NUMBER: 60/057,761
52	EARLIER FILING DATE: 1997-08-22
53	EARLIER APPLICATION NUMBER: 60/047,588
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55	EARLIER APPLICATION NUMBER: 60/047,585
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57	EARLIER APPLICATION NUMBER: 60/047,586
58	EARLIER FILING DATE: 1997-05-23
59	EARLIER APPLICATION NUMBER: 60/047,590
60	EARLIER FILING DATE: 1997-05-23
61	EARLIER APPLICATION NUMBER: 60/047,594
62	EARLIER FILING DATE: 1997-05-23
63	EARLIER APPLICATION NUMBER: 60/047,589
64	EARLIER FILING DATE: 1997-05-23
65	EARLIER APPLICATION NUMBER: 60/047,593

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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
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; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match          71.7%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 66;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGTTTCG 24
Db 878 CAAGTCGAATTGGAAGRACTGTCG 901

RESULT 23
US-09-149-476-226
; Sequence 226, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rozen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-08-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 71.7%; Score 17.2; DB 3; Length 1791;
Best Local Similarity 79.2%; Pred. No. 66;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAAGGCTTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 973 CAAGTCGAATTGAAAGRACTCTCG 996

RESULT 24
US-07-915-922-1
; Sequence 1, Application US/07915922
; Patent No. 5422242
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K.Y.
; TITLE OF INVENTION: Mycobacterium Primers and Probes
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07915,922
; FILING DATE: 19920717
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sias, Stacey R.
; REGISTRATION NUMBER: 32,630
; REFERENCE/DOCKET NUMBER: 8616
; TELECOMMUNICATION INFORMATION:
```

```
;
; TELEPHONE: (510) 814-2863
; TELEFAX: (510) 522-1285
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-915-922-1
Query Match 70.8%; Score 17; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17
Db 7 CAAGTCGAACGGAAGG 23

RESULT 25
US-09-039-866-5
; Sequence 5, Application US/09039866
; Patent No. 6001611
; GENERAL INFORMATION:
; APPLICANT: Will, Stephen G.
; TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 08876
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/039,866
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 1023P
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-039-866-5
Query Match 70.8%; Score 17; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17
Db 7 CAAGTCGAACGGAAGG 23

RESULT 26
US-09-949-016-13974/c
; Sequence 13974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13974
; LENGTH: 106418
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; LOCATION: (1)-(106418)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13974
Query Match 69.2%; Score 16.6; DB 3; Length 106418;
Best Local Similarity 82.6%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCTTTTCG 24
Db 10377 AAGTCCTACGGAAGGCTTTTG 10355

RESULT 27
US-09-949-016-16621/c
; Sequence 16621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 16621
; LENGTH: 108341
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16621
Query Match 69.2%; Score 16.6; DB 3; Length 108341;
Best Local Similarity 82.6%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTC 23
Db 94196 CAAGTCGAAGGAAGGCAATTC 94174

RESULT 28
US-09-949-016-13781/c
; Sequence 13781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13781
; LENGTH: 228851
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(228851)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13781

Query Match 69.2%; Score 16.6; DB 3; Length 228851;
Best Local Similarity 82.6%; Pred. No. 3.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTTTCG 24
||||| ||||| ||||| |||||
Db 132603 AAGTCCTACGGAAGGCCTTTTG 132581

RESULT 29
US-08-485-602-61
; Sequence 61, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
```

```
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
US-08-485-602-61

Query Match 68.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 68;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGAACGGAAGGCCTTTTCG 24
||||| ||||| ||||| |||||
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 30
US-08-757-180-60
; Sequence 60, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium simiae
US-08-757-180-60

Query Match 68.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 68;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGAACGGAAGGCCTTTTCG 24
||||| ||||| ||||| |||||
Db 1 CGAACGGAAGNCCCUUCG 19

RESULT 31
US-08-745-638-61
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; Sequence 61, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium habana
;
US-08-745-638-61

Query Match 68.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 68;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CGAACGGAAGGCGCTTTTCG 24
Db 1 CGAACGGAAGGCGCTTTTCG 19

RESULT 32
US-09-949-016-69524
; Sequence 69524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76807
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-69524

Query Match 67.5%; Score 16.2; DB 3; Length 601;
Best Local Similarity 78.3%; Pred. No. 1.7e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTTCG 24
Db 293 AAGTCCTAYGGAAGGCGCTTTTG 315

RESULT 33
US-09-949-016-76807
; Sequence 76807, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 76807
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
;
US-09-949-016-76807

Query Match 67.5%; Score 16.2; DB 3; Length 601;
Best Local Similarity 78.3%; Pred. No. 1.7e+02;
Matches 18; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTTCG 24
Db 285 AAGTCCTACGGAAGGCGCTTTTG 307

RESULT 34
US-09-533-559-7113
; Sequence 7113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7113

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; LENGTH: 637
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-7113

Query Match      67.5%; Score 16.2; DB 3; Length 637;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21
   |||||||
Db 29 CATGCGAACGGAAGACTT 49

RESULT 35
US-09-974-300-4677/c
; Sequence 4677, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4677
; LENGTH: 972
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(972)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4677

Query Match      67.5%; Score 16.2; DB 5; Length 972;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTT 21
   |||||||
Db 384 CAAGTCGAACGGAAGGCGCTT 364

RESULT 36
US-09-608-285A-45/c
; Sequence 45, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180

Query Match      67.5%; Score 16.2; DB 3; Length 1498;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTT 22
   |||||||
Db 512 AAGTCGAACGGAATGCTGT 492

Query Match      67.5%; Score 16.2; DB 3; Length 1498;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTT 22
   |||||||
Db 512 AAGTCGAACGGAATGCTGT 492

Query Match      67.5%; Score 16.2; DB 3; Length 1498;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTT 22
   |||||||
Db 512 AAGTCGAACGGAATGCTGT 492
```

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RESULT 38
US-09-608-285A-53/c
; Sequence 53, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-53

Query Match      67.5%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 39
US-09-557-800C-53/c
; Sequence 53, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-53

Query Match      67.5%; Score 16.2; DB 3; Length 1588;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      659 AAGTCGAACGGAATGCTCTGT 639

RESULT 40
US-09-608-285A-49/c
; Sequence 49, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-49

Query Match      67.5%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
        |||||
Db      191 AAGTCGAACGGAATGCTCTGT 171
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RESULT 41
US-09-557-800C-49/c
; Sequence 49, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-04-25
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 1999-08-09
; PRIOR FILING DATE: 1999-07-16
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1999-03-19
; PRIOR FILING DATE: 1998-07-24
; PRIOR FILING DATE: 1999-02-04
; PRIOR FILING DATE: 1999-02-04
; PRIOR FILING DATE: 1999-02-04
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-49

Query Match      67.5%; Score 16.2; DB 3; Length 2294;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      191 AAGTCGAACGGAATGCTCTGT 171

RESULT 42
US-09-608-285A-46/c
; Sequence 46, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
```

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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-46

Query Match      67.5%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 43
US-09-557-800C-46/c
; Sequence 46, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2371
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-46

Query Match      67.5%; Score 16.2; DB 3; Length 2371;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      268 AAGTCGAACGGAATGCTCTGT 248

RESULT 44
US-09-608-285A-51/c
; Sequence 51, Application US/09608285A
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; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-51

Query Match      67.5%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      394 AAGTCGAACGGAATGCTCTGT 374

RESULT 45
US-09-557-800C-51/c
; Sequence 51, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
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; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-557-800C-51

Query Match      67.5%; Score 16.2; DB 3; Length 2497;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      394 AAGTCGAACGGAATGCTCTGT 374

RESULT 46
US-09-608-285A-48/c
; Sequence 48, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 2693
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-608-285A-48

Query Match      67.5%; Score 16.2; DB 3; Length 2693;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCCTTT 22
      |||||
Db      590 AAGTCGAACGGAATGCTCTGT 570

RESULT 47
US-09-557-800C-48/c
; Sequence 48, Application US/09557800C
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; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 48  
; LENGTH: 2693  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-800C-48

Query Match 67.5%; Score 16.2; DB 3; Length 2693;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 590 AAGTCGAACGGAATGCTCTGT 570

RESULT 48  
US-09-608-285A-26/c  
; Sequence 26, Application US/09608285A  
; Patent No. 6335013  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
; FILE REFERENCE: 28110/36570  
; CURRENT APPLICATION NUMBER: US/09/608,285A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-608-285A-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (148)..(1599)  
US-09-608-285A-26

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 49  
US-09-608-285A-52/c  
; Sequence 52, Application US/09608285A  
; Patent No. 6335013  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
; FILE REFERENCE: 28110/36570  
; CURRENT APPLICATION NUMBER: US/09/608,285A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-608-285A-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

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RESULT 50
US-09-240-639-1/c
; Sequence 1, Application US/09240639
; Patent No. 6350447
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/240,639
; CURRENT FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-09-240-639-1
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTCTG 639

RESULT 51
US-09-370-265-26/c
; Sequence 26, Application US/09370265
; Patent No. 6447771
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 28111/35508
; CURRENT APPLICATION NUMBER: US/09/370,265
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: PCT/US99/16180
; EARLIER FILING DATE: 1999-07-16
; EARLIER FILING DATE: 1999-07-09
; EARLIER FILING DATE: 1999-03-19
; EARLIER FILING DATE: 1999-02-04
; EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-370-265-26
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTCTG 639

RESULT 52
US-09-557-800C-26/c
; Sequence 26, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (148)..(1599)
US-09-557-800C-26
Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTTT 22
      |||||
Db      659 AAGTCGAACGGAATGCTCTG 639

RESULT 53
US-09-557-800C-52/c
; Sequence 52, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
```

; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 52  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-800C-52

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 54  
US-09-370-625A-26/c  
; Sequence 26, Application US/09370625A  
; Patent No. 6600032  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO NOVEL CD39-LIKE POLYPEPTIDES  
; FILE REFERENCE: 28110/35908  
; CURRENT APPLICATION NUMBER: US/09/370,625A  
; CURRENT FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 26  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (148)..(1599)  
US-09-370-625A-26

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 55  
US-09-510A-1/c  
; Sequence 1, Application US/09908510A  
; Patent No. 6759214  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS  
; FILE REFERENCE: 28110/36120E  
; CURRENT APPLICATION NUMBER: US/09/908,510A

; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
; OTHER INFORMATION:  
US-09-908-510A-1

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 56  
US-09-905-744B-1/c  
; Sequence 1, Application US/09905744B  
; Patent No. 6780410  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND ACIDS  
; FILE REFERENCE: 28110/36120A  
; CURRENT APPLICATION NUMBER: US/09/905,744B  
; CURRENT FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 09/240,639  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2762  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (232)..(1599)  
; OTHER INFORMATION:  
US-09-905-744B-1

Query Match 67.5%; Score 16.2; DB 3; Length 2762;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 57  
US-10-107-660-1/c  
; Sequence 1, Application US/10107660  
; Patent No. 6780977  
; GENERAL INFORMATION:  
; APPLICANT: Chadwick, Brian Paul  
; APPLICANT: Frischauf, Anna-Maria  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND NUCLEIC ACIDS  
; FILE REFERENCE: 9598-066  
; CURRENT APPLICATION NUMBER: US/10/107,660  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: US/09/240,639  
; PRIOR FILING DATE: 1998-01-29

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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
US-10-107-660-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    |||||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 58
US-10-107-576-1/c
; Sequence 1, Application US/10107576
; Patent No. 6783959
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120H
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/10/107,576
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-107-576-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    |||||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 59
US-09-905-732B-1/c
; Sequence 1, Application US/09905732B
; Patent No. 6787328
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120B
; CURRENT APPLICATION NUMBER: US/09/905,732B
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
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; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-732B-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    |||||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 60
US-09-905-743B-1/c
; Sequence 1, Application US/09905743B
; Patent No. 6828423
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120C
; CURRENT APPLICATION NUMBER: US/09/905,743B
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-09-905-743B-1

Query Match          67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    |||||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 61
US-09-905-589-1/c
; Sequence 1, Application US/09905589
; Patent No. 6884872
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Frischauf, Anna-Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
; FILE REFERENCE: 9598-066
; CURRENT APPLICATION NUMBER: US/09/905,589
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US/09/240,639
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (232)..(1599)
US-09-905-589-1
Query Match      67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 62
US-10-108-171A-1/c
; Sequence 1, Application US/10108171A
; Patent No. 6899875
; GENERAL INFORMATION:
; APPLICANT: Chadwick, Brian Paul
; APPLICANT: Friesch, Anna Maria
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES AND
; FILE REFERENCE: 28110/36120F
; CURRENT APPLICATION NUMBER: US/10/108,171A
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 09/240,639
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2762
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(1599)
; OTHER INFORMATION:
US-10-108-171A-1
Query Match      67.5%; Score 16.2; DB 3; Length 2762;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 63
US-09-608-285A-50/c
; Sequence 50, Application US/09608285A
; Patent No. 6335013
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE
; FILE REFERENCE: 28110/36570
; CURRENT APPLICATION NUMBER: US/09/608,285A
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/583,231
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/557,800
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350,836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273,447
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; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/244,444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/122,449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-608-285A-50
Query Match      67.5%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 64
US-09-557-800C-50/c
; Sequence 50, Application US/09557800C
; Patent No. 6476211
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Mulero, Julio
; APPLICANT: Yeung, George
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like
; FILE REFERENCE: 28110/36457
; CURRENT APPLICATION NUMBER: US/09/557,800C
; CURRENT FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/481,238
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 09/370,265
; PRIOR FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/16180
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 09/350836
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/273447
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: 09/122449
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 09/244444
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: 09/118,205
; PRIOR FILING DATE: 1998-07-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 2805
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-557-800C-50
Query Match      67.5%; Score 16.2; DB 3; Length 2805;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAGGCCTTT 22
    ||||| ||||| |||||
Db  659 AAGTCGAACGGAATGCTCTGT 639

RESULT 65
US-09-608-285A-54/c
; Sequence 54, Application US/09608285A
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; Patent No. 6335013  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE  
; TITLE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 28110/36570  
; CURRENT APPLICATION NUMBER: US/09/608,285A  
; CURRENT FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 09/583,231  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 09/557,800  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350,836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273,447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/244,444  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/122,449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 54  
; LENGTH: 2882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-608-285A-54

Query Match 67.5%; Score 16.2; DB 3; Length 2882;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 66  
US-09-557-800C-54/c  
; Sequence 54, Application US/09557800C  
; Patent No. 6476211  
; GENERAL INFORMATION:  
; APPLICANT: Ford, John  
; APPLICANT: Mulero, Julio  
; APPLICANT: Yeung, George  
; TITLE OF INVENTION: Methods and Materials Relating to CD39-Like  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 28110/36457  
; CURRENT APPLICATION NUMBER: US/09/557,800C  
; CURRENT FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/481,238  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: 09/370,265  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR APPLICATION NUMBER: PCT/US99/16180  
; PRIOR FILING DATE: 1999-07-16  
; PRIOR APPLICATION NUMBER: 09/350836  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/273447  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 09/122449  
; PRIOR FILING DATE: 1998-07-24  
; PRIOR APPLICATION NUMBER: 09/244444

; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: 09/118,205  
; PRIOR FILING DATE: 1998-07-16  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 54  
; LENGTH: 2882  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-557-800C-54

Query Match 67.5%; Score 16.2; DB 3; Length 2882;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTT 22  
|||||  
Db 659 AAGTCGAACGGAATGCTCTGT 639

RESULT 67  
US-09-738-274-28  
; Sequence 28, Application US/09738274  
; Patent No. 6664081  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUEZ, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02 UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-28

Query Match 66.7%; Score 16; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCC 19  
|||||  
Db 1 GTCGAACGGAAGGCC 16

RESULT 68  
US-09-974-300-6612/c  
; Sequence 6612, Application US/09974300  
; Patent No. 7018794  
; GENERAL INFORMATION:  
; APPLICANT: Berka, Randy M.  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 10085.500-US  
; CURRENT APPLICATION NUMBER: US/09/974,300  
; CURRENT FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: 09/680,598  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: 60/279,526  
; PRIOR FILING DATE: 2001-03-27



; NUMBER OF SEQ ID NOS: 8481  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6612  
; LENGTH: 161  
; TYPE: DNA  
; ORGANISM: Bacillus clausii  
US-09-974-300-6612

Query Match 66.7%; Score 16; DB 5; Length 161;  
Best Local Similarity 79.2%; Pred. No. 1.6e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCGCTTTTCG 24  
DB 81 CAAGGCAACGGCAATGCGCTTTTCG 58

## RESULT 69

US-09-252-991A-2715/c  
; Sequence 2715, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 2715  
; LENGTH: 417  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-2715

Query Match 66.7%; Score 16; DB 3; Length 417;  
Best Local Similarity 79.2%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCGCTTTTCG 24  
DB 180 CAAGTGAAGGAGAGGCGCTTTCG 157

## RESULT 70

US-09-252-991A-6201  
; Sequence 6201, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; PRIOR FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6201  
; LENGTH: 552  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-6201

Query Match 66.7%; Score 16; DB 3; Length 552;  
Best Local Similarity 79.2%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCGCTTTTCG 24  
DB 44 CAGGCCGTTTCGAAAGGCGCTTCG 67

## RESULT 71

US-09-949-016-79652  
; Sequence 79652, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 79652  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-79652

Query Match 66.7%; Score 16; DB 3; Length 601;  
Best Local Similarity 79.2%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCGCTTTTCG 24  
DB 328 CAAAACGACGCGAAATGCTTTTG 351

## RESULT 72

US-09-949-016-201683/c  
; Sequence 201683, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 201683  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-201683

Query Match 66.7%; Score 16; DB 3; Length 601;  
Best Local Similarity 79.2%; Pred. No. 2.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCGCTTTTCG 24  
DB 228 CAAGTTGAATGGAATTCCTTTGG 205

## RESULT 73

US-09-311-170-1  
; Sequence 1, Application US/09311170  
; Patent No. 6121034  
; GENERAL INFORMATION:  
; APPLICANT: Laroche et al., Andre L.  
; TITLE OF INVENTION: Xylanase cxy1  
; FILE REFERENCE: xylanase cxy1  
; CURRENT APPLICATION NUMBER: US/09/311.170  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1269  
; TYPE: DNA  
; ORGANISM: Coniothyrium minitans  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (25)..(1179)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (88)..(180)  
; OTHER INFORMATION: Cellulose-binding domain  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (181)..(273)  
; OTHER INFORMATION: hinge region  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (274)..(1179)  
; OTHER INFORMATION: catalytic domain  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (25)..(75)  
; OTHER INFORMATION: putative signal peptide  
US-09-311-170-1

Query Match 66.7%; Score 16; DB 3; Length 1269;  
Best Local Similarity 79.2%; Pred. No. 2.5e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTCG 24  
Db 477 CAGTCGAACGGAAGGCTGCTCG 500

## RESULT 74

US-09-252-991A-887  
; Sequence 887, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 887  
; LENGTH: 1698  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-887

Query Match 66.7%; Score 16; DB 3; Length 1698;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGG 17  
Db 361 AAGTCGAACGGAAGG 376

## RESULT 75

US-09-799-451-258  
; Sequence 258, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yundong  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 258  
; LENGTH: 2103  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1184)..(1303)  
US-09-799-451-258

Query Match 66.7%; Score 16; DB 3; Length 2103;  
Best Local Similarity 79.2%; Pred. No. 2.8e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTCG 24  
Db 993 CAAGTCGATTTGAAGACTGTCG 1016

## RESULT 76

US-09-252-991A-6717  
; Sequence 6717, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 6717  
; LENGTH: 2106  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa



; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17398  
; LENGTH: 139150  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17398

Query Match 66.7%; Score 16; DB 3; Length 139150;  
Best Local Similarity 79.2%; Pred. No. 6.5e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTG 24  
||||| ||||| ||||| ||||| |||||  
Db 117041 CAAGTGAATGGAATTCCTTTG 117018

## RESULT 81

US-09-949-016-12879/c  
; Sequence 12879, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12879  
; LENGTH: 139577  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12879

Query Match 66.7%; Score 16; DB 3; Length 139577;  
Best Local Similarity 79.2%; Pred. No. 6.5e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTG 24  
||||| ||||| ||||| ||||| |||||  
Db 117041 CAAGTGAATGGAATTCCTTTG 117018

## RESULT 82

US-09-949-016-14033  
; Sequence 14033, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14033  
; LENGTH: 784019  
; TYPE: DNA

; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(784019)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14033

Query Match 66.7%; Score 16; DB 3; Length 784019;  
Best Local Similarity 79.2%; Pred. No. 7.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTG 24  
||||| ||||| ||||| ||||| |||||  
Db 751665 CAAACGACCGGAATGCCCTTTG 751688

## RESULT 83

US-09-949-016-12777  
; Sequence 12777, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12777  
; LENGTH: 828152  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(828152)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12777

Query Match 66.7%; Score 16; DB 3; Length 828152;  
Best Local Similarity 79.2%; Pred. No. 7.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTG 24  
||||| ||||| ||||| ||||| |||||  
Db 747798 CAAACGACCGGAATGCCCTTTG 747821

## RESULT 84

US-09-489-039A-1391  
; Sequence 1391, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709, 2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 1391  
; LENGTH: 375  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1391

Query Match 65.8%; Score 15.8; DB 3; Length 375;  
Best Local Similarity 89.5%; Pred. No. 2.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 CGAACGGAAGCCTTTCG 24  
|||||

Db 332 CGAACGGAAGCCTTTCG 350  
|||||

RESULT 85  
US-08-008-216-7  
; Sequence 7, Application US/08008216  
; Patent No. 5366887  
; GENERAL INFORMATION:  
; APPLICANT: Slightom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: Ri T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,216  
; FILING DATE: 25-JAN-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhorst, Marnie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020US1  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 573 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: Strain A4  
; IMMEDIATE SOURCE:  
; LIBRARY: Convolvulus arvensis plant cells  
; CLONE: Clone 7  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (1..573)  
; OTHER INFORMATION: /label= ORF7  
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071  
; OTHER INFORMATION: through 5643 of Seq. ID No. 5366887 19. It is read 5' to  
; OTHER INFORMATION: 3' from the complementary strand."  
US-08-008-216-7

Query Match 65.8%; Score 15.8; DB 2; Length 573;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCGAACGGAAGCCTTT 22  
|||||

Db 507 GTCGAACGACAAGGCCTTT 525  
RESULT 86  
US-08-459-569-7  
; Sequence 7, Application US/08459569  
; Patent No. 5543501  
; GENERAL INFORMATION:  
; APPLICANT: Slightom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: Ri T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,569  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/008,216  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhorst, Marnie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 573 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: Strain A4  
; IMMEDIATE SOURCE:  
; LIBRARY: Convolvulus arvensis plant cells  
; CLONE: Clone 7  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (1..573)  
; OTHER INFORMATION: /label= ORF7  
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071  
; Patent No. 5543501  
; OTHER INFORMATION: through 5643 of Seq. ID No. 5543501 19. It is read 5' to  
; OTHER INFORMATION: 3' from the complementary strand."  
US-08-459-569-7

Query Match 65.8%; Score 15.8; DB 2; Length 573;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTCGAACGGAAGCCTTT 22  
|||||

Db 507 GTCGAACGACAAGGCCTTT 525  
|||||

RESULT 87

```
US-08-458-831-7
; Sequence 7, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slighton, Jerry L.
; TITLE OF INVENTION: Polymorphisms in Known Genes Associated
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82725
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82725
Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 437 AGTCAACGGAAGGCATT 455

RESULT 89
US-09-949-016-82726
; Sequence 82726, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726
Query Match 65.8%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 204 AGTCAACGGAAGGCATT 222

RESULT 90
US-09-949-016-82727
; Sequence 82727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016

US-08-458-831-7
; Sequence 7, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slighton, Jerry L.
; TITLE OF INVENTION: Polymorphisms in Known Genes Associated
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/08/458,831
; CURRENT FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; Patent No. 5824866
; OTHER INFORMATION: through 5643 of Seq. ID No. 5824866 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
US-08-458-831-7
Query Match 65.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTT 22
Db 507 GTCGAACGACGAAGGCCTT 525

RESULT 88
US-09-949-016-82725
; Sequence 82725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
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; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82727  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-82727

Query Match 65.8%; Score 15.8; DB 3; Length 601;  
Best Local Similarity 89.5%; Pred. No. 2.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 3 AGTCGAACGGAAGGCCTT 21  
||||| ||||| ||||| ||  
Db 45 AGTCAACGGAAGGCATT 63

## RESULT 91

US-08-008-216-6  
; Sequence 6, Application US/08008216  
; Patent No. 5366887  
; GENERAL INFORMATION:  
; APPLICANT: Slightom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: Ri T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/008,216  
; FILING DATE: 25-JAN-1993  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; NAME: Barnhorst, Marlie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1074 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: Strain A4  
; IMMEDIATE SOURCE:  
; LIBRARY: Convolvulus arvensis plant cells  
; CLONE: Clone 7  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: 1..1074  
; OTHER INFORMATION: /label= ORF6  
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143  
; OTHER INFORMATION: through 6216 of Seq. ID No. 5366887 19."  
US-08-008-216-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;  
Best Local Similarity 89.5%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 4 GTCGAACGGAAGGCCTTT 22  
||||| ||||| ||||| ||  
Db 435 GTCGAACGCAAGGCCTTT 453

## RESULT 92

US-08-459-569-6  
; Sequence 6, Application US/08459569  
; Patent No. 5543501  
; GENERAL INFORMATION:  
; APPLICANT: Slightom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: Ri T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,569  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/008,216  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhorst, Marlie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1074 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: Strain A4  
; IMMEDIATE SOURCE:  
; LIBRARY: Convolvulus arvensis plant cells  
; CLONE: Clone 7  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..1074  
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; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143  
; Patent No. 5543501  
; OTHER INFORMATION: through 6216 of Seq. ID No. 5543501 19."

US-08-459-569-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;  
Best Local Similarity 89.5%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22  
Db 435 GTCGAACGACAGGCCTTT 453

RESULT 93

US-08-458-831-6  
; Sequence 6, Application US/08458831  
; Patent No. 5824866  
; GENERAL INFORMATION:  
; APPLICANT: Slightom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: R1 T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/458,831  
; APPLICATION NUMBER: US/08/458,831  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/008,216  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barthorst, Marnie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1074 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: Strain A4  
; IMMEDIATE SOURCE:  
; LIBRARY: Convolvulus arvensis plant cells  
; CLONE: Clone 7  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..1074  
; OTHER INFORMATION: /label= ORF6  
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143  
; Patent No. 5824866  
; OTHER INFORMATION: through 6216 of Seq. ID No. 5824866 19."

US-08-458-831-6

Query Match 65.8%; Score 15.8; DB 2; Length 1074;  
Best Local Similarity 89.5%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22  
Db 435 GTCGAACGACAGGCCTTT 453

RESULT 94

US-09-583-110-1172  
; Sequence 1172, Application US/09583110  
; Patent No. 6699703  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al.  
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus  
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics  
; FILE REFERENCE: PATH00-07A  
; CURRENT APPLICATION NUMBER: US/09/583,110  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/107,433  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/085,131  
; PRIOR FILING DATE: 1998-05-12  
; PRIOR APPLICATION NUMBER: US 60/051,553  
; PRIOR FILING DATE: 1997-07-02  
; NUMBER OF SEQ ID NOS: 5322  
; SEQ ID NO 1172  
; LENGTH: 1551  
; TYPE: DNA  
; ORGANISM: Streptococcus pneumoniae  
US-09-583-110-1172

Query Match 65.8%; Score 15.8; DB 3; Length 1551;  
Best Local Similarity 89.5%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20  
Db 299 AAGCCGAAGTGAAGGCCT 317

RESULT 95

US-09-107-433-1056  
; Sequence 1056, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011



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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 1056:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1566 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...1566
; SEQUENCE DESCRIPTION: SEQ ID NO: 1056:
US-09-107-433-1056
Query Match 65.8%; Score 15.8; DB 3; Length 1566;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20
Db 314 AAGCGGAACGGAAGGCCT 332

RESULT 96
US-09-270-767-163
; Sequence 163, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-163
Query Match 65.8%; Score 15.8; DB 3; Length 4029;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 1400 AGCGGAACGGAAGGCCAT 1418

RESULT 97
US-09-270-767-15445
; Sequence 15445, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-15445
Query Match 65.8%; Score 15.8; DB 3; Length 4029;
Best Local Similarity 89.5%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 21
Db 1400 AGCGGAACGGAAGGCCAT 1418

RESULT 98
US-08-961-527-19
; Sequence 19, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4820 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-19
Query Match 65.8%; Score 15.8; DB 3; Length 4820;
Best Local Similarity 89.5%; Pred. No. 4.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCT 20
Db 2907 AAGCGGAACGGAAGGCCT 2925

RESULT 99
US-08-008-216-19
; Sequence 19, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
```

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; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
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; NAME/KEY: misc feature
; LOCATION: complement (937..2262)
; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF2SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
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; OTHER INFORMATION: /label= ORF3SUBSEQUENCE
; FEATURE:
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; OTHER INFORMATION: /label= ORF4SUBSEQUENCE
; FEATURE:
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; LOCATION: complement (4607..4918)
; OTHER INFORMATION: /label= ORF5SUBSEQUENCE
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; LOCATION: 6609..8888
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE

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; OTHER INFORMATION: /label= ORF10SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF11SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF13SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF14SUBSEQUENCE
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; NAME/KEY: misc feature
; LOCATION: complement (17737..18189)
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; US-08-008-216-19
; Query Match 65.8%; Score 15.8; DB 2; Length 21126;
; Best Local Similarity 89.5%; Pred. No. 5.7e+02;
; Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTT 22
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Db 5577 GTCGAACGACAGGCCTTT 5595

RESULT 100
US-08-459-569-19
; Sequence 19, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marlie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
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; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF3SUBSEQUENCE
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; NAME/KEY: misc feature
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; OTHER INFORMATION: /label= ORF4SUBSEQUENCE
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; OTHER INFORMATION: /label= ORF5SUBSEQUENCE
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
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; LOCATION: 6603..8888
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (6576..6830)
; OTHER INFORMATION: /label= ORF9SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9748..10044
; OTHER INFORMATION: /label= ORF10SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (10509..11282)
; OTHER INFORMATION: /label= ORF11SUBSEQUENCE
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 12466..13002
; OTHER INFORMATION: /label= ORF12SUBSEQUENCE
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; NAME/KEY: misc feature
; LOCATION: 13723..14319
; OTHER INFORMATION: /label= ORF13SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15659..16210
; OTHER INFORMATION: /label= ORF14SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (16517..17545)
; OTHER INFORMATION: /label= ORF15SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (17737..18189)
; OTHER INFORMATION: /label= ORF16SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (18177..18743)
; OTHER INFORMATION: /label= ORF17SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (19031..19390)
; OTHER INFORMATION: /label= ORF18SUBSEQUENCE
; US-08-459-569-19
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Query Match 65.8%; Score 15.8; DB 2; Length 21126;
Best Local Similarity 89.5%; Pred. No. 5,7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 4 GTCCGACGCGAAGGCCTTT 22
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Db 5577 GTCGACGACGAAGGCCTTT 5595
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Search completed: May 19, 2006, 01:01:54
Job time : 91.4458 secs
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91	16.6	69.2	25	10	US-10-956-157-105929	Sequence 105929,	c 164	16.2	67.5	2693	7	US-10-286-926-48	Sequence 48, Appl
92	16.6	69.2	552	4	US-09-925-065A-738727	Sequence 738727,	c 165	16.2	67.5	2693	7	US-10-231-913-35	Sequence 35, Appl
93	16.6	69.2	552	5	US-09-925-065A-738727	Sequence 738727,	c 166	16.2	67.5	2692	6	US-10-932-063-26	Sequence 26, Appl
94	16.6	69.2	572	4	US-09-925-065A-646509	Sequence 646509,	c 167	16.2	67.5	2762	7	US-10-286-926-26	Sequence 26, Appl
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113	16.6	69.2	2077	13	US-11-097-143-4424	Sequence 4424, Ap	c 186	16.2	66.7	60	6	US-10-149-187-4	Sequence 4, Appl
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c 267 15.8 65.8 5166 11 US-10-714-995-47 Sequence 47, Appl
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c 277 15.6 65.0 25 9 US-10-719-900-945960 Sequence 945960,
c 278 15.6 65.0 25 10 US-10-956-157-105927 Sequence 105927, A
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c 296 15.6 65.0 394 8 US-10-437-963-19564 Sequence 19564, A
c 297 15.6 65.0 437 8 US-10-437-963-54697 Sequence 54697, A
c 298 15.6 65.0 445 9 US-10-425-115-139266 Sequence 139266,
c 299 15.6 65.0 455 9 US-10-856-499-60 Sequence 60, Appl
c 300 15.6 65.0 455 9 US-10-856-499-1958 Sequence 1958, Ap
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## ALIGNMENTS

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RESULT 1
US-09-738-274-22
; Sequence 22, Application US/09738274
; Publication No. US20030165824A1
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; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-22
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Query Match 100.0%; Score 24; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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## RESULT 2

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US-10-665-708-22
; Sequence 22, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-22
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Query Match 100.0%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
Db 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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## RESULT 3

US-09-738-274-21  
; Sequence 21, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-21

Query Match 100.0%; Score 24; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24  
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DB 2 CAAGTCGAACGGAAGGCCCTTTCG 25

RESULT 4  
US-10-665-708-21  
; Sequence 21, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-21

Query Match 100.0%; Score 24; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24  
|||||  
DB 2 CAAGTCGAACGGAAGGCCCTTTCG 25

RESULT 5  
US-10-697-802A-6  
; Sequence 6, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 6  
; LENGTH: 1449  
; TYPE: DNA  
; ORGANISM: Mycobacterium fortuitum  
US-10-697-802A-6

Query Match 93.3%; Score 22.4; DB 10; Length 1449;  
Best Local Similarity 95.8%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24  
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DB 21 CAAGTCGAACGGAAGGCCCTTTCG 44

RESULT 6  
US-10-697-802A-13  
; Sequence 13, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 13  
; LENGTH: 1455  
; TYPE: DNA  
; ORGANISM: Mycobacterium mucogenicum  
US-10-697-802A-13

Query Match 93.3%; Score 22.4; DB 10; Length 1455;  
Best Local Similarity 95.8%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCCTTTCG 24  
|||||  
DB 31 CAAGTCGAACGGAAGGCCCTTTCG 54

RESULT 7  
US-10-697-802A-5  
; Sequence 5, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 5  
; LENGTH: 1482  
; TYPE: DNA  
; ORGANISM: Mycobacterium farcinogenes  
US-10-697-802A-5



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Query Match      93.3%; Score 22.4; DB 10; Length 1482;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGGCGCTTTCG 24
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Db 29 CAAGTCGAACGAAAGGCGCTTTCG 52

RESULT 8
US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      87.5%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGAAAGGCGCTTTCG 24
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Db 1 GTCGAACGAAAGGCGCTTTCG 21

RESULT 9
US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

Query Match      93.3%; Score 22.4; DB 10; Length 1482;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGGCGCTTTCG 24
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Db 29 CAAGTCGAACGAAAGGCGCTTTCG 52

RESULT 8
US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      87.5%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGAAAGGCGCTTTCG 24
   |||||
Db 1 GTCGAACGAAAGGCGCTTTCG 21

RESULT 9
US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-23

Query Match      93.3%; Score 22.4; DB 10; Length 1482;
Best Local Similarity 95.8%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGGCGCTTTCG 24
   |||||
Db 29 CAAGTCGAACGAAAGGCGCTTTCG 52

RESULT 8
US-09-738-274-23
; Sequence 23, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      87.5%; Score 21; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGAAAGGCGCTTTCG 24
   |||||
Db 1 GTCGAACGAAAGGCGCTTTCG 21

RESULT 9
US-10-665-708-23
; Sequence 23, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/1172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

Query Match      87.5%; Score 21; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTCGAACGAAAGGCGCTTTCG 24
   |||||
Db 1 GTCGAACGAAAGGCGCTTTCG 21

RESULT 10
US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kasanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES
; FILE REFERENCE: 4115-180
; CURRENT APPLICATION NUMBER: US/10/522,454
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: PCT/USO3/24238
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Actinomyces sp.
US-10-522-454-1

Query Match      86.7%; Score 20.8; DB 10; Length 1403;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAAGGCGCTTTCG 24
   |||||
Db 26 CAAGTCGAACGAAAGGCGCTTTCG 49

RESULT 11
US-11-035-296-1
; Sequence 1, Application US/11035296
; Publication No. US20050203005A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-195
; CURRENT APPLICATION NUMBER: US/11/035,296
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
```

```
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-035-296-1

Query Match      86.7%; Score 20.8; DB 13; Length 1443;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 31 CAAGTCGAGCGGAAAGGCGCTTTCG 54

RESULT 12
US-11-045-628-1
; Sequence 1, Application US/11045628
; Publication No. US20050233952A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Imaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; TITLE OF INVENTION: ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      86.7%; Score 20.8; DB 13; Length 1443;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 31 CAAGTCGAGCGGAAAGGCGCTTTCG 54

RESULT 13
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
```

```
; ORGANISM: Mycobacterium gordonae
US-10-697-802A-7

Query Match      86.7%; Score 20.8; DB 10; Length 1461;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 21 CAAGTCGAACGGAAGGCGCTTTCG 44

RESULT 14
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
   ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAAGGCGCTTTCG 74

RESULT 15
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
```

```

; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-8

Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAAGTCGAACGGAAAGCCCTTCG 24
      ||||| ||||| ||||| |||||
DB 51 CAAAGTCAGCGGAAGGCCCTTCG 74

RESULT 17
US-11-228-416-9
; Sequence 9, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODU
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH964 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA
US-11-228-416-9

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```
Query Match      86.7%; Score 20.8; DB 16; Length 1480;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 18
US-11-228-416-3
; Sequence 3, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; CURRENT APPLICATION NUMBER: US/11/228,416
; PRIOR FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1424)..(1424)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-3

Query Match      86.7%; Score 20.8; DB 16; Length 1481;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 19
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
```

```
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1425)..(1425)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
; US-11-228-416-4

Query Match      86.7%; Score 20.8; DB 16; Length 1482;
Best Local Similarity 91.7%; Pred. No. 8.1;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

RESULT 20
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
```

; LOCATION: (351)..(351)  
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (443)..(443)  
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (444)..(444)  
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1426)..(1426)  
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-7

Query Match 86.7%; Score 20.8; DB 16; Length 1483;  
Best Local Similarity 91.7%; Pred. No. 8.1; Mismatches 2; Indels 0; Gaps 0;  
Matches 22; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
Db 51 CAAGTCGAGCGGAAGGCGCTTTCG 74

## RESULT 21

US-09-738-972-7  
; Sequence 7, Application US/09738972  
; Patent No. US20020012918A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: primer  
US-09-738-972-7

Query Match 85.0%; Score 20.4; DB 3; Length 32;  
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 22  
Db 2 CAAGTCGAACGGAAGGCGCTTCT 23

## RESULT 22

US-09-738-972-14/c  
; Sequence 14, Application US/09738972  
; Patent No. US20020012918A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR FILING DATE: 1999-12-15

; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: probe  
US-09-738-972-14

Query Match 85.0%; Score 20.4; DB 3; Length 32;  
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 22  
Db 31 CAAGTCGAACGGAAGGCGCTTCT 10

## RESULT 23

US-10-862-026-7  
; Sequence 7, Application US/10862026  
; Publication No. US20040224348A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/10/862,026  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: primer  
US-10-862-026-7

Query Match 85.0%; Score 20.4; DB 9; Length 32;  
Best Local Similarity 95.5%; Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;  
Matches 21; Conservative 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 22  
Db 2 CAAGTCGAACGGAAGGCGCTTCT 23

## RESULT 24

US-10-862-026-14/c  
; Sequence 14, Application US/10862026  
; Publication No. US20040224348A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/10/862,026  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-862-026-14

Query Match      85.0%; Score 20.4; DB 9; Length 32;
Best Local Similarity 95.5%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
    |||||
Db 31 CAAGTCGAACGGAAGGCCTCT 10
    |||||

RESULT 25
US-10-478-633A-23
; Sequence 23, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-478-633A-23

Query Match      85.0%; Score 20.4; DB 10; Length 560;
Best Local Similarity 95.5%; Pred. No. 12;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
    |||||
Db 31 CAAGTCGAACGGAAGGCCTCT 52
    |||||

RESULT 26
US-10-697-802A-12
; Sequence 12, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 12
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium lentiflavum
US-10-697-802A-12

Query Match      85.0%; Score 20.4; DB 10; Length 1421;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
    |||||
Db 21 CAAGTCGAACGGAAGGCCTCT 42
    |||||

RESULT 27
US-10-697-802A-2
; Sequence 2, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 2
; LENGTH: 1454
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-697-802A-2

Query Match      85.0%; Score 20.4; DB 10; Length 1454;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
    |||||
Db 31 CAAGTCGAACGGAAGGCCTCT 52
    |||||

RESULT 28
US-10-029-397A-32
; Sequence 32, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 32
; LENGTH: 1465
; TYPE: DNA
; ORGANISM: Mycobacterium avium
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (298)..(891)
; OTHER INFORMATION: N = A, C, G or T/U
US-10-029-397A-32

Query Match      85.0%; Score 20.4; DB 7; Length 1465;
Best Local Similarity 95.5%; Pred. No. 13;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTT 22
    |||||
Db 21 CAAGTCGAACGGAAGGCCTCT 42
    |||||

RESULT 29
US-10-831-286A-1517
; Sequence 1517, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
```

; PRIOR APPLICATION NUMBER: 60/464,955  
; PRIOR FILING DATE: 2003-04-24  
; NUMBER OF SEQ ID NOS: 48788  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1517  
; LENGTH: 30  
; TYPE: DNA  
; ORGANISM: Corynebacterium diphtheriae  
US-10-831-286A-1517

Query Match 83.3%; Score 20; DB 11; Length 30;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20  
|||||  
Db 1 CAAGTCGAACGGAAGGCCT 20  
|||||

## RESULT 30

US-10-831-286A-8212  
; Sequence 8212, Application US/10831286A  
; Publication No. US20060046246A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENG, QIANDONG  
; APPLICANT: CHATELIER, SONIA  
; APPLICANT: MOIR, DONALD T.  
; APPLICANT: LACROIX, BRUNA  
; APPLICANT: CHILDRESS, DARRELL  
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
; FILE REFERENCE: 032796-174.001  
; CURRENT APPLICATION NUMBER: US/10/831.286A  
; CURRENT FILING DATE: 2004-04-26  
; PRIOR APPLICATION NUMBER: 60/464,955  
; PRIOR FILING DATE: 2003-04-24  
; NUMBER OF SEQ ID NOS: 48788  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8212  
; LENGTH: 30  
; TYPE: DNA

; ORGANISM: Corynebacterium kutscheri  
US-10-831-286A-8212

Query Match 80.8%; Score 19.4; DB 11; Length 30;  
Best Local Similarity 95.2%; Pred. No. 33;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21  
|||||  
Db 1 CAAGTCGAACGGAAGGCCTT 21  
|||||

## RESULT 31

US-10-438-774-15  
; Sequence 15, Application US/10438774  
; Publication No. US20040010504A1  
; GENERAL INFORMATION:  
; APPLICANT: Hinrichs, Steven  
; APPLICANT: Mohammed, Amr  
; APPLICANT: Ali, Hesham  
; APPLICANT: Kuyper, Dan  
; TITLE OF INVENTION: Custom Sequence Databases and Methods of  
; FILE REFERENCE: UNMC.63174-US  
; CURRENT APPLICATION NUMBER: US/10/438,774  
; CURRENT FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: 60/381,015  
; PRIOR FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 454  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-438-774-15

Query Match 80.8%; Score 19.4; DB 7; Length 454;  
Best Local Similarity 95.2%; Pred. No. 37;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24  
|||||  
Db 1 GTCGAACGGAAGGCCTTTCG 21  
|||||

## RESULT 32

US-10-085-871C-1  
; Sequence 1, Application US/10085871C  
; Publication No. US20030199047A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Chung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/085.871C  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1437  
; TYPE: DNA

; ORGANISM: Saccharothrix 44442  
US-10-085-871C-1

Query Match 80.0%; Score 19.2; DB 7; Length 1437;  
Best Local Similarity 87.5%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24  
|||||  
Db 31 CAAGTCGAGCGTAAGGCCTTTCG 54  
|||||

## RESULT 33

US-10-727-643-1  
; Sequence 1, Application US/10727643  
; Publication No. US20050064566A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Chung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/727,643  
; CURRENT FILING DATE: 2003-12-03  
; PRIOR APPLICATION NUMBER: US/10/085,871  
; PRIOR FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1437  
; TYPE: DNA

; ORGANISM: Saccharothrix 44442  
US-10-727-643-1

Query Match 80.0%; Score 19.2; DB 10; Length 1437;  
Best Local Similarity 87.5%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;





; APPLICANT: Hwang, Byong Kook  
; APPLICANT: Lee, Jung Yeop  
; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant  
; FILE REFERENCE: 4228-102  
; CURRENT APPLICATION NUMBER: US/10/756,683  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: KP 10-2003-0015628  
; PRIOR FILING DATE: 2003-03-13  
; PRIOR APPLICATION NUMBER: KP 10-2003-0015629  
; PRIOR FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1488  
; TYPE: DNA  
; ORGANISM: Lechevalieria aerocolonigenes  
US-10-756-683-1

Query Match 80.0%; Score 19.2; DB 9; Length 1488;  
Best Local Similarity 87.5%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24  
Db 43 CAAGTCGAGCGTAAGGCCCTTCG 66

RESULT 39  
US-10-875-161-2  
; Sequence 2, Application US/10875161  
; Publication No. US20050009151A1  
; GENERAL INFORMATION:  
; APPLICANT: Chase, Matthew  
; APPLICANT: Clayton, Robert  
; APPLICANT: Landis, Bryan  
; APPLICANT: Banerjee, Amit  
; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric  
; FILE REFERENCE: S0-3262-2-PR-US  
; CURRENT APPLICATION NUMBER: US/10/875,161  
; CURRENT FILING DATE: 2004-06-22  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 1514  
; TYPE: DNA  
; ORGANISM: Rhodococcus opacus  
; FEATURE:  
; NAME/KEY: rRNA  
; LOCATION: (1)..(1514)  
; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus  
; FEATURE:  
; NAME/KEY: misc.difference  
; LOCATION: (1)..(1514)  
; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of  
US-10-875-161-2

Query Match 80.0%; Score 19.2; DB 9; Length 1514;  
Best Local Similarity 87.5%; Pred. No. 49;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24  
Db 54 CAAGTCGAGCGTAAGGCCCTTCG 77

RESULT 40  
US-09-738-274-27  
; Sequence 27, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:

; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-27

Query Match 79.2%; Score 19; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 41  
US-10-665-708-27  
; Sequence 27, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-27

Query Match 79.2%; Score 19; DB 10; Length 23;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19  
Db 1 CAAGTCGAACGGAAGGCC 19

RESULT 42  
US-10-830-943-11

```
; Sequence 11, Application US/10830943
; Publication No. US20050009053A1
; GENERAL INFORMATION:
; APPLICANT: Boecker, Sebastian
; APPLICANT: van den Boom, Dirk
; TITLE OF INVENTION: FRAGMENTATION-BASED METHODS AND SYSTEMS
; TITLE OF INVENTION: FOR DE NOVO SEQUENCING
; FILE REFERENCE: 17082-079001
; CURRENT APPLICATION NUMBER: US/10/830,943
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/466,006
; PRIOR FILING DATE: 2003-04-25
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: amplicon sequence
US-10-830-943-11

Query Match          79.2%; Score 19; DB 9; Length 80;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCC 19
Db 51 CAAGTCGAACGGAAGGCC 69

RESULT 43
US-10-478-633A-24
; Sequence 24, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for
; FILE REFERENCE: 683232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 24
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
US-10-478-633A-24

Query Match          79.2%; Score 19; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCC 19
Db 43 CAAGTCGAACGGAAGGCC 61

RESULT 44
US-10-697-802A-11
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
US-10-697-802A-14

Query Match          79.2%; Score 19; DB 10; Length 145;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCC 19
Db 16 CAAGTCGAACGGAAGGCC 34

RESULT 45
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
US-10-697-802A-14

Query Match          79.2%; Score 19; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCC 19
Db 15 CAAGTCGAACGGAAGGCC 33

RESULT 46
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          79.2%; Score 19; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCC 19
Db 1 CAAGTCGAACGGAAGGCC 19
```

```
Db      39 CAAGTCGAACGGAAGGCC 57

RESULT 47
US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US20030162244A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US/09/463,618
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: H10-166226
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match      79.2%; Score 19; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCC 19
      |||||
Db      39 CAAGTCGAACGGAAGGCC 57

RESULT 48
US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match      79.2%; Score 19; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCC 19
      |||||
Db      21 CAAGTCGAACGGAAGGCC 39

RESULT 49
US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
```

```
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15

Query Match      79.2%; Score 19; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCC 19
      |||||
Db      21 CAAGTCGAACGGAAGGCC 39

RESULT 50
US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8

Query Match      79.2%; Score 19; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCC 19
      |||||
Db      45 CAAGTCGAACGGAAGGCC 63

RESULT 51
US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02 UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14
```

Query Match 78.3%; Score 18.8; DB 3; Length 32;  
Best Local Similarity 90.9%; Pred. No. 65;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
| | | | | | | | | | | | | | | | | | | |  
DB 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 52  
US-10-665-708-14  
; Sequence 14, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAI, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; MYCOBACTERIUM SPECIES  
; FILE REFERENCE: Gp107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665.708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
US-10-665-708-14

Query Match 78.3%; Score 18.8; DB 10; Length 32;  
Best Local Similarity 90.9%; Pred. No. 65;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
| | | | | | | | | | | | | | | | | | | |  
DB 2 CAAGTCGAACGGAAGGCCTCT 23

RESULT 53  
US-10-697-802A-17  
; Sequence 17, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697.802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 17  
; LENGTH: 1416  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-10-697-802A-17

Query Match 78.3%; Score 18.8; DB 10; Length 1416;  
Best Local Similarity 90.9%; Pred. No. 76;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
| | | | | | | | | | | | | | | | | | | |

Db 21 CAAGTCGAACGGAAGGCCTCT 42

RESULT 54  
US-10-697-802A-3  
; Sequence 3, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697.802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 3  
; LENGTH: 1421  
; TYPE: DNA  
; ORGANISM: Mycobacterium bovis  
US-10-697-802A-3

Query Match 78.3%; Score 18.8; DB 10; Length 1421;  
Best Local Similarity 90.9%; Pred. No. 76;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
| | | | | | | | | | | | | | | | | | | |  
DB 21 CAAGTCGAACGGAAGGCCTCT 42

RESULT 55  
US-10-697-802A-10  
; Sequence 10, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697.802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 10  
; LENGTH: 1463  
; TYPE: DNA  
; ORGANISM: Mycobacterium kansasii  
US-10-697-802A-10

Query Match 78.3%; Score 18.8; DB 10; Length 1463;  
Best Local Similarity 90.9%; Pred. No. 76;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22  
| | | | | | | | | | | | | | | | | | | |  
DB 20 CAAGTCGAACGGAAGGCCTCT 41

RESULT 56  
US-09-726-774-7  
; Sequence 7, Application US/09726774  
; Patent No. US20020082226A1  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Antisense Antibacterial Method and  
; Composition  
; FILE REFERENCE: 0450-0032.30  
; CURRENT APPLICATION NUMBER: US/09/726,774  
; CURRENT FILING DATE: 2000-11-29  
; PRIOR APPLICATION NUMBER: US 60/168,150  
; PRIOR FILING DATE: 1999-11-29  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7

```
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match      78.3%; Score 18.8; DB 3; Length 1464;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTT 22
Db 21 CAACTCGAACGGAAGGCTCT 42

RESULT 57
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7

Query Match      78.3%; Score 18.8; DB 8; Length 1464;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTT 22
Db 21 CAACTCGAACGGAAGGCTCT 42

RESULT 58
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; TITLE OF INVENTION: Mycobacterium and Method of Use
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match      78.3%; Score 18.8; DB 8; Length 1524;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CAACTCGAACGGAAGGCTTT 22
Db 51 CAACTCGAACGGAAGGCTCT 72

RESULT 59
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match      78.3%; Score 18.8; DB 7; Length 1536;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTT 22
Db 60 CAACTCGAACGGAAGGCTCT 81

RESULT 60
US-10-029-397A-34
; Sequence 34, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match      78.3%; Score 18.8; DB 7; Length 1536;
Best Local Similarity 90.9%; Pred. No. 76;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAACTCGAACGGAAGGCTTT 22
Db 60 CAACTCGAACGGAAGGCTCT 81

RESULT 61
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
```

```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match      75.8%; Score 18.2; DB 4; Length 600;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTTC 23
   ||||| ||| ||||| |||||
Db 298 CAAGTGGACCTGAAAGGCCTTC 276

RESULT 62
US-09-925-065A-906221/c
; Sequence 906221, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906221
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-925-065A-906221

Query Match      75.8%; Score 18.2; DB 5; Length 600;
Best Local Similarity 87.0%; Pred. No. 1.4e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTTC 23
   ||||| ||| ||||| |||||
Db 298 CAAGTGGACCTGAAAGGCCTTC 276

RESULT 63
US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match      75.0%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAACGGAAGGCCTTTCG 24
   ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 64
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match      75.0%; Score 18; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAACGGAAGGCCTTTCG 24
   ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCCTTTCG 18

RESULT 65
US-10-425-114-30427
; Sequence 30427, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
```

```
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30427
; LENGTH: 1366
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73019F09_FLI
US-10-425-114-30427

Query Match          74.2%; Score 17.8; DB 8; Length 1366;
Best Local Similarity 90.5%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 896 CAAGTGAACGAAAGGCCTT 916

RESULT 66
US-09-917-800A-1684
; Sequence 1684, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1684
; LENGTH: 4540
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_021266
US-09-917-800A-1684
```

Query Match 74.2%; Score 17.8; DB 3; Length 4540;

```
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 105 CAAGTCGAACGAAAGGACTT 125

RESULT 67
US-11-136-527-299
; Sequence 299, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 299
; LENGTH: 4770
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-299
```

Query Match 74.2%; Score 17.8; DB 16; Length 4770;
Best Local Similarity 90.5%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| ||||| |||||
Db 105 CAAGTCGAACGAAAGGACTT 125
```

```
RESULT 68
US-10-087-192-1004
; Sequence 1004, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1004
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-087-192-1004
```

Query Match 73.3%; Score 17.6; DB 6; Length 960;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 CAAGTCGAACGGAAGGCCTTTCG 24
    ||||| ||||| ||||| |||||
Db 811 CAAGTCGAGCAGAAAGTCCTTACG 834
```

RESULT 69
US-10-956-157-9594

```
; Sequence 9594, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9594
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-956-157-9594

Query Match      73.3%; Score 17.6; DB 10; Length 1400;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 554 CAAGTCGAATTGAAAGGACTGTGCG 577

RESULT 70
US-10-956-157-4359
; Sequence 4359, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4359
; LENGTH: 1786
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-956-157-4359

Query Match      73.3%; Score 17.6; DB 10; Length 1786;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 940 CAAGTCGAATTGAAAGGACTGTGCG 963

RESULT 71
US-10-087-192-1003
; Sequence 1003, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
```

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; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 43800
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-087-192-1003

Query Match      73.3%; Score 17.6; DB 6; Length 43800;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 33651 CAAGTCGAGCAGAAAGTCCTTACG 33674

RESULT 72
US-10-697-802A-9
; Sequence 9, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 9
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Mycobacterium intracellulare
; US-10-697-802A-9

Query Match      72.5%; Score 17.4; DB 10; Length 1452;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCC 19
    ||||| ||||| ||||| |||||
Db 11 CAAGTCGAACGGAAGGCC 29

RESULT 73
US-10-767-701-31297
; Sequence 31297, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31297
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: 18066455
; US-10-767-701-31297

Query Match      71.7%; Score 17.2; DB 8; Length 622;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AGTCGACGGAAGGCGCTTTTCG 24
    ||||| ||||| ||||| |||||
Db 31 AGTCGGAAGGAATGGCGCTTTTCG 52
```



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RESULT 74
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          71.7%; Score 17.2; DB 4; Length 654;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAGTCGAACGGAAGGCCTTTC 23
Db      403 AAGTGAACGGAACGGCCTTTC 424

RESULT 75
US-09-925-065A-481777
; Sequence 481777, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 481777
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-481777

Query Match          71.7%; Score 17.2; DB 5; Length 654;
Best Local Similarity 86.4%; Pred. No. 4.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      2 AAGTCGAACGGAAGGCCTTTC 23
Db      403 AAGTGAACGGAACGGCCTTTC 424

RESULT 76
US-09-809-391-59
; Sequence 59, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
US-09-809-391-59

Query Match          71.7%; Score 17.2; DB 3; Length 1776;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy      1 CAAGTCGAACGGAAGGCCTTTCG 24
Db      878 CAAGTCGAATTGAAGRACGTCTCG 901

RESULT 77
US-09-882-171-59
; Sequence 59, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
US-09-882-171-59
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7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,877	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,889	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,893	
7	PRIOR FILING DATE: 1997-08-22	
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7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,878	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,662	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,872	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,882	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,637	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,903	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,888	
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7	PRIOR APPLICATION NUMBER: 60/056,910	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,864	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,631	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,845	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/056,892	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/057,761	
7	PRIOR FILING DATE: 1997-08-22	
7	PRIOR APPLICATION NUMBER: 60/047,595	
7	PRIOR FILING DATE: 1997-05-23	
7	PRIOR APPLICATION NUMBER: 60/047,599	
7	PRIOR FILING DATE: 1997-05-23	
7	PRIOR APPLICATION NUMBER: 60/047,588	
7	PRIOR FILING DATE: 1997-05-23	
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7	PRIOR FILING DATE: 1997-05-23	
7	PRIOR APPLICATION NUMBER: 60/047,585	
7	PRIOR FILING DATE: 1997-05-23	
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7	PRIOR FILING DATE: 1997-05-23	
7	PRIOR APPLICATION NUMBER: 60/043,578	
7	PRIOR FILING DATE: 1997-04-11	
7	PRIOR APPLICATION NUMBER: 60/043,576	
7	PRIOR FILING DATE: 1997-04-11	
7	PRIOR APPLICATION NUMBER: 60/047,501	
7	PRIOR FILING DATE: 1997-05-23	

; PRIOR APPLICATION NUMBER: 60/043,670  
 ; PRIOR FILING DATE: 1997-04-11  
 ; PRIOR APPLICATION NUMBER: 60/056,632  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,664  
 ; PRIOR FILING DATE: 1997-08-22  
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 ; PRIOR APPLICATION NUMBER: 60/056,909  
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 ; PRIOR APPLICATION NUMBER: 60/056,875  
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 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/056,887  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/057,650  
 ; PRIOR FILING DATE: 1997-09-05  
 ; PRIOR APPLICATION NUMBER: 60/056,884  
 ; PRIOR FILING DATE: 1997-08-22  
 ; PRIOR APPLICATION NUMBER: 60/057,669  
 ; PRIOR FILING DATE: 1997-09-05

Query Match 71.7%; Score 17.2; DB 3; Length 1776;  
 Best Local Similarity 79.2%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 Db 878 CAAGTCGAATTGAAGRACTGTGC 901

RESULT 78  
 US-10-164-861-59  
 ; Sequence 59, Application US/10164861  
 ; Publication No. US2003022548A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P1  
 ; CURRENT APPLICATION NUMBER: US/10/164,861  
 ; CURRENT FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION NUMBER: US/09/149,476  
 ; PRIOR FILING DATE: 1998-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493  
 ; PRIOR FILING DATE: 1998-03-06  
 ; NUMBER OF SEQ ID NOS: 757  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 59  
 ; LENGTH: 1776  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (713)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (862)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (1752)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (1773)

; OTHER INFORMATION: n equals a,t,g, or c  
 US-10-164-861-59

Query Match 71.7%; Score 17.2; DB 7; Length 1776;  
 Best Local Similarity 79.2%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 Db 878 CAAGTCGAATTGAAGRACTGTGC 901

RESULT 79  
 US-11-144-947-59  
 ; Sequence 59, Application US/11144947  
 ; Publication No. US20060084082A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruben et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: P2002P2C2  
 ; CURRENT APPLICATION NUMBER: US/11/144,947  
 ; CURRENT FILING DATE: 2005-06-06  
 ; PRIOR APPLICATION NUMBER: 09/882,171  
 ; PRIOR FILING DATE: 2005-06-03  
 ; PRIOR APPLICATION NUMBER: 09/809,391  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/190,068  
 ; PRIOR FILING DATE: 2000-03-17  
 ; PRIOR APPLICATION NUMBER: 10/164,861  
 ; PRIOR FILING DATE: 2002-06-10  
 ; PRIOR APPLICATION NUMBER: 09/149,476  
 ; PRIOR FILING DATE: 1998-09-08  
 ; PRIOR APPLICATION NUMBER: PCT/US98/04493  
 ; PRIOR FILING DATE: 1998-03-06  
 ; PRIOR APPLICATION NUMBER: 60/040,162  
 ; PRIOR FILING DATE: 1997-03-07  
 ; PRIOR APPLICATION NUMBER: 60/040,333  
 ; PRIOR FILING DATE: 1997-03-07  
 ; PRIOR APPLICATION NUMBER: 60/038,621  
 ; PRIOR FILING DATE: 1997-03-07  
 ; PRIOR APPLICATION NUMBER: 60/040,626  
 ; PRIOR FILING DATE: 1997-03-07  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 761  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 59  
 ; LENGTH: 1776  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (713)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (862)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (1752)  
 ; OTHER INFORMATION: n equals a,t,g, or c  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (1773)  
 ; OTHER INFORMATION: n equals a,t,g, or c

US-11-144-947-59  
 Query Match 71.7%; Score 17.2; DB 16; Length 1776;  
 Best Local Similarity 79.2%; Pred. No. 4.6e+02;  
 Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTCG 24  
 Db 878 CAAGTCGAATTGAAGRACTGTGC 901

Db	878	CAAGTCGAATTGAAAGRACTGTGC	901
RESULT 80			
US-09-809-391-226			
; Sequence 226, Application US/09809391			
; Publication No. US20030049618A1			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: 186 Human Secreted proteins			
; FILE REFERENCE: P2002P2			
; CURRENT APPLICATION NUMBER: US/09/809,391			
; CURRENT FILING DATE: 2001-03-16			
; Prior application data removed - consult PALM or file wrapper			
; NUMBER OF SEQ ID NOS: 761			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 226			
; LENGTH: 1791			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-09-809-391-226			
 Query Match                71.7%; Score 17.2; DB 3; Length 1791;			
Best Local Similarity     79.2%; Pred. No. 4.6e+02;			
Matches    19; Conservative    1; Mismatches    4; Indels    0; Gaps    0;			
Qy	1	CAAGTCGAACGGAAAGCCTTTCG	24
Db	973	CAAGTCGAATTGAAAGRACTGTGC	996
RESULT 81			
US-09-882-171-226			
; Sequence 226, Application US/09882171			
; Publication No. US20030175858A1			
; GENERAL INFORMATION:			
; APPLICANT: Ruben et al.			
; TITLE OF INVENTION: 186 Human Secreted proteins			
; FILE REFERENCE: P2002P2			
; CURRENT APPLICATION NUMBER: US/09/882,171			
; CURRENT FILING DATE: 2001-06-18			
; PRIOR APPLICATION NUMBER: 09/809,391			
; PRIOR FILING DATE: 2001-03-16			
; PRIOR APPLICATION NUMBER: 09/149,476			
; PRIOR FILING DATE: 1998-09-08			
; PRIOR APPLICATION NUMBER: PCT/US98/04493			
; PRIOR FILING DATE: 1998-03-06			
; PRIOR APPLICATION NUMBER: 60/040,162			
; PRIOR FILING DATE: 1997-03-07			
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; PRIOR FILING DATE: 1997-03-07			
; PRIOR APPLICATION NUMBER: 60/047,600			
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-05-23
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; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
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; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
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; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/056,862
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; PRIOR APPLICATION NUMBER: 60/056,908
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; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05
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Query Match 71.7%; Score 17.2; DB 3; Length 1791;

Best Local Similarity 79.2%; Pred. No. 4.6e+02; Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
      ||||| ||||| ||||| |||||
Db 973 CAAGTCGAATTGAAAGRACTGTCG 996
```

#### RESULT 82

```
US-10-164-861-226
; Sequence 226, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-164-861-226
```

Query Match 71.7%; Score 17.2; DB 7; Length 1791;

Best Local Similarity 79.2%; Pred. No. 4.6e+02; Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 CAAGTCGAACGGAAGGCTTTTCG 24
      ||||| ||||| ||||| |||||
Db 973 CAAGTCGAATTGAAAGRACTGTCG 996
```

#### RESULT 83

```
US-11-144-947-226
; Sequence 226, Application US/11144947
; Publication No. US20060084082A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
```

```
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 226
; LENGTH: 1791
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-144-947-226

Query Match          71.7%; Score 17.2; DB 16; Length 1791;
Best Local Similarity 79.2%; Pred. No. 4.6e+02;
Matches 19; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTTCG 24
    ||||| ||||| ||||| ||||| |||||
Db 973 CAAGTCGAATGGAAGACTGTCG 996

RESULT 84
US-09-925-065A-553599
; Sequence 553599, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 4; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 85
US-09-925-065A-553599
; Sequence 553599, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 4; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 86
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.7%; Score 17.2; DB 7; Length 2919;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 2385 CACGGCAACGCAAGGCCTTT 2364

RESULT 87
US-10-425-115-40860/c
; Sequence 40860, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 553599
; LENGTH: 2258
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-553599

Query Match          71.7%; Score 17.2; DB 5; Length 2258;
Best Local Similarity 86.4%; Pred. No. 4.6e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 1256 CAAGTCGAACGAAAGGCCTGT 1277

RESULT 86
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.7%; Score 17.2; DB 7; Length 2919;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGAAAGGCCTTT 22
    ||||| ||||| ||||| ||||| |||||
Db 2385 CACGGCAACGCAAGGCCTTT 2364

RESULT 87
US-10-425-115-40860/c
; Sequence 40860, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 40860
; LENGTH: 3096
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MFT4577_137265C.1
US-10-425-115-40860

Query Match          71.7%; Score 17.2; DB 9; Length 3096;
Best Local Similarity 86.4%; Pred. No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAAGGCCTTTC 23
Db  3089 AAGTCGAACGGAAAGGCCTTTC 3068

RESULT 88
US-10-831-286A-12801
; Sequence 12801, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12801
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-12801

Query Match          70.8%; Score 17; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 AGTCGAACGGAAAGGCC 19
Db  4 AGTCGAACGGAAAGGCC 20

RESULT 89
US-10-831-286A-23905
; Sequence 23905, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
```

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; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23905
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium ulcerans
US-10-831-286A-23905

Query Match          70.8%; Score 17; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  3 AGTCGAACGGAAAGGCC 19
Db  3 AGTCGAACGGAAAGGCC 19

RESULT 90
US-10-956-157-105928
; Sequence 105928, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105928
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-105928

Query Match          69.2%; Score 16.6; DB 10; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  2 AAGTCGAACGGAAAGGCCTTTCG 24
Db  1 AAGTCGAATTCGAAGGACTGTGCG 23

RESULT 91
US-10-956-157-105929
; Sequence 105929, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 105929
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-105929

Query Match          69.2%; Score 16.6; DB 10; Length 25;
Best Local Similarity 82.6%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy  1 CAAGTCGAACGGAAAGGCCTTTC 23
Db  1 CAAGTCGAACGGAAAGGCCTTTC 23
```

Db 3 CAAGTCGAATTGAAAGGACTGTC 25

## RESULT 92

US-09-925-065A-738727/c  
; Sequence 738727, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 738727  
; LENGTH: 552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-738727

Query Match 69.2%; Score 16.6; DB 4; Length 552;  
Best Local Similarity 82.6%; Pred. No. 8.6e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTC 23  
Db 487 CAAGCGGAATGGAAGGCATTTC 465

## RESULT 93

US-09-925-065A-738727/c  
; Sequence 738727, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 738727  
; LENGTH: 552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-738727

Query Match 69.2%; Score 16.6; DB 5; Length 552;  
Best Local Similarity 82.6%; Pred. No. 8.6e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTC 23  
Db 487 CAAGCGGAATGGAAGGCATTTC 465

## RESULT 94

US-09-925-065A-646509/c  
; Sequence 646509, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 646509  
; LENGTH: 572  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-646509

Query Match 69.2%; Score 16.6; DB 4; Length 572;  
Best Local Similarity 82.6%; Pred. No. 8.6e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTTC 23  
Db 125 CAAGGCGAAGAAAGGCTTTC 103

## RESULT 95

US-09-925-065A-646509/c  
; Sequence 646509, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 646509  
; LENGTH: 572  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-646509

Query Match 69.2%; Score 16.6; DB 5; Length 552;  
Best Local Similarity 82.6%; Pred. No. 8.6e+02;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;



```
Query Match      69.2%; Score 16.6; DB 5; Length 572;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
Db      125 CAAGGCCAAGAAAGGCGCTTTC 103

RESULT 96
US-10-972-079-55955/c
; Sequence 55955, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM11110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 55955
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_1
US-10-972-079-55955

Query Match      69.2%; Score 16.6; DB 10; Length 600;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
Db      480 CAAGGGGACGGAAGGACTTTC 458

RESULT 97
US-10-972-079-55956/c
; Sequence 55956, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEER
; FILE REFERENCE: MM11110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 55956
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Chicken 19866894310123_2
US-10-972-079-55956

Query Match      69.2%; Score 16.6; DB 10; Length 600;
Best Local Similarity 82.6%; Pred. No. 8.6e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
Db      113 CAAGGGGACGGAAGGACTTTC 91

RESULT 98
US-10-301-480-553054/c
; Sequence 553054, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-301-480-553054

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Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCGCTTTC 23
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; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-08-09
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; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
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; NUMBER OF SEQ ID NOS: 78614
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GenCore version 5.1.8  
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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	16	66.7	2397	7	US-11-217-529-254 Sequence 254, App
4	15.2	63.3	1260	7	US-11-217-529-5375 Sequence 5375, App
5	15.2	63.3	11611	6	US-10-541-993-4 Sequence 4, Appli
6	15	62.5	1157	6	US-10-196-749-391 Sequence 391, App
7	15	62.5	1157	7	US-11-101-316-145 Sequence 145, App
8	15	62.5	2952	7	US-11-217-529-4946 Sequence 4946, App
9	14.8	61.7	497	6	US-10-488-619-2075 Sequence 2075, App
10	14.8	61.7	599	6	US-10-488-619-2155 Sequence 2155, App
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14	14.6	60.8	1350	7	US-11-217-529-514 Sequence 514, App
15	14.6	60.8	2541	7	US-11-217-529-82268 Sequence 82268, A
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c 130	13.2	55.0	3330	7	US-11-217-529-3415	Sequence 3415, Ap	c 204	12.8	53.3	711	6	US-10-488-619-1859	Sequence 1859, Ap
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c 146	13	54.2	1065	7	US-11-217-529-80744	Sequence 80744, A	c 220	12.8	53.3	1542	7	US-11-217-529-3998	Sequence 3998, Ap
c 147	13	54.2	1080	7	US-11-217-529-77409	Sequence 77409, A	c 221	12.8	53.3	1584	7	US-11-217-529-76285	Sequence 76285, A
c 148	13	54.2	1095	7	US-11-217-529-77804	Sequence 77804, A	c 222	12.8	53.3	1647	7	US-11-217-529-2853	Sequence 2853, Ap
c 149	13	54.2	1098	7	US-11-217-529-494	Sequence 494, App	c 223	12.8	53.3	1653	6	US-10-468-193-25	Sequence 25, Appl
c 150	13	54.2	1119	7	US-11-217-529-81068	Sequence 81068, A	c 224	12.8	53.3	1660	6	US-10-196-749-147	Sequence 147, App
c 151	13	54.2	1173	7	US-11-217-529-77948	Sequence 77948, A	c 225	12.8	53.3	1660	7	US-11-101-316-31	Sequence 31, Appl
c 152	13	54.2	1203	7	US-11-217-529-998	Sequence 998, App	c 226	12.8	53.3	1689	7	US-11-217-529-81231	Sequence 81231, A
c 153	13	54.2	1212	7	US-11-217-529-77899	Sequence 77899, A	c 227	12.8	53.3	1695	7	US-11-217-529-4098	Sequence 4098, Ap
c 154	13	54.2	1350	7	US-11-217-529-76294	Sequence 76294, A	c 228	12.8	53.3	1785	7	US-11-217-529-81561	Sequence 81561, A
c 155	13	54.2	1383	7	US-11-217-529-78730	Sequence 78730, A	c 229	12.8	53.3	1804	7	US-11-251-465-7	Sequence 7, Appli
c 156	13	54.2	1413	7	US-11-217-529-2672	Sequence 2672, Ap	c 230	12.8	53.3	1854	7	US-11-217-529-1678	Sequence 1678, Ap
c 157	13	54.2	1413	7	US-11-217-529-81595	Sequence 81595, A	c 231	12.8	53.3	1887	7	US-11-217-529-76204	Sequence 76204, A
c 158	13	54.2	1449	7	US-11-217-529-906	Sequence 906, App	c 232	12.8	53.3	1915	6	US-10-196-749-275	Sequence 275, App
c 159	13	54.2	1467	7	US-11-217-529-5430	Sequence 5430, Ap	c 233	12.8	53.3	1915	7	US-11-217-529-173838	Sequence 173838
c 160	13	54.2	1491	7	US-11-217-529-6034	Sequence 6034, Ap	c 234	12.8	53.3	2157	7	US-11-217-529-76599	Sequence 76599, A
c 161	13	54.2	1542	7	US-11-217-529-3917	Sequence 3917, Ap	c 235	12.8	53.3	2223	7	US-11-217-529-78291	Sequence 78291, A
c 162	13	54.2	1725	7	US-11-217-529-77670	Sequence 77670, A	c 236	12.8	53.3	2331	7	US-11-217-529-5632	Sequence 5632, Ap
c 163	13	54.2	1737	7	US-11-217-529-82238	Sequence 82238, A	c 237	12.8	53.3	2343	7	US-11-217-529-4231	Sequence 4231, Ap
c 164	13	54.2	1758	7	US-11-217-529-1422	Sequence 1422, Ap	c 238	12.8	53.3	2387	7	US-11-226-605-50	Sequence 50, Appl
c 165	13	54.2	1887	7	US-11-217-529-2426	Sequence 2426, Ap	c 239	12.8	53.3	2454	7	US-11-217-529-6038	Sequence 6038, Ap
c 166	13	54.2	1980	7	US-11-217-529-82112	Sequence 82112, A	c 240	12.8	53.3	2823	7	US-11-217-529-4032	Sequence 4032, Ap
c 167	13	54.2	2015	7	US-11-217-529-2923	Sequence 2923, Ap	c 241	12.8	53.3	2910	7	US-11-217-529-77545	Sequence 77545, A
c 168	13	54.2	2115	7	US-11-217-529-76502	Sequence 76502, Ap	c 242	12.8	53.3	2976	7	US-11-217-529-80319	Sequence 80319, A
c 169	13	54.2	2193	7	US-11-217-529-81384	Sequence 81384, A	c 243	12.8	53.3	3108	7	US-11-217-529-3251	Sequence 3251, Ap
c 170	13	54.2	2212	6	US-10-196-749-325	Sequence 325, App	c 244	12.8	53.3	3396	6	US-10-505-928-346	Sequence 346, App
c 171	13	54.2	2217	7	US-11-217-529-80740	Sequence 80740, A							

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245 12.8 53.3 3588 6 US-10-505-928-84 Sequence 84, Appl
246 12.8 53.3 3930 7 US-11-217-529-76026 Sequence 76026, A
247 12.8 53.3 5071 6 US-10-505-928-616 Sequence 616, App
c 248 12.8 53.3 7873 6 US-10-485-397-7 Sequence 7, Appli
c 249 12.8 53.3 7943 6 US-10-485-397-8 Sequence 8, Appli
c 250 12.8 53.3 8090 7 US-11-228-605-86 Sequence 86, Appl
c 251 12.8 53.3 9246 7 US-11-217-529-3285 Sequence 3285, App
c 252 12.8 53.3 128361 6 US-10-505-928-151 Sequence 151, App
c 253 12.6 52.5 25 7 US-11-217-529-10285 Sequence 10285, A
c 254 12.6 52.5 25 7 US-11-217-529-27271 Sequence 27271, A
c 255 12.6 52.5 25 7 US-11-217-529-162183 Sequence 162183,
c 256 12.6 52.5 25 7 US-11-217-529-168245 Sequence 168245,
c 257 12.6 52.5 25 7 US-11-217-529-168252 Sequence 168252,
c 258 12.6 52.5 162 7 US-11-217-529-166599 Sequence 166599,
c 259 12.6 52.5 321 7 US-11-217-529-80939 Sequence 80939, A
c 260 12.6 52.5 381 7 US-11-217-529-166545 Sequence 166545,
c 261 12.6 52.5 435 7 US-11-217-529-75873 Sequence 75873, A
c 262 12.6 52.5 576 6 US-10-511-917-366 Sequence 366, App
c 263 12.6 52.5 670 6 US-10-488-619-2286 Sequence 2286, App
c 264 12.6 52.5 732 7 US-11-217-529-82430 Sequence 82430, A
c 265 12.6 52.5 756 7 US-11-217-529-3092 Sequence 3092, A
c 266 12.6 52.5 822 7 US-11-217-529-75872 Sequence 75872, A
c 267 12.6 52.5 829 7 US-11-252-080-11 Sequence 11, Appl
c 268 12.6 52.5 837 7 US-11-217-529-173884 Sequence 173884,
c 269 12.6 52.5 872 6 US-10-488-619-1544 Sequence 1544, App
c 270 12.6 52.5 909 6 US-10-473-173-50 Sequence 50, Appl
c 271 12.6 52.5 990 7 US-11-217-529-4134 Sequence 4134, App
c 272 12.6 52.5 1062 7 US-11-217-529-1585 Sequence 1585, App
c 273 12.6 52.5 1065 7 US-11-217-529-82055 Sequence 82055, A
c 274 12.6 52.5 1083 7 US-11-242-505A-2 Sequence 2, Appli
c 275 12.6 52.5 1098 7 US-11-217-529-1708 Sequence 1708, App
c 276 12.6 52.5 1158 7 US-11-217-529-190921 Sequence 190921,
c 277 12.6 52.5 1224 7 US-11-217-529-81416 Sequence 81416, A
c 278 12.6 52.5 1254 7 US-11-217-529-406 Sequence 406, App
c 279 12.6 52.5 1254 7 US-11-217-529-5416 Sequence 5416, App
c 280 12.6 52.5 1275 7 US-11-217-529-79354 Sequence 79354, A
c 281 12.6 52.5 1287 7 US-11-217-529-3812 Sequence 3812, App
c 282 12.6 52.5 1326 7 US-11-217-529-1929 Sequence 1929, App
c 283 12.6 52.5 1344 7 US-11-217-529-6073 Sequence 6073, App
c 284 12.6 52.5 1398 7 US-11-217-529-2602 Sequence 2602, App
c 285 12.6 52.5 1413 7 US-11-217-529-5563 Sequence 5563, App
c 286 12.6 52.5 1467 7 US-11-217-529-398 Sequence 398, App
c 287 12.6 52.5 1614 7 US-11-217-529-6108 Sequence 6108, App
c 288 12.6 52.5 1653 6 US-10-505-928-587 Sequence 587, App
c 289 12.6 52.5 1716 7 US-11-226-605-42 Sequence 42, Appl
c 290 12.6 52.5 1716 7 US-11-217-529-78630 Sequence 78630, A
c 291 12.6 52.5 1790 7 US-11-242-505A-1 Sequence 1, Appli
c 292 12.6 52.5 1833 7 US-11-217-529-4667 Sequence 4667, App
c 293 12.6 52.5 1854 7 US-11-217-529-1678 Sequence 1678, App
c 294 12.6 52.5 1947 7 US-11-217-529-4699 Sequence 4699, App
c 295 12.6 52.5 2007 7 US-11-217-529-81504 Sequence 81504, A
c 296 12.6 52.5 2043 7 US-11-217-529-2687 Sequence 2687, App
c 297 12.6 52.5 2043 6 US-10-981-760-1 Sequence 1, Appli
c 298 12.6 52.5 2200 6 US-10-981-760-3 Sequence 3, Appli
c 299 12.6 52.5 2225 6 US-10-505-928-24 Sequence 24, Appl
300 12.6 52.5 2341 6 US-10-511-937-349 Sequence 349, App

ALIGNMENTS

RESULT 1
US-11-217-529-80747
; Sequence 80747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
DB 265 CAATCCAACTGAATGGCTTTCG 288

RESULT 2
US-11-217-529-79690/c
; Sequence 79690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
|||||
DB 265 CAATCCAACTGAATGGCTTTCG 288

RESULT 3
US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

Query Match 66.7%; Score 16; DB 7; Length 1824;
Best Local Similarity 79.2%; Pred. No. 9.1;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCGCTTTCG 24
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DB 752 CAATCGACGGAATGACTTACG 729
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30

; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 391  
; LENGTH: 1157  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-196-749-391

Query Match 62.5%; Score 15; DB 6; Length 1157;  
Best Local Similarity 78.3%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23  
||||| ||||| ||||| ||||| |||||  
Db 155 CAAGTGAACGGAAGGCGCCTGC 177

RESULT 7  
US-11-101-316-145  
; Sequence 145, Application US/11101316  
; Publication No. US20060099657A1  
; GENERAL INFORMATION:  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID  
; FILE REFERENCE: P3230R1C17C1  
; CURRENT APPLICATION NUMBER: US/11/101,316  
; CURRENT FILING DATE: 2005-04-06  
; PRIOR APPLICATION NUMBER: 10/063526  
; PRIOR FILING DATE: 2002-05-03  
; PRIOR APPLICATION NUMBER: 10/006867  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/23328  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 09/380137  
; PRIOR FILING DATE: 1999-08-25  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: 60/087759  
; PRIOR FILING DATE: 1998-06-02  
; NUMBER OF SEQ ID NOS: 170  
; SEQ ID NO 145  
; LENGTH: 1157  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-11-101-316-145

Query Match 62.5%; Score 15; DB 7; Length 1157;  
Best Local Similarity 78.3%; Pred. No. 27;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23  
||||| ||||| ||||| ||||| |||||  
Db 155 CAAGTGAACGGAAGGCGCCTGC 177

RESULT 8  
US-11-217-529-4946/c  
; Sequence 4946, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA

; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4946  
; LENGTH: 2952  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-4946

Query Match 62.5%; Score 15; DB 7; Length 2952;  
Best Local Similarity 78.3%; Pred. No. 31;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTCG 24  
||||| ||||| ||||| ||||| |||||  
Db 2664 AATTCGATCTGGAAGGCCCTTCG 2642

RESULT 9  
US-10-488-619-2075  
; Sequence 2075, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2075  
; LENGTH: 497  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-2075

Query Match 61.7%; Score 14.8; DB 6; Length 497;  
Best Local Similarity 88.9%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18  
||||| ||||| ||||| |||||  
Db 69 CCAGTCGCACGGAAGGC 86

RESULT 10  
US-10-488-619-2156  
; Sequence 2156, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2156  
; LENGTH: 599  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-2156

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Query Match      61.7%; Score 14.8; DB 6; Length 599;
Best Local Similarity 88.9%; Pred. No. 31;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18
    ||||| ||||| |||||
Db 537 CCAAGTCGACGGAAGGC 554

RESULT 11
US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      61.7%; Score 14.8; DB 6; Length 784;
Best Local Similarity 88.9%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGC 18
    ||||| ||||| |||||
Db 397 CCAAGTCGACGGAAGGC 380

RESULT 12
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      60.8%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24
    ||||| ||||| |||||
Db 5 GTCCACGGAAGAACCGCGTCG 25

RESULT 13
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US 10/932,182
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match      60.8%; Score 14.6; DB 7; Length 471;
Best Local Similarity 81.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GTCGAACGGAAGGCCTTTCG 24
    ||||| ||||| |||||
Db 152 GTCCACGGAAGAACCGCGTCG 172

RESULT 14
US-11-217-529-730
; Sequence 730, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 730
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-730

Query Match      60.8%; Score 14.6; DB 7; Length 1350;
Best Local Similarity 81.0%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTT 21
    ||||| ||||| |||||
Db 1128 CCAAGTCGACGACAGTCCTT 1148

RESULT 15
US-11-217-529-514/c
; Sequence 514, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```



```
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 514
; LENGTH: 2541
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-514

Query Match      60.8%; Score 14.6; DB 7; Length 2541;
Best Local Similarity 81.0%; Pred. No. 48;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      ||||| ||||| ||||| ||||| |||||
Db      2480 AAGTCAATGTAATGCGCTTT 2460

RESULT 16
US-11-217-529-82268/c
; Sequence 82268, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82268
; LENGTH: 2883
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82268

Query Match      60.8%; Score 14.6; DB 7; Length 2883;
Best Local Similarity 81.0%; Pred. No. 49;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCCTTT 22
      ||||| ||||| ||||| ||||| |||||
Db      2230 AAGTAGAAGGAACGCGCTTT 2210

RESULT 17
US-11-217-529-56270/c
; Sequence 56270, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
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; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56270
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-56270

Query Match      60.0%; Score 14.4; DB 7; Length 25;
Best Local Similarity 93.8%; Pred. No. 32;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGG 17
      ||||| ||||| ||||| |||||
Db      18 AAGTCGAATGGAAGG 3

RESULT 18
US-11-217-529-4661
; Sequence 4661, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4661
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4661

Query Match      60.0%; Score 14.4; DB 7; Length 750;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCCTTCG 24
      ||||| ||||| ||||| ||||| |||||
Db      297 CAAGTCGATGAAGAGGCCGTAG 320

RESULT 19
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; APPLICANT: GICQUEL, BRIGITTE
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCObACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
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; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
US-11-324-517-36

Query Match          60.0%; Score 14.4; DB 7; Length 1600;
Best Local Similarity 75.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 1476 CAAGTCGACCGGAAGCGCGTACG 1499

RESULT 20
US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

Query Match          60.0%; Score 14.4; DB 7; Length 1872;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 163 CGATTCTGATGGAATGCTTTTG 140

RESULT 21
US-11-217-529-75610/c
; Sequence 75610, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
```

```
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75610
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75610

Query Match          60.0%; Score 14.4; DB 7; Length 2013;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 527 CAATTCAATCTGAAAGTCCCTTTTG 504

RESULT 22
US-11-217-529-3183
; Sequence 3183, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3183
; LENGTH: 2376
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3183

Query Match          60.0%; Score 14.4; DB 7; Length 2376;
Best Local Similarity 75.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTTCG 24
Db 1306 CAAGTCGAAGCTAACGGGATTTTCG 1329

RESULT 23
US-11-217-529-6038
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-6038

Query Match          60.0%; Score 14.4; DB 7; Length 2454;
Best Local Similarity 93.8%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      8 AACGGAAGGCTTTC 23
Db      1022 AATGGAAGGCTTTC 1037

RESULT 24
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match          60.0%; Score 14.4; DB 7; Length 3663;
Best Local Similarity 75.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      1 CAAGTCGAACGGAAGGCTTTCG 24
Db      348 CAAATCTAACGTAAGGCTTCTTG 325

RESULT 25
US-11-217-529-4529/c
; Sequence 4529, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369
```

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; SEQ ID NO 4529
; LENGTH: 4365
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4529

Query Match          60.0%; Score 14.4; DB 7; Length 4365;
Best Local Similarity 93.8%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGG 17
Db      4147 AAGTCGAATCGAAGG 4132

RESULT 26
US-11-217-529-75552
; Sequence 75552, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75552
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75552

Query Match          59.2%; Score 14.2; DB 7; Length 480;
Best Local Similarity 84.2%; Pred. No. 61;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGGCTT 20
Db      212 AAGACGAATGGAGAGGCT 230

RESULT 27
US-11-217-529-1257/c
; Sequence 1257, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1257
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1257
```

```
Query Match          59.2%; Score 14.2; DB 7; Length 858;
Best Local Similarity 84.2%; Pred. NO.66;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 5 TCGAACGGAAGGCCCTTC 23  
Db 187 TCGAAGAGAAAGGCCCTTC 169

```

RESULT 28
US-11-217-529-77141/c
; Sequence 77141, Application US/11217529
; Publication No. US2006099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 9-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77141
; LENGTH: 858
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77141

```

	Query Match	59.2%	Score
	Best Local Similarity	84.2%	Percent
	Matches	16;	Conservative
		0;	1
QY	5	TCGAACGGAAGGCGCTTTC	23
Db	187	TCGAACGGAAGGCGCTTTC	169

```

RESULT 29
US-11-217-529-60921/c
; Sequence 60921, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 60921
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-60921

```

Query Match 58.3%; Score 14; DB 7; Length 25;  
Best Local Similarity 77.3%; Pred. NO. 51;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```

QY      2  AAGTCGAACGGAAGGCCCTTC  23
        |||||
Db      22  AATTCGATTCGGAAGGCCCTTC  1
        |||||

RESULT 30
US-11-217-529-117575/c
; Sequence 117575, Application US/11217529
; Publication No. US2006009612A1
; GENERAL INFORMATION:

```

```

RESULT 30
US-11-217-529-117575/c
; Sequence 117575, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIRO
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 8-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/9332,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 117575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-117575

```

```

Query Match          58.3%; Score
Best Local Similarity 77.3%; Pred.
Matches 17; Conservative 0; Mismatches 10
QY 1 CAGTTCGAACGGAAAGGCCCTTT 22
    |||||
DB 22 CAGTTCGAAGGTATATGACTTT 1

```

RESULT 31  
US-11-217-529-152173  
; Sequence 152173, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 152173  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: *Saccharomyces pastorianus*  
US-11-217-529-152173

	Query Match	58.3%;	Score
	Best Local Similarity	77.3%;	Pred.
	Matches	17; Conservative	0; Mismatch
Qy	1	CAAGTCGAACGGAAAGGCCCTTT	228
Db	4	CAAGTCTTCGGAAAGGCCCTCT	250

```
RESULT 32
US-11-139-257-9
; Sequence 9, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-139-257-9

Query Match      58.3%; Score 14; DB 7; Length 150;
Best Local Similarity 77.3%; Pred. No. 65;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 10 CATGACAAACGGCAAGGCTTT 31

RESULT 33
US-11-139-257-14
; Sequence 14, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 210
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Positive internal control
US-11-139-257-14

Query Match      58.3%; Score 14; DB 7; Length 210;
Best Local Similarity 77.3%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 40 CATGACAAACGGCAAGGCTTT 61

RESULT 34
US-11-139-257-12
; Sequence 12, Application US/11139257
; Publication No. US2006008849A1
; GENERAL INFORMATION:
; APPLICANT: Happe, Scott
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis of Group B
; FILE OF INVENTION: Streptococcus Infection
; FILE REFERENCE: 25436/2512
; CURRENT APPLICATION NUMBER: US/11/139,257
; CURRENT FILING DATE: 2005-05-27
; PRIOR APPLICATION NUMBER: US 60/575,124
; PRIOR FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Control Sequence
US-11-139-257-12

Query Match      58.3%; Score 14; DB 7; Length 213;
Best Local Similarity 77.3%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 41 CATGACAAACGGCAAGGCTTT 62

RESULT 35
US-11-217-529-81538
; Sequence 81538, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81538
; LENGTH: 363
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81538

Query Match      58.3%; Score 14; DB 7; Length 363;
Best Local Similarity 77.3%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCTTT 22
Db 90 CAAGTTCTTCGAAAGGCTCT 111

RESULT 36
US-11-217-529-79564/c
; Sequence 79564, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79564
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-79564

Query Match      58.3%; Score 14; DB 7; Length 381;
Best Local Similarity 77.3%; Pred. No. 74;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
Db 108 CAAGTCGATCGGAAGTGACTCT 87

RESULT 37
US-11-217-529-78815
; Sequence 78815, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78815
; LENGTH: 438
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-78815

Query Match      58.3%; Score 14; DB 7; Length 438;
Best Local Similarity 77.3%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AAGTCGAACGGAAGGCCTTTC 23
Db 1 ATGTCGAAGGAAGGTTTTC 22

RESULT 38
US-11-217-529-2487
; Sequence 2487, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2487
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-2487

Query Match      58.3%; Score 14; DB 7; Length 579;
Best Local Similarity 77.3%; Pred. No. 79;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CAAGTCGAACGGAAGGCCTTT 22
Db 86 CAATTCCACTAAAGGACTTT 107

RESULT 39
US-11-217-529-81387
; Sequence 81387, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81387
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-81387

Query Match      58.3%; Score 14; DB 7; Length 666;
Best Local Similarity 77.3%; Pred. No. 80;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AACTCGAACGGAAGGCCTTTC 23
Db 374 AAGTGAATGGAAGGCTCTCC 395

RESULT 40
US-11-217-529-4416
; Sequence 4416, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4416
; LENGTH: 837
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-4416

Query Match      58.3%; Score 14; DB 7; Length 837;
Best Local Similarity 77.3%; Pred. No. 83;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2  AAGTCGAACGGAAGGCCTTTC 23
      ||||| || ||||| || |||||
Db      176 AAGTCGAAGGAATGTCATTTC 197
      ||||| || ||||| || |||||

RESULT 41
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7

Query Match      58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3  AGTCGAACGGAAGGCCTTTC 24
      ||||| || ||||| || |||||
Db      1014 AGTCGAAGACTGGGCCTTTC 1035
      ||||| || ||||| || |||||

RESULT 42
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9

Query Match      58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3  AGTCGAACGGAAGGCCTTTC 24
      ||||| || ||||| || |||||
Db      1014 AGTCGAAGACTGGGCCTTTC 1035
      ||||| || ||||| || |||||

RESULT 43
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
```

```
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH Variant RC-35
US-10-975-697-11

Query Match      58.3%; Score 14; DB 6; Length 1080;
Best Local Similarity 77.3%; Pred. No. 86;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      3  AGTCGAACGGAAGGCCTTTC 24
      ||||| || ||||| || |||||
Db      1014 AGTCGAAGACTGGGCCTTTC 1035
      ||||| || ||||| || |||||

RESULT 44
US-11-217-529-78457/c
; Sequence 78457, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78457
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78457

Query Match      58.3%; Score 14; DB 7; Length 1194;
Best Local Similarity 77.3%; Pred. No. 87;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1  CAAGTCGAACGGAAGGCCTTT 22
      || ||||| || || |||||
Db      980  CAGTCGAAGGGTAATGACTTT 959
      || ||||| || || |||||

RESULT 45
US-10-196-749-223/c
; Sequence 223, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 223
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-196-749-223

Query Match      58.3%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||||| ||||| ||||| |||||
Db      807 AAGGCGCCCGGAAGGCGGTGC 786

RESULT 46
US-09-949-925-62/c
; Sequence 62, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P203P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; ORGANISM: Homo Sapien

Query Match      58.3%; Score 14; DB 6; Length 1245;
Best Local Similarity 77.3%; Pred. No. 88;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||||| ||||| ||||| |||||
Db      807 AAGGCGCCCGGAAGGCGGTGC 786

RESULT 47
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match      58.3%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||||| ||||| ||||| |||||
Db      971 AAGTCGAACGGAAGGCGCTTTC 950

RESULT 48
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-62

Query Match      58.3%; Score 14; DB 1; Length 1452;
Best Local Similarity 77.3%; Pred. No. 90;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||||| ||||| ||||| |||||
Db      947 AAGTATAAGTAAAGGCGCTTGC 926

RESULT 47
US-11-217-529-1925/c
; Sequence 1925, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1925
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1925

Query Match      58.3%; Score 14; DB 7; Length 1887;
Best Local Similarity 77.3%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 AAGTCGAACGGAAGGCGCTTTC 23
      ||||| ||||| ||||| |||||
Db      971 AAGTCGAACGGAAGGCGCTTTC 950

RESULT 48
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876
```





```
RESULT 53
US-11-217-529-3215/c
; Sequence 3215, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3215
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3215

Query Match      58.3%; Score 14; DB 7; Length 3093;
Best Local Similarity 77.3%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTT 22
Db 1579 CAAGTTGATGAAGAAAGCGGTTT 1558

RESULT 54
US-11-217-529-82660/c
; Sequence 82660, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82660
; LENGTH: 4806
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82660

Query Match      58.3%; Score 14; DB 7; Length 4806;
Best Local Similarity 77.3%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCGCTTTC 23
Db 836 AATTCAAACGGAATAGGCTTTC 815

RESULT 55
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-29

Query Match      58.3%; Score 14; DB 6; Length 6805;
Best Local Similarity 77.3%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCGCTTTCG 24
Db 1258 AGTCGAAGAGACTGGGCGCTTTCG 1237

RESULT 56
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-31

Query Match      58.3%; Score 14; DB 6; Length 7330;
Best Local Similarity 77.3%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCGCTTTCG 24
Db 1258 AGTCGAAGAGACTGGGCGCTTTCG 1237

RESULT 57
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-25
```

```
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:glya overexpression
; OTHER INFORMATION: plasmid
US-10-520-210-25

Query Match      58.3%; Score 14; DB 6; Length 7701;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AGTCGAACGGAAGGCCTTCG 24
      ||||| | |||||
Db      1263 AGTCGAAGACTGGCCTTCG 1242

RESULT 58
US-10-520-210-24/c
; Sequence 24, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; TITLE OF INVENTION: PANTOTHENATE
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 7926
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:serA overexpression
; OTHER INFORMATION: plasmid
US-10-520-210-24

Query Match      58.3%; Score 14; DB 6; Length 7926;
Best Local Similarity 77.3%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      3 AGTCGAACGGAAGGCCTTCG 24
      ||||| | |||||
Db      1263 AGTCGAAGACTGGCCTTCG 1242

RESULT 59
US-10-519-335-37/c
; Sequence 37, Application US/10519335
; Publication No. US20060099210A1
; GENERAL INFORMATION:
; APPLICANT: Cavarec, Laurent
```

```
; APPLICANT: Chumakov, Ilya
; APPLICANT: Destenaves, Benoit
; APPLICANT: Gonthier, Catherine
; APPLICANT: Elias, Isabelle
; TITLE OF INVENTION: NOVEL KCNQ POLYPEPTIDES, MODULATORS THEREOF, AND THEIR USES IN TH
; TITLE OF INVENTION: TREATMENT OF MENTAL DISORDERS
; FILE REFERENCE: G-194US03PCT
; CURRENT APPLICATION NUMBER: US/10/519,335
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 60/391,359
; PRIOR FILING DATE: 2002-06-25
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 151830
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (10)..(10)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60402)..(60402)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61110)..(61110)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98207)..(98207)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98208)..(98208)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98209)..(98209)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98210)..(98210)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (98211)..(98211)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (99743)..(99743)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (108055)..(108055)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109094)..(109094)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (109125)..(109125)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (118900)..(118900)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (119024)..(119024)
; OTHER INFORMATION: n = a or c or g or t
```

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;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119053)..(119112)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119115)..(119121)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (119123)..(119123)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (141674)..(141674)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142063)..(142063)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142137)..(142137)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (142967)..(142967)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143077)..(143077)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143506)..(143506)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143587)..(143587)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (143629)..(143629)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (149079)..(149079)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5363)..(5363)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8080)..(8080)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10296)..(10296)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14528)..(14528)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15336)..(15336)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15457)..(15457)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
;

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; NAME/KEY: misc feature
; LOCATION: (16288)..(16288)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16306)..(16307)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16316)..(16316)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16397)..(16397)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (56012)..(56012)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (57662)..(57662)
; OTHER INFORMATION: n = a or c or g or t
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(54)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (55)..(124)
; OTHER INFORMATION: exon 1
; FEATURE:
; NAME/KEY: exon
; LOCATION: (91147)..(91244)
; OTHER INFORMATION: exon 2
; FEATURE:
; NAME/KEY: exon
; LOCATION: (93669)..(93834)
; OTHER INFORMATION: exon 3
; FEATURE:
; NAME/KEY: exon
; LOCATION: (96310)..(96422)
; OTHER INFORMATION: exon 4
; FEATURE:
; NAME/KEY: exon
; LOCATION: (99546)..(99723)
; OTHER INFORMATION: exon 5
; FEATURE:
; NAME/KEY: exon
; LOCATION: (125441)..(125605)
;

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Query Match 58.3%; Score 14; DB 6; Length 151830;  
Best Local Similarity 77.3%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CAAGTCGACGGAAAGGCGCTTT 22  
|||||  
Db 127951 CAAGGCGATCAAGGGCGCTTT 127930  
|||||

RESULT 60  
US-10-506-549-3/c  
; Sequence 3, Application US/10506549  
; Publication No. US20060100417A1  
; GENERAL INFORMATION:  
; APPLICANT: APPLERA CORPORATION  
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
; TITLE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: CL001361-US  
; CURRENT APPLICATION NUMBER: US/10/506,549  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: 60/361,343

; PRIOR FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 394191  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(394191)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-506-549-3

Query Match 58.3%; Score 14; DB 6; Length 394191;  
Best Local Similarity 77.3%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTTCG 24  
Db 388331 AGGCAATGGAAGGCTTTAG 388310

## RESULT 61

US-11-217-529-75992  
; Sequence 75992, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 75992  
; LENGTH: 1236  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-75992

Query Match 57.5%; Score 13.8; DB 7; Length 1236;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGG 17  
Db 1176 CAAGTCGAAGGGAATG 1192

## RESULT 62

US-11-217-529-79704  
; Sequence 79704, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 79704  
; LENGTH: 1380  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-79704

Query Match 57.5%; Score 13.8; DB 7; Length 1380;  
Best Local Similarity 88.2%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGC 18  
Db 1061 AATTCGAACGGAAGGC 1077

## RESULT 63

US-09-949-925-78/c  
; Sequence 78, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 67 Human secreted proteins  
; FILE REFERENCE: P2023P2  
; CURRENT APPLICATION NUMBER: US/09/949,925  
; CURRENT FILING DATE: 2001-09-12  
; PRIOR APPLICATION NUMBER: US 60/232,150  
; PRIOR FILING DATE: 2000-12-09  
; PRIOR APPLICATION NUMBER: PCT/US99/01621  
; PRIOR FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,167  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,162  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,161  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: US 60/073,170  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 298  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 78  
; LENGTH: 1931  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1212)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-949-925-78

Query Match 57.5%; Score 13.8; DB 1; Length 1931;  
Best Local Similarity 88.2%; Pred. No. 1.2e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 TCGAACGGAAGGCCTT 21  
Db 248 TCGAACGGAAGGCATT 232

## RESULT 64

US-09-949-925-12/c  
; Sequence 12, Application US/09949925  
; Publication No. US20060099575A9  
; GENERAL INFORMATION:

```
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2021P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-12

Query Match      57.5%; Score 13.8; DB 1; Length 1932;
Best Local Similarity 88.2%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 TCGAACGGAAGGCCTT 21
        ||||| ||||| ||||| |||||
Db      248 TCGAAGGGAAGGCATT 232

RESULT 65
US-11-217-529-98883
; Sequence 98883, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-98883

Query Match      56.7%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AAGTCGACGGAAGGCCTT 21
        ||||| ||||| ||||| |||||
Db      3 AACTCTACCTGAAAGGCCTT 22

RESULT 66
US-11-217-529-130040/c
; Sequence 130040, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 130040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-130040

Query Match      56.7%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CAAGTCGACGGAAGGCCT 20
        ||||| ||||| ||||| |||||
Db      21 CAAGTCGATCGGAAGTGACT 2

RESULT 67
US-11-217-529-188129
; Sequence 188129, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-188129

Query Match      56.7%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AAGTCGACGGAAGGCCTT 21
        ||||| ||||| ||||| |||||
Db      3 AACTCTACCTGAAAGGCCTT 22

RESULT 68
US-10-488-619-2026
```

```
Db      6 AAGTCACACGCAAAAGGCCT 25

RESULT 66
US-11-217-529-130040/c
; Sequence 130040, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 130040
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-130040

Query Match      56.7%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CAAGTCGACGGAAGGCCT 20
        ||||| ||||| ||||| |||||
Db      21 CAAGTCGATCGGAAGTGACT 2

RESULT 67
US-11-217-529-188129
; Sequence 188129, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 188129
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-188129

Query Match      56.7%; Score 13.6; DB 7; Length 25;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 AAGTCGACGGAAGGCCTT 21
        ||||| ||||| ||||| |||||
Db      3 AACTCTACCTGAAAGGCCTT 22

RESULT 68
US-10-488-619-2026
```

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; Sequence 2026, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2026

Query Match          56.7%; Score 13.6; DB 6; Length 523;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 22
Db 257 AATCAAGGAAGGACTTT 276

RESULT 69
US-11-217-529-4440
; Sequence 4440, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4440
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4440

Query Match          56.7%; Score 13.6; DB 7; Length 903;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 TCGAACGGAAGGCCTTCG 24
Db 268 TCGAACGGAAGGACTTGG 287

RESULT 70
US-10-473-173-107/c
; Sequence 107, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
```

```
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107

Query Match          56.7%; Score 13.6; DB 6; Length 927;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCT 20
Db 564 CAGGAAGCAGCAAGGCCT 545

RESULT 71
US-11-217-529-174359
; Sequence 174359, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174359
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174359

Query Match          56.7%; Score 13.6; DB 7; Length 984;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTT 21
Db 837 AACTCTACCTGAAAGGCCTT 856

RESULT 72
US-11-217-529-3863
; Sequence 3863, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3863
; LENGTH: 1224
; TYPE: DNA
```

; ORGANISM: Saccharomyces pastorianus															
US-11-217-529-3863															
Query Match 56.7%; Score 13.6; DB 7; Length 1224;															
Best Local Similarity 80.0%; Pred. No. 1.4e+02;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
QY	4	GTGCAACGGAAGGCGCTTTC	23												
Db	309	GTGCAAAAGGAAGGCGCTTGC	328												
RESULT 73															
US-11-217-529-78935															
; Sequence 78935, Application US/11217529															
; Publication No. US20060099612A1															
; GENERAL INFORMATION:															
; APPLICANT: SUNTORY LIMITED															
; APPLICANT: NAKAO, YOSHIHIRO															
; APPLICANT: NAKAMURA, NORIHISA															
; APPLICANT: KODAMA, YUKIKO															
; APPLICANT: FUJIMURA, TOMOKO															
; APPLICANT: ASHIKARI, TOSHIHIKO															
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS															
; FILE REFERENCE: S-38-285															
; CURRENT APPLICATION NUMBER: US/11/217,529															
; PRIOR FILING DATE: 2005-09-02															
; PRIOR APPLICATION NUMBER: US 10/932,182															
; PRIOR FILING DATE: 2004-09-02															
; NUMBER OF SEQ ID NOS: 197023															
; SOFTWARE: PatentIn version 3.3															
; SEQ ID NO 78935															
; LENGTH: 1242															
; TYPE: DNA															
; ORGANISM: Saccharomyces pastorianus															
US-11-217-529-78935															
Query Match 56.7%; Score 13.6; DB 7; Length 1242;															
Best Local Similarity 80.0%; Pred. No. 1.4e+02;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
QY	5	TCGAACGGAAGGCGCTTTCG	24												
Db	63	TCGAACAGTAAGGCGCTTTTG	82												
RESULT 74															
US-11-217-529-76764															
; Sequence 76764, Application US/11217529															
; Publication No. US20060099612A1															
; GENERAL INFORMATION:															
; APPLICANT: SUNTORY LIMITED															
; APPLICANT: NAKAO, YOSHIHIRO															
; APPLICANT: NAKAMURA, NORIHISA															
; APPLICANT: KODAMA, YUKIKO															
; APPLICANT: FUJIMURA, TOMOKO															
; APPLICANT: ASHIKARI, TOSHIHIKO															
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS															
; FILE REFERENCE: S-38-285															
; CURRENT APPLICATION NUMBER: US/11/217,529															
; PRIOR FILING DATE: 2005-09-02															
; PRIOR APPLICATION NUMBER: US 10/932,182															
; PRIOR FILING DATE: 2004-09-02															
; NUMBER OF SEQ ID NOS: 197023															
; SOFTWARE: PatentIn version 3.3															
; SEQ ID NO 76764															
; LENGTH: 1479															
; TYPE: DNA															
; ORGANISM: Saccharomyces pastorianus															
US-11-217-529-76764															
Query Match 56.7%; Score 13.6; DB 7; Length 1479;															
Best Local Similarity 80.0%; Pred. No. 1.4e+02;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
QY	3	AGTCGAACGGAAGGCGCTTTT	22												
Db	7	AGTCGAACACTACAGGCGCTTT	26												
RESULT 75															
US-10-505-928-419															
; Sequence 419, Application US/10505928															
; Publication No. US20060088532A1															
; GENERAL INFORMATION:															
; APPLICANT: Ludwig Institute for Cancer Research et al.															
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES															
; FILE REFERENCE: 28967/39178															
; CURRENT APPLICATION NUMBER: US/10/505,928															
; CURRENT FILING DATE: 2004-08-27															
; PRIOR APPLICATION NUMBER: US 60/363,019															
; PRIOR FILING DATE: 2002-03-07															
; NUMBER OF SEQ ID NOS: 866															
; SOFTWARE: PatentIn 3.2															
; SEQ ID NO 419															
; LENGTH: 1667															
; TYPE: DNA															
; ORGANISM: Homo sapiens															
US-10-505-928-419															
Query Match 56.7%; Score 13.6; DB 6; Length 1667;															
Best Local Similarity 80.0%; Pred. No. 1.5e+02;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
QY	1	CAAGTCGAACGGAAGGCGCT	20												
Db	370	CAAGTCGAGCGCAAGCACT	389												
RESULT 76															
US-11-217-529-82107															
; Sequence 82107, Application US/11217529															
; Publication No. US20060099612A1															
; GENERAL INFORMATION:															
; APPLICANT: SUNTORY LIMITED															
; APPLICANT: NAKAO, YOSHIHIRO															
; APPLICANT: NAKAMURA, NORIHISA															
; APPLICANT: KODAMA, YUKIKO															
; APPLICANT: FUJIMURA, TOMOKO															
; APPLICANT: ASHIKARI, TOSHIHIKO															
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS															
; FILE REFERENCE: S-38-285															
; CURRENT APPLICATION NUMBER: US/11/217,529															
; CURRENT FILING DATE: 2005-09-02															
; PRIOR APPLICATION NUMBER: US 10/932,182															
; PRIOR FILING DATE: 2004-09-02															
; NUMBER OF SEQ ID NOS: 197023															
; SOFTWARE: PatentIn version 3.3															
; SEQ ID NO 82107															
; LENGTH: 1797															
; TYPE: DNA															
; ORGANISM: Saccharomyces pastorianus															
US-11-217-529-82107															
Query Match 56.7%; Score 13.6; DB 7; Length 1797;															
Best Local Similarity 80.0%; Pred. No. 1.5e+02;															
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;															
QY	1	CAAGTCGAACGGAAGGCGCT	20												
Db	485	CAAGCTCAACGATAGGCGCT	504												
RESULT 77															
US-11-217-529-5081															
; Sequence 5081, Application US/11217529															
; Sequence 5081, Application US/11217529															
; Sequence 5081, Application US/11217529															



```
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5081
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5081

Query Match          56.7%; Score 13.6; DB 7; Length 2040;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 AGTCGAACGGAAGGCCTT 22
Db 62 AGACGAACCTTAAGGCATT 81

RESULT 78
US-11-217-529-82283/c
; Sequence 82283, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82283
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82283

Query Match          56.7%; Score 13.6; DB 7; Length 2436;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTT 21
Db 1920 AACTTGAAGGGAAGGCCTT 1901

RESULT 79
US-11-217-529-76785
; Sequence 76785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
```

```
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76785
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76785

Query Match          56.7%; Score 13.6; DB 7; Length 2595;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGGCCTT 21
Db 2545 AAGTCACACGCAAGGCCTT 2564

RESULT 80
US-11-217-529-32547/c
; Sequence 32547, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32547
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-32547

Query Match          55.8%; Score 13.4; DB 7; Length 25;
Best Local Similarity 73.9%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCCTTTC 23
Db 23 CAAATGGAACGTCAAAGTCTTTC 1

RESULT 81
US-11-217-529-94649
; Sequence 94649, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 94649
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-94649

Query Match          55.8%; Score 13.4; DB 7; Length 25;
Best Local Similarity 73.9%; Pred. No. 1.e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
Db 2 CAACGCGACGGAAGAACTACTTTC 24

RESULT 82
US-11-217-529-166591
; Sequence 166591, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 166591
; LENGTH: 393
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-166591

Query Match          55.8%; Score 13.4; DB 7; Length 393;
Best Local Similarity 73.9%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
Db 253 CAAGTCGTATGGAAGGAAGCTTC 275

RESULT 83
US-10-488-619-2473/c
; Sequence 2473, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2473
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2473
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Query Match          55.8%; Score 13.4; DB 6; Length 487;
Best Local Similarity 73.9%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
Db 78 CAAGTCCTAAAGGAATGGCTTAC 56

RESULT 84
US-10-488-619-2474
; Sequence 2474, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2474
; LENGTH: 510
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2474

Query Match          55.8%; Score 13.4; DB 6; Length 510;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
Db 399 CAAGTCCTAAAGGAATGGCTTAC 421

RESULT 85
US-10-488-619-2770/c
; Sequence 2770, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2770
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2770

Query Match          55.8%; Score 13.4; DB 6; Length 562;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23
Db 206 CAAGTCGGCGGCGAGGCATTC 184

RESULT 86
US-11-301-554-1914
; Sequence 1914, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
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; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US 11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1914
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-301-554-1914

Query Match          55.8%; Score 13.4; DB 7; Length 624;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAG 16
        |||||
Db      502 AAGTCGAACGGAAG 516

RESULT 87
US-11-301-554-1668
; Sequence 1668, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
```

```
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-301-554-1668

Query Match          55.8%; Score 13.4; DB 7; Length 636;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAG 16
        |||||
Db      505 AAGTCGAACGGAAG 519

RESULT 88
US-11-217-529-79746
; Sequence 79746, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79746
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-79746

Query Match          55.8%; Score 13.4; DB 7; Length 696;
Best Local Similarity 73.9%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2 AAGTCGAACGGAAGCCTTCG 24
        |||||
```

```

Db      418 AATCAGACGAGAGCCCTTGC 440

RESULT 89
US-11-217-529-5130/c
; Sequence 5130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5130
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5130

Query Match      55.8%; Score 13.4; DB 7; Length 762;
Best Local Similarity 93.3%; Pred. No. 1.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 AACGGAAGGCCTTT 22
      ||||||| |||||
Db      539 AACGGAAGGCCTTT 525

RESULT 90
US-10-525-126-124/c
; Sequence 124, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR FILING DATE: 2003-08-22
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 124
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Platichthys stellatus
US-10-525-126-124

Query Match      55.8%; Score 13.4; DB 6; Length 814;
Best Local Similarity 93.3%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 AACGGAAGGCCTTT 22
      ||||||| |||||
Db      254 AAAGGAAGGCCTTT 240

RESULT 91
US-11-217-529-5478
; Sequence 5478, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5478
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5478

Query Match      55.8%; Score 13.4; DB 7; Length 918;
Best Local Similarity 73.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      2 AACTCGAACGGAAGGCCTTTCG 24
      ||||||| |||||
Db      139 AATACCAGCGCAAGGCCTTTGG 161

RESULT 92
US-11-217-529-191032
; Sequence 191032, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191032
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-191032

Query Match      55.8%; Score 13.4; DB 7; Length 990;
Best Local Similarity 73.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 CAAGTCGAACGGAAGGCCTTTC 23
      ||||||| |||||
Db      847 CAAGTCGTATGGAAGGGAACCTTC 869

RESULT 93
US-11-217-529-1564
; Sequence 1564, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO

```

```
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1564
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1564

Query Match      55.8%; Score 13.4; DB 7; Length 1107;
Best Local Similarity 73.9%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGCGCTTTC 23
   |||||  |||||  |||||  |||||
Db 592 CAAGTCGAGCGCAACGCGCATATC 614

RESULT 94
US-11-217-529-82255/c
; Sequence 82255, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82255
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82255

Query Match      55.8%; Score 13.4; DB 7; Length 1515;
Best Local Similarity 73.9%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGGAAGCGCTTTCG 24
   |||||  |||||  |||||  |||||
Db 1013 AATTCGAATCTAAAGGCTTTTG 991

RESULT 95
US-11-256-221-1
; Sequence 1, Application US/11256221
; Publication No. US20060094094A1
; GENERAL INFORMATION:
; APPLICANT: Sugio, Tsuyoshi
; APPLICANT: Miura, Akira
; APPLICANT: Parada Valdecantos, Pilar A.
; APPLICANT: Badilla Ohlbaum, Ricardo
; TITLE OF INVENTION: BACTERIA STRAIN WENELEN DSM 16786, USE OF SAID BACTERIA FOR
; TITLE OF INVENTION: LEACHING OF ORES OR CONCENTRATES CONTAINING METALLIC SULFIDE
; TITLE OF INVENTION: MINERAL SPECIES AND LEACHING PROCESSES BASED ON THE USE OF SAID
; TITLE OF INVENTION: BACTERIA OR MIXTURES THAT CONTAIN SAID BACTERIA
; FILE REFERENCE: 15053.15US01
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; CURRENT APPLICATION NUMBER: US/11/256,221
; CURRENT FILING DATE: 2005-10-21
; PRIOR APPLICATION NUMBER: CL 2731-2004
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1531
; TYPE: DNA
; ORGANISM: Bacteria
US-11-256-221-1

Query Match      55.8%; Score 13.4; DB 7; Length 1531;
Best Local Similarity 93.3%; Pred. No. 1.8e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAA 15
   |||||  |||||  |||||  |||||
Db 54 CAAGTCGAACGGTAA 68

RESULT 96
US-11-301-554-316
; Sequence 316, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-301-554-316
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Query Match 55.8%; Score 13.4; DB 7; Length 1633;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAG 16  
|||||  
Db 567 AAGTCGAACGAAAG 581

## RESULT 97

US-11-301-554-788  
; Sequence 788, Application US/11301554  
; Publication No. US20060088527A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Sleath, Paul R.  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Durham, Margarita  
; APPLICANT: Carter, Darick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangut, Chaitanya S.  
; APPLICANT: McNabb, Andria

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.478C21  
; CURRENT APPLICATION NUMBER: US/11/301,554  
; CURRENT FILING DATE: 2005-12-13  
; PRIOR APPLICATION NUMBER: US 10/283,017  
; PRIOR FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US 10/113,872  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 10/017,754  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: US 09/902,941  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 09/849,626  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 09/736,457  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: US 09/702,705  
; PRIOR FILING DATE: 2000-10-30  
; PRIOR APPLICATION NUMBER: US 09/677,419  
; PRIOR FILING DATE: 2000-10-06  
; PRIOR APPLICATION NUMBER: US 09/671,325  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/658,824  
; PRIOR FILING DATE: 2000-09-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2157  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 788  
; LENGTH: 1633  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-301-554-788

Query Match 55.8%; Score 13.4; DB 7; Length 1633;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAG 16  
|||||  
Db 567 AAGTCGAACGAAAG 581

## RESULT 98

US-11-217-529-80937  
; Sequence 80937, Application US/11217529

; Publication No. US20060099612A1  
; GENERAL INFORMATION: LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 80937  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-80937

Query Match 55.8%; Score 13.4; DB 7; Length 1647;  
Best Local Similarity 93.3%; Pred. No. 1.8e+02;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGAAA 15  
|||||  
Db 160 CAAGTCGAACGAAA 174

## RESULT 99

US-11-217-529-2385  
; Sequence 2385, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 2385  
; LENGTH: 1710  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2385

Query Match 55.8%; Score 13.4; DB 7; Length 1710;  
Best Local Similarity 73.9%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 AAGTCGAACGAAAGCCTTCG 24  
|||||  
Db 1112 AAGTCGATGGAAACCTTATCG 1134

## RESULT 100

US-11-217-529-2406/c  
; Sequence 2406, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2406  
; LENGTH: 1716  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-2406

Query Match 55.8%; Score 13.4; DB 7; Length 1716;  
Best Local Similarity 73.9%; Pred. No. 1.8e+02;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CAAGTCGAACGGAAGGCGCTTTC 23  
||| ||||| ||| |||||  
Db 1297 CAATGGACGTCGAAGTCCTTC 1275

Search completed: May 19, 2006, 05:38:17  
Job time : 16.8916 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 259.361 Seconds  
(without alignments)  
591.412 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22  
Sequence: 1 gtcgaacggaagccttcgg 22

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- N\_Geneseq\_8:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002as:\*
  - 7: Geneseqn2002bs:\*
  - 8: Geneseqn2003as:\*
  - 9: Geneseqn2003bs:\*
  - 10: Geneseqn2003cs:\*
  - 11: Geneseqn2003ds:\*
  - 12: Geneseqn2004as:\*
  - 13: Geneseqn2004bs:\*
  - 14: Geneseqn2005s:\*
  - 15: Geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	4	AD11273 Mycobacte
2	22	100.0	22	10	ADG88354 Mycobacte
3	22	100.0	22	14	AEAO8229 Mycobacte
4	21	95.5	24	4	AD11272 Mycobacte
5	21	95.5	24	10	ADG88353 Mycobacte
6	21	95.5	24	14	AEAO8228 Mycobacte
7	21	95.5	25	4	AD11271 Mycobacte
8	21	95.5	25	10	ADG88352 Mycobacte
9	21	95.5	25	14	AEAO8227 Mycobacte
10	20.4	92.7	500	13	AD220587 Formaldeh
11	20.4	92.7	1449	14	AEAO82405 Mycobacte
12	20.4	92.7	1455	14	AEAO82412 Mycobacte
13	20.4	92.7	1482	14	AEAO82404 Mycobacte
14	19	86.4	19	4	AD11274 Mycobacte
15	19	86.4	19	10	ADG88355 Mycobacte
16	19	86.4	19	14	AEAO8230 Mycobacte
17	18.8	85.5	50	12	ADP94057 Microorga
18	18.8	85.5	166	2	AAX32481 Preferred

c	92	16	72.7	1344	12	AD085868	Ado85868	Gordonia	165	15.6	70.9	3111	11	ACH97300	Ach97300 Klebsiell
	93	16	72.7	1415	14	AEa22413	Aea22413 Mycobacte		c 166	15.6	70.9	3257	4	AAC84585	Aac84585 Wheat mag
	94	16	72.7	1460	3	Aaz22765	Aaz22765 Corynebac		c 167	15.6	70.9	12368	4	AAS46271	Aas46271 DNA encod
	95	16	72.7	1462	14	AEa22415	Aea22415 Mycobacte		c 168	15.6	70.9	39949	12	ADF31997	Adf31997 Full leng
	96	16	72.7	1484	14	AEa22414	Aea22414 Mycobacte		c 169	15.6	70.9	43800	11	ACN44516	Acn44516 Mouse gen
	97	16	72.7	1517	12	ADM92517	Adm92517 Gordonia		c 170	15.6	70.9	48200	12	ADF31998	Adf31998 Cosmid 2A
	98	16	72.7	1517	12	AD071823	Ado71823 DNA of RN		c 171	15.6	70.9	86453	14	ADY25730	Ady25730 SULF rela
	99	16	72.7	1527	14	AEa22407	Aea22407 Mycobacte		c 172	15.6	70.9	110000	6	ABQ69245_16	Continuation (17 o
	100	15.8	71.8	32	4	AD11264	Ad11264 Mycobacte		c 173	15.6	70.9	110000	6	ABQ67195_1	Continuation (2 of
	101	15.8	71.8	32	10	ADG88345	Adg88345 Mycobacte		c 174	15.6	70.9	110000	10	ACF65385_3	Continuation (4 of
	102	15.8	71.8	32	14	AEA08220	Aea08220 Mycobacte		c 175	15.6	70.9	110000	10	ACF65385_4	Continuation (5 of
	103	15.8	71.8	50	2	AAX99199	Aax99199 M. kansas		c 176	15.6	70.9	110000	10	ACF67367_33	Continuation (34 o
	104	15.8	71.8	50	2	AAX99194	Aax99194 M. bovis		c 177	15.6	70.9	264965	12	ADN16203	Adn16203 Human sul
	105	15.8	71.8	50	2	AAX99193	Aax99193 M. tuberc		c 178	15.6	70.9	268685	6	ABS56563	Abs56563 Human SUL
	106	15.8	71.8	50	12	ADP94055	Adp94055 Microorga		c 179	15.4	70.0	27	2	AAV24410	Aav24410 Target se
	107	15.8	71.8	50	12	ADP94047	Adp94047 Microorga		c 180	15.4	70.0	27	2	AAV13018	Aav13018 Mycobacte
	108	15.8	71.8	170	3	AAA31293	Aaa31293 Plant mic		c 181	15.4	70.0	28	4	AAD11025	Aad11025 Probe #5
	109	15.8	71.8	203	2	AAQ94742	Aaq94742 DNA fragm		c 182	15.4	70.0	28	4	AAD11018	Aad11018 PCR prime
	110	15.8	71.8	209	14	AEb98764	Aeb98764 Mycobacte		c 183	15.4	70.0	36	14	ADU69991	Adu69991 LAMP reac
	111	15.8	71.8	211	14	AEb98761	Aeb98761 Mycobacte		c 184	15.4	70.0	37	14	ADU69989	Adu69989 LAMP reac
	112	15.8	71.8	305	3	AAA31415	Aaa31415 Plant mic		c 185	15.4	70.0	39	14	ADU69984	Adu69984 LAMP reac
	113	15.8	71.8	349	13	ADV99481	Adv99481 Meningitil		c 186	15.4	70.0	39	14	ADU69983	Adu69983 LAMP reac
	114	15.8	71.8	375	11	ACH95956	Ach95956 Klebsiell		c 187	15.4	70.0	39	14	ADU69985	Adu69985 LAMP reac
	115	15.8	71.8	381	5	AAS77874	Aas77874 DNA encod		c 188	15.4	70.0	39	14	AEb98765	Aeb98765 Mycobacte
	116	15.8	71.8	576	5	AAS67301	Aas67301 DNA encod		c 189	15.4	70.0	39	14	AEb98779	Aeb98779 Mycobacte
	117	15.8	71.8	1271	2	AAV24293	Aav24293 Mycobacte		c 190	15.4	70.0	39	15	AEF95350	Aef95350 Nucleic a
	118	15.8	71.8	1416	14	AEa22416	Aea22416 Mycobacte		c 191	15.4	70.0	41	14	ADU69960	Adu69960 LAMP reac
	119	15.8	71.8	1421	14	AEa22402	Aea22402 Mycobacte		c 192	15.4	70.0	41	14	ADU69958	Adu69958 LAMP reac
	120	15.8	71.8	1463	14	AEa22409	Aea22409 Mycobacte		c 193	15.4	70.0	42	14	ADU69959	Adu69959 LAMP reac
	121	15.8	71.8	1464	3	AAZ35571	Aaz35571 Mycobacte		c 194	15.4	70.0	42	14	ADU69957	Adu69957 LAMP reac
	122	15.8	71.8	1464	5	AAS11027	Aas11027 Mycobacte		c 195	15.4	70.0	455	3	ACAS5929	Aac55929 Eucalyptu
	123	15.8	71.8	1469	13	ADR90574	Adr90574 M. kansas		c 196	15.4	70.0	455	3	ACAS57218	Aac57218 Eucalyptu
	124	15.8	71.8	1524	4	AAS30719	Aas30719 Mycobacte		c 197	15.4	70.0	861	14	ACL67957	ACL67957 M. xanthu
	125	15.8	71.8	1536	10	ADB61681	Adb61681 16S rRNA		c 198	15.4	70.0	1164	13	ADS56576	Ads56576 Bacterial
	126	15.8	71.8	1536	10	ADB61682	Adb61682 16S rRNA		c 199	15.4	70.0	2642	4	ABL23018	Ab123018 Drosophil
	127	15.8	71.8	1537	10	ADF41649	Adf41649 Mycobacte		c 200	15.4	70.0	3581	4	ABL23036	Ab123036 Drosophil
	128	15.8	71.8	1849	14	AEA51361	Aea51361 Mouse gen		c 201	15.4	70.0	5433	4	ABL04331	Ab104331 Drosophil
	129	15.8	71.8	2000	11	ACL36116	ACL36116 Rice stre		c 202	15.4	70.0	7162	4	ABL04330	Ab104330 Drosophil
	130	15.8	71.8	2896	10	ACC47372	Acc47372 Human lat		c 203	15.4	70.0	23677	14	ACL64755	ACL64755 M. xanthu
	131	15.8	71.8	2898	12	ADC35344	Adc35344 Murine se		c 204	15.2	69.1	365	12	ADF20374	Adf20374 Pinus rad
	132	15.8	71.8	2919	13	ADS59960	Ads59960 Bacterial		c 205	15.2	69.1	409	13	AAU09116	Aaf09116 Fusarium
	133	15.8	71.8	3054	10	ACC47371	Acc47371 Rat late		c 206	15.2	69.1	409	13	ADU53157	Adu53157 Fusarium
	134	15.8	71.8	6883	4	AAI36998	Aai36998 Human mus		c 207	15.2	69.1	409	14	ADZ91160	Adz91160 Fusarium
	135	15.8	71.8	6883	8	ABX59986	Abx59986 cDNA enco		c 208	15.2	69.1	413	14	ACL61303	ACL61303 Human col
	136	15.8	71.8	6883	12	ADJ30736	Adj30736 Human mus		c 209	15.2	69.1	414	5	AAE65015	Aaf65015 Novel hum
	137	15.8	71.8	21126	1	AAAN0970	Aan0970 TL-DNA re		c 210	15.2	69.1	416	4	AAI87098	Aai87098 Human pol
	138	15.8	71.8	21126	12	AD055765	Ado55765 Agrobacte		c 211	15.2	69.1	475	6	ABL78115	Ab178115 Human ova
	139	15.8	71.8	36241	10	ADB74385	Adb74385 Mycobacte		c 212	15.2	69.1	499	9	ACH13049	Ach13049 Human adu
	140	15.8	71.8	36470	10	ADB74374	Adb74374 Mycobacte		c 213	15.2	69.1	561	3	AAU98000	Aac98000 Human col
	141	15.8	71.8	110000	4	AAI99682_14	Continuation (15 o		c 214	15.2	69.1	585	4	AAH10759	Aah10759 Human cdn
	142	15.8	71.8	110000	4	AAI99683_14	Continuation (15 o		c 215	15.2	69.1	622	4	AAU00309	Aas00309 S. pneumo
	143	15.6	70.9	227	9	ADB82110	Adb82110 Human cdn		c 216	15.2	69.1	671	13	ADQ79174	Adq79174 Novel can
	144	15.6	70.9	331	6	ABQ89167	Abq89167 Human pro		c 217	15.2	69.1	861	10	ABZ39185	Abz39185 N. gonorr
	145	15.6	70.9	439	4	AAAC84579	Aac84579 Corn magn		c 218	15.2	69.1	978	6	ABN74125	Abn74125 Bovine em
	146	15.6	70.9	465	10	ADB57680	Adb57680 Toxicity-		c 219	15.2	69.1	1374	10	ADBE64000	Adbe64000 Rat gene
	147	15.6	70.9	471	10	ACC61674	Acc61674 Gene sequ		c 220	15.2	69.1	1374	10	ADBE63996	Adbe63996 Rat gene
	148	15.6	70.9	471	10	ADK64173	Adk64173 Disease t		c 221	15.2	69.1	1392	2	AAZ11765	Aaz11765 Maize his
	149	15.6	70.9	524	10	ADB57597	Abx57597 Arabidops		c 222	15.2	69.1	1420	3	AAU69580	Aac69580 Human sec
	150	15.6	70.9	624	10	ADC72425	Adc72425 DNA Seq I		c 223	15.2	69.1	1542	10	ADH84376	Adh84376 Enterococ
	151	15.6	70.9	633	10	ACF70237	Accf70237 Phototrab		c 224	15.2	69.1	1733	5	AAH90021	Aah90021 Human bon
	152	15.6	70.9	784	3	AAAC49475	Aac49475 Arabidops		c 225	15.2	69.1	1929	11	ACL38184	ACL38184 Rice stre
	153	15.6	70.9	960	11	ACN44517	Acn44517 Mouse mRN		c 226	15.2	69.1	2501	2	AAV58761	Aav58761 Human sec
	154	15.6	70.9	1101	13	AD742264	Adt42264 Bacterial		c 227	15.2	69.1	2635	8	ABT18506	Abt18506 Aspergill
	155	15.6	70.9	1111	13	ADX13192	Adx13192 Plant ful		c 228	15.2	69.1	2796	4	AAH18563	Aah18563 Human cdn
	156	15.6	70.9	1418	8	ABZ25595	Abz25595 Rhodococc		c 229	15.2	69.1	2937	8	ACT23290	Act23290 Prokaryot
	157	15.6	70.9	1662	11	ACH97324	Ach97324 Klebsiell		c 230	15.2	69.1	2964	8	ABT20322	Abt20322 Aspergill
	158	15.6	70.9	1675	13	ADS56900	Ads56900 Bacterial		c 231	15.2	69.1	3485	2	AAI313220	Aai313220 Enterococ
	159	15.6	70.9	1718	13	AD081352	Ado81352 Plant ful		c 232	15.2	69.1	3485	6	ABU99015	Abu99015 Enterococ
	160	15.6	70.9	2427	13	ADX60109	Adx60109 Plant ful		c 233	15.2	69.1	3628	10	ADG15051	Adg15051 Human SEC
	161	15.6	70.9	2444	3	AAU56089	Aac56089 Eucalyptu		c 234	15.2	69.1	3846	10	AD121796	Adi21796 Novel hum
	162	15.6	70.9	2460	14	ADW16476	Adw16476 Eucalyptu		c 235	15.2	69.1	3908	4	AAU11067	Aad11067 Human sec
	163	15.6	70.9	2982	6	ABZ14720	Abz14720 Arabidops		c 236	15.2	69.1	3918	5	AHH89908	Aah89908 Human bon
	164	15.6	70.9	2982	10	ADF75190	Adf75190 Thale cre		c 237	15.2	69.1	4001	10	AAH42453	Adf42453 Human PP7



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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 23; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTCGAACGGAAAGGCTTTTCGG 22
DB |||||||||||||||||||
1 GTCGAACGGAAAGGCTTTTCGG 22

RESULT 3
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX
AC AEA08229;
XX
XX 14-JUL-2005 (first entry)
XX
XX Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX
XX Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
XX Mycobacterium celatum.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX
Query Match 95.5%; Score 21; DB 4; Length 24;

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XX Claim 8; SEQ ID NO 23; 21pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
XX amplifying non-T7 PCR primer.
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 22; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GTCGAACGGAAAGGCTTTTCGG 22
DB |||||||||||||||||||
1 GTCGAACGGAAAGGCTTTTCGG 22

RESULT 4
AAD11272
ID AAD11272 standard; DNA; 24 BP.
XX
AC AAD11272;
XX
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying primer #16.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
XX
Query Match 95.5%; Score 21; DB 4; Length 24;

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 5
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 6
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX
KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PS (JUCK/) JUCKER M T.
PS (DELG/) DELGADO F D.
PS (CLEU/) CLEUZIAT P.
PS (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 22; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTTTCG 21
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 7
AAD11271
ID AAD11271 standard; DNA; 25 BP.
XX
AC AAD11271;
XX
DT 24-SEP-2001 (first entry)
DE Mycobacterium 16S rRNA amplifying primer #15.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOT7; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.

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PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 36; 44pp; English.
XX
CC The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCG 21
DB 5 GTCGAACGGAAGGCCTTTCG 25

RESULT 8
ADG88352
ID ADG88352 standard; DNA; 25 BP.
XX
AC ADG88352;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #21.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 21; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCG 21
DB 5 GTCGAACGGAAGGCCTTTCG 25

RESULT 9
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX
AC AEA08227;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX
KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 21; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S-rRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 95.5%; Score 21; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCG 21

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Db      5  GTCGAACGGAAGGCGCTTTCG 25

RESULT 10
ID      ADZ20587
XX      ADZ20587 standard; DNA; 500 BP.
XX      AC      ADZ20587;
XX      DT      16-JUN-2005 (first entry)
XX      DE      Formaldehyde decomposition related Mycobacterium sp. DNA.
XX      KW      decomposition; formaldehyde; ds.
XX      OS      Mycobacterium sp.
XX      PN      JP2003284548-A.
XX      PD      07-OCT-2003.
XX      PF      27-MAR-2002; 2002JP-00089307.
XX      PR      27-MAR-2002; 2002JP-00089307.
XX      PA      (KUMO-) KUMOMOTO KEN PREFECTURE.
XX      PA      (MITS-) MITSUWA CORP YG.
XX      PA      (MITS-) MITSUWA BIPO KK.
XX      DR      WPI; 2004-172963/17.
XX      DE      Decomposing formaldehyde by Mycobacterium and/or growth medium of the
XX      PT      cells.
XX      PS      Example 1; SEQ ID NO 1; 20pp; Japanese.
XX      CC      The invention relates to a novel method for decomposing formaldehyde by
XX      CC      using microbial cells that belong to Mycobacterium sp. or Fusarium
XX      CC      oxysporum, and/or the growth medium of the microbial cells. The invention
XX      CC      further comprises: microbial cells which belong to Mycobacterium sp.
XX      CC      having the ability to decompose formaldehyde; a formaldehyde
XX      CC      decomposition agent comprising Mycobacterium sp. and/or the growth medium
XX      CC      of the microbial cells; and a formaldehyde decomposition agent comprising
XX      CC      F. oxysporum and/or its growth medium. The method is useful for
XX      CC      decomposing formaldehyde in sea water by Mycobacterium sp. or F.
XX      CC      oxysporum that is deposited under FERM P-S18690 or FERM P-18483,
XX      CC      respectively. This polynucleotide sequence represents the Mycobacterium
XX      CC      sp. DNA of the invention.
XX      SQ      Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;

Query Match      92.7%; Score 20.4; DB 13; Length 500;
Best Local Similarity 95.5%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCG 22
        |||||
Db      57  GTCGAACGGAAGGCGCTTTCG 78

RESULT 11
ID      AEA22405
XX      AEA22405 standard; DNA; 1449 BP.
XX      AC      AEA22405;
XX      DT      25-AUG-2005 (first entry)
XX      DE      Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.
XX      KW      microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX      OS      Mycobacterium fortuitum.

XX      US2005130168-A1.
XX      PN      16-JUN-2005.
XX      PD      31-OCT-2003; 2003US-00697802.
XX      PF      31-OCT-2003; 2003US-00697802.
XX      PR      (HANX/) HAN X.
XX      PA      (PHAM/) PHAM A S.
XX      PI      Han X, Pham AS;
XX      DR      WPI; 2005-424597/43.
XX      DE      Determining a bacterium species comprises providing oligonucleotide
XX      PT      primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX      PS      Disclosure; SEQ ID NO 6; 74pp; English.
XX      CC      The invention relates to a method (M1) for determining a bacterium
XX      CC      species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX      CC      extracting a genomic nucleotide from the bacterium to provide a
XX      CC      nucleotide template; (c) annealing a region of a nucleotide template to a
XX      CC      specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX      CC      complimentary fashion, the primer set designed to provide a product
XX      CC      having a predetermined size dictated by a complementary primer set; (d)
XX      CC      amplifying the region of the nucleotide template to produce the product;
XX      CC      and (e) determining a species of a bacterium in a nucleotide sequence of
XX      CC      the product. Also described is an alternative method (M2) for determining
XX      CC      a bacterium species comprising: (a) providing a specimen or a sample
XX      CC      having a template; (b) providing a pair of primers selected from: (i) a
XX      CC      first forward primer having consecutive bases of an AFB-f comprising any
XX      CC      of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX      CC      or variations and a first reverse primer having consecutive bases of an
XX      CC      AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX      CC      or their fragments or variations, (ii) a second forward primer having
XX      CC      consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX      CC      bp (AEA22489-AEA22516) or their fragments or variations and a second
XX      CC      reverse primer having consecutive bases of an UB-r comprising any of the
XX      CC      28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX      CC      variations, or (iii) a first forward primer having consecutive bases of
XX      CC      an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX      CC      second reverse primer having consecutive bases of an UB-r of AEA22517-
XX      CC      AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX      CC      comparing the product from the specimen with a nucleotide sequence from a
XX      CC      database to determine the bacterium species present in the specimen. The
XX      CC      methods are useful for determining a bacterium species. The present
XX      CC      sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide
XX      CC      sequence, which is used in the exemplification of the present invention.
XX      SQ      Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;

Query Match      92.7%; Score 20.4; DB 14; Length 1449;
Best Local Similarity 95.5%; Pred. No. 3.4;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCGCTTTCG 22
        |||||
Db      24  GTCGAACGGAAGGCGCTTTCG 45

RESULT 12
AEA22412
ID      AEA22412 standard; DNA; 1455 BP.
XX      AC      AEA22412;
XX      DT      25-AUG-2005 (first entry)
XX      DE      Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.
XX      OS

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AC AAD11274;
XX
XX 24-SEP-2001 (first entry)
XX
XX Mycobacterium 16S rRNA amplifying primer #18.
XX
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 19; DB 4; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCGCTTTCGG 22
XX | | | | | | | | | | | | | | | | | |
XX Db 1 GAACGGAAGGCGCTTTCGG 19
XX
XX RESULT 15
XX ADG88355
XX ID ADG88355 standard; DNA; 19 BP.
XX
XX AC ADG88355;
XX
XX 11-MAR-2004 (first entry)
XX
XX Mycobacterium amplifying PCR primer #24.
XX
XX In vitro amplification; PCR; primer; ss.
XX
XX Mycobacterium xenopi.
XX
XX US2003165824-A1.
XX
XX 04-SEP-2003.
XX
XX

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PF 15-DEC-2000; 2000US-00738274.
XX
XX 17-DEC-1999; 99US-0172190P.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 24; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 86.4%; Score 19; DB 10; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCGCTTTCGG 22
XX | | | | | | | | | | | | | | | | | |
XX Db 1 GAACGGAAGGCGCTTTCGG 19
XX
XX RESULT 16
XX AEA08230
XX ID AEA08230 standard; DNA; 19 BP.
XX
XX AC AEA08230;
XX
XX 14-JUL-2005 (first entry)
XX
XX Mycobacterium xenopi 16SrRNA amplifying non-T7 primer, SEQ ID NO: 24.
XX
XX DNA amplification; microorganism detection; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
XX Mycobacterium xenopi; ATCC 19250.
XX
XX US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid

```

PT amplification and detection of amplified products.  
 XX  
 PS Claim 1; SEQ ID NO 24; 21pp; English.  
 XX  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample. The method involves using in  
 CC vitro nucleic acid amplification and detection of amplified products. The  
 CC invention is useful for diagnostic detection of pathogenic bacteria such  
 CC as Mycobacterium species. The present sequence is the Mycobacterium  
 CC xenopi (ATCC 19250) 16S ribosomal RNA (16S rRNA) amplifying non-T7 PCR  
 CC primer.  
 XX  
 SQ Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 86.4%; Score 19; DB 14; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 GAACGGAAAGGCTTTCGG 22  
 Db 1 GAACGGAAAGGCTTTCGG 19  
 |||||  
 RESULT 17  
 ADF94057  
 ID ADF94057 standard; DNA; 50 BP.  
 XX  
 AC ADF94057;  
 XX  
 DT 11-MAR-2004 (first entry)  
 XX  
 DE Microorganism detection probe, SEQ ID 150.  
 XX  
 KW Probe; detection; identification; microorganism; food; drug;  
 KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
 XX  
 OS Mycobacterium gordonae.  
 XX  
 PN W02003106676-A1.  
 XX  
 PD 24-DEC-2003.  
 XX  
 PF 16-JUN-2003; 2003WO-JP007620.  
 XX  
 PR 14-JUN-2002; 2002JP-00174564.  
 XX  
 PA (HISF) HITACHI SOFTWARE ENG CO LTD.  
 PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.  
 XX  
 PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
 PI Shimadzu M, Kobayashi I, Ishiko H;  
 XX  
 DR WPI; 2004-071565/07.  
 XX  
 XX 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
 PT microorganism for specific detection and identification of the  
 PT microorganism in foods and drug compositions.  
 XX  
 PS Claim 2; SEQ ID NO 150; 150pp; Japanese.  
 XX  
 CC The present invention relates to probes (ADF93908-ADF94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADF94060 and ADF94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetocombitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia

CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquatium, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.  
 XX  
 SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;  
 Query Match 85.5%; Score 18.8; DB 12; Length 50;  
 Best Local Similarity 90.9%; Pred. No. 15;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GTCGAACGGAAAGGCTTTCGG 22  
 Db 7 GTCGAACGGTAAGGCCCTTCGG 28  
 |||||  
 RESULT 18  
 AAX32481  
 ID AAX32481 standard; DNA; 166 BP.  
 XX  
 AC AAX32481;  
 XX  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE Preferred probe of the invention.  
 XX  
 KW 16S rRNA; maduromycetes; hybridisation; streptomycetes; probe; ss.  
 XX  
 OS Synthetic.  
 OS Streptomyces ambofaciens.  
 XX  
 PN W09914361-A1.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 16-SEP-1998; 98WO-EP006038.  
 XX  
 PR 18-SEP-1997; 97US-0059295P.  
 PR 16-DEC-1997; 97US-0069748P.  
 XX  
 PA (MERI) MERCK SHARP & DOHME ESPANA SAE.  
 XX  
 PI Genilloud O, Mellado RP, Parro V, Rodriguez V;  
 XX  
 DR WPI; 1999-229548/19.  
 XX  
 XX New probes used for detection of maduromycetes bacteria and to  
 PT differentiate between maduromycetes and streptomycetes.  
 XX  
 PS Disclosure; Fig 1; 22pp; English.  
 XX  
 CC The invention relates to a novel nucleic acid probe hybridises to a  
 CC nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria  
 CC under hybridisation conditions, and does not hybridise to nucleic acids  
 CC encoding a portion of 16S rRNA of streptomycetes under identical  
 CC hybridisation conditions. The probes can be used for detecting the  
 CC presence of maduromycetes bacteria in a sample and for differentiating  
 CC between maduromycetes and streptomycetes bacteria in a sample. The  
 CC present sequence represents a preferred probe of the invention  
 XX

SQ Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 2; Length 166;  
Best Local Similarity 90.9%; Pred. No. 18;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22  
Db 60 GTCGACGGAAGGCGCTTCGG 81

RESULT 19  
ABZ76674  
ID ABZ76674 standard; DNA; 460 BP.  
XX AC  
XX ABZ76674;  
DT 30-APR-2003 (first entry)  
XX Microtrasporea recticatena IF014525 DNA sequence SEQ ID NO:5.  
DE Streptomyces sp. TM-7; pravastatin; compactin; hyperlipidaemia;  
KW antilipaeamic; microorganism; gene; ds.  
KW  
XX  
OS Nonomuraea recticatena.  
XX  
XX WO200299109-A1.  
XX  
XX  
PD 12-DEC-2002.  
XX  
XX 30-MAY-2002; 2002WO-JP005252.  
PF  
XX  
XX 01-JUN-2001; 2001JP-00166412.  
XX  
XX (SAOC ) MERCIAN CORP.  
PA  
XX  
XX Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ieshiki K;  
FI  
XX  
XX WPI; 2003-148672/14.  
DR  
XX  
XX Novel Streptomyces sp. produced polypeptide for hydroxylation of  
PT compactin at 6beta-position and its encoded DNA, applicable in  
PT constructing transformant microbes to synthesize pravastatin for treating  
PT hyperlipedemia.  
XX  
XX  
PS Disclosure; Page 50-51; 67pp; Japanese.  
XX  
XX The present invention describes a DNA sequence which contains a base  
CC sequence from bases 544-1758 in the sequence of (1) with 1992 base pairs,  
CC or a DNA hybridisable with the DNA under stringent conditions and  
CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-  
CC position. Also described: (1) DNA containing base sequences from bases  
CC 544-1758 and from bases 1782-1970 in the sequence of (1) or a DNA  
CC hybridisable with the DNA under stringent conditions and encoding a  
CC polypeptide with hydroxylase activity on compactin at the 6beta-position;  
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid  
CC sequence based on the polypeptide but with some amino acids deleted,  
CC substituted or added and having hydroxylase activity on compactin at the  
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of  
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a  
CC process for producing pravastatin by culturing the transformant  
CC microorganism before isolating the culture liquor or cells, and addition  
CC of compactin for reaction to give pravastatin for recovery; and (6)  
CC Streptomyces sp. TM-6 (FERM BP-8002) or TM-7 (FERM BP-8003). (1) has  
CC antilipaeamic activity. The polypeptide and its encoded DNA are applicable  
CC in constructing transformant microorganisms to synthesise pravastatin for  
CC treating hyperlipidaemia. With the recombinant microorganisms,  
CC pravastatin can be produced efficiently, with much less galpha  
CC hydroxylated epimer formed. The present sequence represents a  
CC Microtrasporea recticatena IF014525 nucleotide sequence, which is given  
CC in the exemplification of the present invention  
XX  
XX Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 8; Length 460;  
Best Local Similarity 90.9%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22  
Db 34 GTCGACGGAAGGCGCTTCGG 55

RESULT 20  
ABZ7673  
ID AEB7673 standard; DNA; 497 BP.  
XX AC  
XX AEB7673;  
DT 06-OCT-2005 (first entry)  
XX Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.  
DE cyclosporin; cyclosporin A; ds.  
KW Streptosporangium sp.  
OS  
XX JP2005198543-A.  
PN  
XX 28-JUL-2005.  
PD  
XX 15-JAN-2004; 2004JP-00007488.  
PF  
XX 15-JAN-2004; 2004JP-00007488.  
PR  
XX (SAOC ) MERCIAN CORP.  
PA  
XX  
XX Ota K, Uematsu H, Kaneko K, Tsuchida T;  
FI  
XX  
XX WPI; 2005-537020/55.  
DR  
XX  
XX Producing cyclosporin derivative useful as reference standard for  
PT quantitative measurement of cyclosporin A in blood, by incubating  
PT cyclosporin A in presence of Dactylosporangium and extracting cyclosporin  
PT derivative.  
XX  
XX Disclosure; SEQ ID NO 2; 12pp; Japanese.  
PS  
XX  
XX The invention relates to a novel method for producing a cyclosporin  
CC derivative. The method involves incubating cyclosporin A in the presence  
CC of a strain belonging to Dactylosporangium, Streptomyces, Nocardi, and  
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and  
CC extracting the cyclosporin derivative from the incubated liquid. The  
CC cyclosporin derivative is used as a reference standard for quantitative  
CC measurement of cyclosporin A and its metabolite in blood and urine. This  
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in  
CC the cyclosporin production method of the invention.  
XX  
XX Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 85.5%; Score 18.8; DB 14; Length 497;  
Best Local Similarity 90.9%; Pred. No. 20;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22  
Db 57 GTCGACGGAAGGCGCTTCGG 78

RESULT 21  
AED64356  
ID AED64356 standard; DNA; 500 BP.  
XX AC  
XX AED64356;  
DT 12-JAN-2006 (first entry)

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XX Rhodococcus sp. 16S rDNA, SEQ ID 1.
DE 16S ribosomal RNA; 16S rRNA; ds.
KW Rhodococcus sp.; 2-35-1 strain.
OS JP2005304498-A.
PN 04-NOV-2005.
XX 22-MAR-2005; 2005JP-00081977.
XX 23-MAR-2004; 2004JP-00083956.
XX (SANYO-) SANYO FINE KK.
XX Isobe K, Matsura A, Sakaguchi T;
XX WPI; 2005-762911/78.
XX Producing alpha-L- or -D-amino adipic acid semialdehyde derivative or its
PT salt, involves oxidatively deaminating aminomethyl group of alpha-amino
PT protecting group of L- or D-lysine, by utilizing oxidase derived from
PT Rhodococcus.
XX Disclosure; SEQ ID NO 1; 30pp; Japanese.
XX The present invention relates to a method (M1) for producing alpha-L- or
CC -D-amino adipic acid semialdehyde derivatives. The method involves
CC oxidatively deaminating the aminomethyl group of the alpha-amino
CC protecting group of L- or D-lysine into an aldehyde group, by utilizing
CC an oxidase derived from Rhodococcus. The present sequence was used to
CC illustrate the invention.
XX Sequence 500 BP; 113 A; 120 C; 173 G; 88 T; 0 U; 6 Other;
SQ Query Match 85.5%; Score 18.8; DB 14; Length 500;
Best Local Similarity 90.9%; Pred. No. 20;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCTTTCGG 22
Db ||||| ||||| ||||| ||||| |||||
57 GTCGAGCGGTAAAGCCTTTCGG 78

RESULT 22
AD080217/c
ID AD080217 standard; DNA; 1343 BP.
XX AC AD080217;
XX 29-JUL-2004 (first entry)
XX Rhodococcus sp. GR-002 strain 16S rDNA.
DE cyclic hydrocarbon degrading agent; Rhodococcus; gram positive bacillus;
XX catalase test positive; nitrate-reduction ability positive;
KW pyrazinamidase negative; pyrrolidonyl allyl amidase negative;
KW alkali phosphatase positive; beta-glucuronidase negative;
KW beta-galactosidase negative; alpha-glucosidase positive;
KW N-acetyl-beta-glucosaminidase negative; urease positive; GR-002 strain;
KW FERM P-18804; waste engine oil; aromatic hydrocarbon;
KW cycloaliphatic hydrocarbon; polycyclic aromatic hydrocarbon; ds.
XX Rhodococcus sp.
OS JP2004113197-A.
XX 15-APR-2004.
XX 27-SEP-2002; 2002JP-00284521.
XX

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PR 27-SEP-2002; 2002JP-00284521.
XX (GEIT-) GEITO KK.
XX WPI; 2004-322544/30.
XX Novel cyclic hydrocarbon degrading Rhodococcus species GR-002 strain
PT having biochemical properties e.g. gram positive bacillus, catalase test
PT positive, pyrazinamidase negative, useful for degrading waste engine oil.
XX Claim 2; SEQ ID NO 1; 13pp; Japanese.
XX The invention relates to a novel cyclic hydrocarbon degrading agent from
XX the Rhodococcus genus. The cyclic hydrocarbon degrading agent having
CC biochemical properties such as: gram positive bacillus, catalase test
CC positive, nitrate-reduction ability positive, pyrazinamidase negative,
CC pyrrolidonyl allyl amidase negative, alkali phosphatase positive, beta-
CC glucuronidase negative, beta-galactosidase negative, alpha-glucosidase
CC positive, N-acetyl-beta-glucosaminidase negative, urease positive. The
CC novel Rhodococcus microorganism is Rhodococcus sp. GR-002 strain having
CC the accession number FERM P-18804. The cyclic hydrocarbon degrading agent
CC is useful for processing a cyclic hydrocarbon-containing substance, such
CC as a waste engine oil. The novel Rhodococcus microorganism is useful for
CC degrading cyclic hydrocarbons containing aromatic hydrocarbons,
CC cycloaliphatic hydrocarbons, and/or polycyclic aromatic hydrocarbons.
CC This polynucleotide represents the novel Rhodococcus microorganism 16S
CC rDNA sequence of the invention.
XX Sequence 1343 BP; 263 A; 452 C; 320 G; 308 T; 0 U; 0 Other;
SQ Query Match 85.5%; Score 18.8; DB 12; Length 1343;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGCCTTTCGG 22
Db ||||| ||||| ||||| ||||| |||||
1290 GTCGAGCGGTAAAGCCTTTCGG 1269

RESULT 23
ADW16264
ID ADW16264 standard; DNA; 1390 BP.
XX AC ADW16264;
XX 07-APR-2005 (first entry)
XX DNA copy of the N_albus 16S ribosomal RNA EN46 isolate Seq 16.
DE 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
XX disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX Nocardioides albus.
OS WO2005003328-A1.
XX 13-JAN-2005.
XX 07-JUL-2004; 2004WO-AU000914.
XX 07-JUL-2003; 2003US-0485241P.
XX 22-SEP-2003; 2003US-0504703P.
XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX Franco CMM, Coombs JT;
XX WPI; 2005-091806/10.
XX Improving plant productivity comprises introducing into the plant or
PT propagation material an endophytic actinomycete that facilitates

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PT induction of at least one characteristic related to improved
XX productivity.
PS Claim 1; SEQ ID NO 16; 235pp; English.
XX
CC This invention relates to a novel method for improving plant
CC productivity. Specifically, it refers to introducing into the plant or
CC propagation material an endophytic actinomycetes or variant thereof,
CC where the actinomycetes facilitate induction of a characteristic related
CC to improved productivity. The present invention further describes
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
CC or cytokinin that are able to induce disease resistance in plants i.e.
CC provide disease bio-control capabilities against pathogen infection.
CC Accordingly, the method facilitates the improvement of cereal crop
CC productivity including increasing germination by up-regulating plant
CC growth promoting activities, as well as improving plant vigor or flower
CC and fruit yield. Furthermore, the new actinomycete or metabolite is
CC useful in the manufacture of a medicament for the therapeutic and/or
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
CC plant. As such, this method provides plant protectants and plant growth
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
CC insecticide and nematocide activities. This polynucleotide is the DNA
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
XX
SQ Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;
Query Match 85.5%; Score 18.8; DB 14; Length 1390;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GTCGAACGGAAAGCGCTTTCGG 22
Db 7 GTCGAGCGGAAGGCGCTTTCGG 28
||||| ||||||| |||||
RESULT 24
ADJ38609
ID ADJ38609 standard; DNA; 1403 BP.
XX
AC ADJ38609;
XX
DT 06-MAY-2004 (first entry)
XX
DE Micronospora sp. M42 16S rRNA, SEQ ID 1.
XX
KW Protozoa; Tuberculostatic; Antitubercular; Antimalarial;
KW Cerebroprotective; Actinomycete ; manzamine; 16S rRNA ; antibiotic; ds.
XX
OS Micronospora sp. M42.
XX
FN WO2004013297-A2.
XX
PD 12-FEB-2004.
XX
PF 01-AUG-2003; 2003WO-US024238.
XX
PR 01-AUG-2002; 2002US-0400330P.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY.
XX
PA (UMIS ) UNIV MISSISSIPPI.
XX
PI Hill RT, Hamann MT, Peraud O, Kasanah N;
XX
DR WPI; 2004-169330/16.
XX
PT New isolated actinomycete useful for producing antibiotics produces
XX manzamine having antituberculosis and antimalarial activity.
XX
PS Claim 19; SEQ ID NO 1; 46pp; English.
XX
CC The present invention relates to an isolated actinomycete (A1) producing
CC manzamine, which comprises a 16S rRNA (ADJ38609). (A1) is useful for
CC producing manzamine by fermentation, which involves culturing (A1) having
induction of at least one characteristic related to improved
productivity.
Claim 1; SEQ ID NO 16; 235pp; English.
This invention relates to a novel method for improving plant
productivity. Specifically, it refers to introducing into the plant or
propagation material an endophytic actinomycetes or variant thereof,
where the actinomycetes facilitate induction of a characteristic related
to improved productivity. The present invention further describes
metabolites of the actinomycetes microorganism such as auxin, gibberellin
or cytokinin that are able to induce disease resistance in plants i.e.
provide disease bio-control capabilities against pathogen infection.
Accordingly, the method facilitates the improvement of cereal crop
productivity including increasing germination by up-regulating plant
growth promoting activities, as well as improving plant vigor or flower
and fruit yield. Furthermore, the new actinomycete or metabolite is
useful in the manufacture of a medicament for the therapeutic and/or
prophylactic treatment of a mammalian or non-mammalian subject i.e.
plant. As such, this method provides plant protectants and plant growth
stimulants that exhibit antibacterial, antimicrobial, fungicide,
insecticide and nematocide activities. This polynucleotide is the DNA
sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.
SQ Sequence 1390 BP; 324 A; 348 C; 443 G; 266 T; 0 U; 9 Other;
Query Match 85.5%; Score 18.8; DB 14; Length 1390;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1 GTCGAACGGAAAGCGCTTTCGG 22
Db 7 GTCGAGCGGAAGGCGCTTTCGG 28
||||| ||||||| |||||
RESULT 25
ADJ16290
ID ADJ16290 standard; DNA; 1427 BP.
XX
AC ADJ16290;
XX
DT 07-APR-2005 (first entry)
XX
DE DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.
XX
KW 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;
KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX
OS Actinomycetales.
XX
FN WO2005003328-A1.
XX
PD 13-JAN-2005.
XX
PF 07-JUL-2004; 2004WO-AU000914.
XX
PR 07-JUL-2003; 2003US-0485241P.
XX
PR 22-SEP-2003; 2003US-0504703P.
XX
PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX
PI Franco CMM, Coombs JT;
XX
DR WPI; 2005-091806/10.
XX
PT Improving plant productivity comprises introducing into the plant or
PT propagation material an endophytic actinomycete that facilitates
PT induction of at least one characteristic related to improved
PT productivity.
XX
PS Example 18; Fig 19; 235pp; English.
XX
CC This invention relates to a novel method for improving plant
CC productivity. Specifically, it refers to introducing into the plant or
CC propagation material an endophytic actinomycetes or variant thereof,
CC where the actinomycetes facilitate induction of a characteristic related
CC to improved productivity. The present invention further describes
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
CC or cytokinin that are able to induce disease resistance in plants i.e.
CC provide disease bio-control capabilities against pathogen infection.
CC Accordingly, the method facilitates the improvement of cereal crop
CC productivity including increasing germination by up-regulating plant
CC growth promoting activities, as well as improving plant vigor or flower
CC and fruit yield. Furthermore, the new actinomycete or metabolite is
CC useful in the manufacture of a medicament for the therapeutic and/or
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
CC plant. As such, this method provides plant protectants and plant growth
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
CC insecticide and nematocide activities. This polynucleotide is the DNA
CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

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XX
SQ Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match      85.5%; Score 18.8; DB 14; Length 1427;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGGAAGGCCCTTCGG 22
Db 28 GTCGACGGGAAGGCCCTTCGG 49

RESULT 26
ADZ35975
ID ADZ35975 standard; DNA; 1440 BP.
XX
AC ADZ35975;
XX
DT 30-JUN-2005 (first entry)
XX
DE Verrucosisspora sp. AB-18-032 16S rRNA gene.
XX
KW ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
KW polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;
KW vitamin; abyssomicin B; abyssomicin C; abyssomicin D;
KW Staphylococcus aureus infection; protozoal infection;
KW Plasmodium infection; Leishmania infection; chagas disease;
KW Gram positive bacteria infection; mrsa infection .
XX
OS Verrucosisspora sp. AB-18-032.
XX
XX
XX WO2005033114-A1.
XX
PD 14-APR-2005.
XX
XX 23-SEP-2004; 2004WO-EP010661.
XX
XX 01-OCT-2003; 2003DE-01047472.
XX
XX 11-NOV-2003; 2003DE-01053300.
XX
PA (UYTU-) UNIV TUEBINGEN.
XX
XX Fiedler H, Suessmuth R, Zaehner H, Bull A;
XX
XX WPI; 2005-296122/30.
XX
XX New abyssomicin polycyclic macrolactone compounds, useful as antibiotics
XX and antiprotozoal agents effective against multiresistant strains,
XX prepared using bacteria of genus Verrucosisspora.
XX
XX Disclosure; SEQ ID NO 1; 47pp; German.
XX
XX This invention describes novel polycyclic macrolactones and their
XX derivatives , prepared using bacteria of genus Verrucosisspora and
XX designated abyssomicins. The polycyclic macrolactones have at least one
XX oxa-bicyclo system as a partial structure and at least one Michael system
XX as double bond system. The polycyclic macrolactones are prepared by
XX culturing Verrucosisspora strain AB 18-032, recovering a culture
XX supernatant from the culture, optionally preparing a culture filtrate and
XX optionally isolating one or more polycyclic macrolactones from the
XX supernatant and/or filtrate. Alternatively the microorganism is cultured
XX followed by isolating one or more polycyclic macrolactones from the
XX microorganism. The Verrucosisspora strain AB 18-032 was isolated from
XX marine sediment collected at a depth of 1000m in Sagami bay in the
XX Japanese sea and is deposited as DSM No. 15899. The polycyclic
XX macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
XX essential component in the biosynthesis of folic acid) from chorismic
XX acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is
XX essential to the life of microorganisms, especially prokaryotes and
XX protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of
XX folic acid in mammals (including humans), and thus have no adverse
XX effects on mammalian cells. Three polycyclic macrolactones are
XX specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin

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CC D. Abyssomicin C strongly inhibited growth of methicillin-resistant
CC Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus
CC aureus strain Mu50. The products of the invention are useful as
CC antibiotics (especially effective against Gram positive bacteria) and
CC antiprotozoal agents, specifically effective against bacteria and
CC protozoa resistant (especially multi-resistant) to conventional
CC antibiotics. Typically polycyclic macrolactones are useful for combating
CC tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping
CC sickness and Chagas disease) and infections caused by resistant Gram
CC positive bacteria such as methicillin- and vancomycin-resistant
CC Staphylococcus aureus strains. Polycyclic macrolactones are also useful
CC as disinfectants (especially in hospitals and other medical
CC establishments) and as lead structures for the development of further
CC active agents. This sequence represents the Verrucosisspora strain AB 18-
CC 032 16S rRNA DNA which is used to phylogenically classify the bacterial
CC strain.
XX
SQ Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other;

Query Match      85.5%; Score 18.8; DB 14; Length 1440;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGGAAGGCCCTTCGG 22
Db 4 GTCGACGGGAAGGCCCTTCGG 25

RESULT 27
ADX38843
ID ADX38843 standard; DNA; 1443 BP.
XX
AC ADX38843;
XX
DT 05-MAY-2005 (first entry)
XX
DE Microbispora 16S rDNA.
XX
KW antibiotic; bacterial infection; animal growth; 16S rDNA; ds;
KW antibacterial; anabolic.
XX
OS Microbispora sp. ATCC PTA-5024.
XX
XX WO2005014628-A1.
XX
XX 17-FEB-2005.
XX
XX 12-JUL-2004; 2004WO-EP007658.
XX
XX 18-JUL-2003; 2003EP-00016306.
XX
XX (VICU-) VICURON PHARM INC.
XX
XX Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
XX Marinelli F, Selva E, Parenti F;
XX WPI; 2005-173079/18.
XX
XX New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
XX having specified physico-chemical characteristics, used to form
XX medicament for the treatment or prevention of bacterial infections, or
XX used as animal growth promoter.
XX
XX Disclosure; SEQ ID NO 1; 85pp; English.
XX
XX The invention relates to an antibiotic 107891 complex comprising Factor
XX A1 and Factor A2. The antibiotic is used to form a pharmaceutical
XX composition used as medicament for the treatment or prevention of
XX bacterial infections, or as animal growth promoter. The present sequence
XX represents the Microbispora 16S rDNA.
XX
SQ Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

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XX	Query Match	85.5%; Score 18.8; DB 14; Length 1443;	
SQ	Best Local Similarity	90.9%; Pred. No. 22;	
	Matches	20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1	GTCGAACGGAAGGCTTTTCGG 22	
DB	34	GTCGACGGGAAGGCTTTTCGG 55	
RESULT 28			
AEA22406			
ID	AEA22406	standard; DNA; 1461 BP.	
XX	AEA22406;		
AC	25-AUG-2005	(first entry)	
XX			
DT	Mycobacterium gordonae	16S rRNA sequence SEQ ID NO:7.	
DE	microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.		
KW	Mycobacterium gordonae.		
OS	US2005130168-A1.		
XX	16-JUN-2005.		
XX	31-OCT-2003; 2003US-00697802.		
PF	31-OCT-2003; 2003US-00697802.		
XX			
PR	(HANK/) HAN X.		
PA	(PHAM/) PHAM A S.		
XX	Han X, Pham AS;		
PI	WPI; 2005-424597/43.		
XX			
DR	Determining a bacterium species comprises providing oligonucleotide		
PT	primer set comprising SEQ-FOR and SEQ-REV in a complementary fashion.		
XX	Disclosure; SEQ ID NO 7; 74pp; English.		
XX			
CC	The invention relates to a method (M1) for determining a bacterium		
CC	species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)		
CC	extracting a genomic nucleotide from the bacterium to provide a		
CC	nucleotide template; (c) annealing a region of a nucleotide template to a		
CC	specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a		
CC	complementary fashion, the primer set designed to provide a product		
CC	having a predetermined size dictated by a complementary primer set; (d)		
CC	amplifying the region of the nucleotide template to produce the product;		
CC	and (e) determining a species of a bacterium in a nucleotide sequence of		
CC	the product. Also described is an alternative method (M2) for determining		
CC	a bacterium species comprising: (a) providing a specimen or a sample		
CC	having a template; (b) providing a pair of primers selected from: (i) a		
CC	first forward primer having consecutive bases of an APB-f comprising any		
CC	of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments		
CC	or variations and a first reverse primer having consecutive bases of an		
CC	APB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)		
CC	or their fragments or variations, (ii) a second forward primer having		
CC	consecutive bases of an UB-f comprising any of the 28 sequences of 15-21		
CC	bp (AEA22489-AEA22516) or their fragments or variations and a second		
CC	reverse primer having consecutive bases of an UB-r comprising any of the		
CC	28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or		
CC	variations, or (iii) a first forward primer having consecutive bases of		
CC	an APB-f of AEA22417-AEA22452 or their fragments or variations and a		
CC	second reverse primer having consecutive bases of an UB-r of AEA22517-		
CC	AEA22544 or their fragments or variations; (c) the specimen; and (d)		
CC	comparing the product from the specimen with a nucleotide sequence from a		
CC	database to determine the bacterium species present in the specimen. The		
CC	methods are useful for determining a bacterium species. The present		
CC	invention represents a Mycobacterium gordonae 16S rRNA nucleotide		
CC	sequence, which is used in the exemplification of the present invention.		

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CC and renal inflammatory diseases, hepatitis, sepsis/septic shock, hypoxic
CC shock, acute respiratory distress syndrome (ARDS), rheumatic arthritis,
CC gouty arthritis, aortic regurgitation, juvenile chronic arthritis,
CC osteoarthritis, nephritis, induction of tolerance, contact
CC hypersensitivity, inflammatory bowel disease, sexual dysfunction,
CC transplantation, pain, disease progression of HIV, post inflammatory hypo
CC pigmentation, tinea versicolor, idiopathic guttate hypomelanosis, fever,
CC functional bowel disease, obesity, satiety effect, diabetes mellitus,
CC modulation of dermal exocrine function, canities (canities
CC circumscripta), gray hair, pancreatitis, fibrotic disorders (hypertrophic
CC scars, keloids, localized scleroderma, systemic sclerosis, sclerodermic
CC graft versus host disease of the skin, cirrhosis of the liver, idiopathic
CC and bleomycin induced lung fibrosis, cyclosporin induced nephropathy),
CC uveitis (especially in Behcet's syndrome and sarcoidosis), vasculitis,
CC microbial infections, celliac disease, vulvar vestibulitis syndrome,
CC melanoma invasion or anorexia in human or an animal.
XX
SQ Sequence 1483 BP; 320 A; 360 C; 509 G; 289 T; 0 U; 5 Other;

  Query Match      85.5%; Score 18.8; DB 14; Length 1483;
  Best Local Similarity 90.9%; Pred. No. 22;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
   ||||| ||| ||||| |||||
Db 35 GTCGAGCGGTAAAGCCTTTCGG 56

RESULT 30
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
AC ADR90327;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WP1; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
Claim 1; SEQ ID NO 3; 33pp; Japanese.
XX
The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

  Query Match      85.5%; Score 18.8; DB 13; Length 1511;
  Best Local Similarity 90.9%; Pred. No. 22;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
   ||||| ||| ||||| |||||
Db 54 GTCGAGCGGTAAAGCCTTTCGG 75

RESULT 32
ADR11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

  Query Match      85.5%; Score 18.8; DB 13; Length 1511;
  Best Local Similarity 90.9%; Pred. No. 22;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
   ||||| ||| ||||| |||||
Db 54 GTCGAGCGGTAAAGCCTTTCGG 75

RESULT 32
ADR11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;
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```
Query Match      85.5%; Score 18.8; DB 13; Length 1511;
Best Local Similarity 90.9%; Pred. No. 22;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
   ||||| ||| ||||| |||||
Db 54 GTCGAGCGGTAAAGCCTTTCGG 75

RESULT 31
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
AC ADR90325;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WP1; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
Claim 1; SEQ ID NO 1; 33pp; Japanese.
XX
The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

  Query Match      85.5%; Score 18.8; DB 13; Length 1511;
  Best Local Similarity 90.9%; Pred. No. 22;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22
   ||||| ||| ||||| |||||
Db 54 GTCGAGCGGTAAAGCCTTTCGG 75

RESULT 32
ADR11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;
```



DE Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.  
 XX degradation; aliphatic hydrocarbon; bioremediation; oil degradation;  
 KW pollutant; degradation; groundwater decontamination; 16S rRNA;  
 KW 16S ribosomal RNA; gene; ds.  
 OS Rhodococcus erythropolis.  
 XX JP2005261218-A.  
 PN 29-SEP-2005.  
 PD 16-MAR-2004; 2004JP-00074370.  
 PF 16-MAR-2004; 2004JP-00074370.  
 PR (EBAR ) EBARA CORP.  
 XX Karube M, Tamatsubo K, Miya A;  
 PI WPI; 2005-678804/70.  
 DR Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic  
 PT hydrocarbon, useful for bioremediation of oil-polluted environment such  
 PT as river water, underground water, ocean, sea cost.  
 PS Claim 1; SEQ ID NO 1; 14pp; Japanese.  
 XX The invention relates to a novel Rhodococcus erythropolis M-13 strain  
 CC capable of degrading aliphatic hydrocarbons. The invention further  
 CC provides the 16S rRNA gene of the novel strain showing 98% or more  
 CC homology with a nucleotide sequence of a fully defined 1511 nucleotide  
 CC (AED11327) sequence given in specification. The novel strain is useful  
 CC for the bioremediation of an oil-polluted environment, such as river  
 CC water, underground water, ocean, sea cost, etc. The novel strain degrades  
 CC linear or branched aliphatic hydrocarbons efficiently. This  
 CC polynucleotide sequence represents the DNA of the novel Rhodococcus  
 CC erythropolis M-13 strain 16S rRNA gene of the invention.  
 XX  
 SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;  
 Query Match 85.5%; Score 18.8; DB 14; Length 1511;  
 Best Local Similarity 90.9%; Pred. No. 22;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCTTTCGG 22  
 Db 54 GTCGAGCGTAAGGCTTTCGG 75  
 RESULT 33  
 ADE41084  
 ID ADE41084 standard; rRNA; 1584 BP.  
 XX ADE41084;  
 AC 29-JAN-2004 (first entry)  
 DT . corallina partial 16S rRNA sequence.  
 XX Antibiotic; ss; 16S rRNA; MF-BA-1768alpal; MF-BA-1768betal;  
 KW Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;  
 KW bacterial infection.  
 XX Microbispora corallina; strain NRRL 30420.  
 OS US5551591-B1.  
 XX 22-APR-2003.  
 PD 07-SEP-2001; 2001US-00949230.  
 PF 07-SEP-2001; 2001US-00949230.  
 XX 07-SEP-2001; 2001US-00949230.

XX (ESSE-) ESSENTIAL THERAPEUTICS INC.  
 PA Lee MD;  
 PI WPI; 2003-895156/82.  
 DR Novel antibiotics isolated from fermentation broth of novel strain of  
 XX Microbispora corallina, useful for treating a wide range of bacterial  
 PT infections.  
 PT Disclosure; SEQ ID NO 1; 20pp; English.  
 PS The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal  
 XX or its pharmaceutically acceptable salt, having physicochemical  
 CC characteristics in the non-salt form as detailed in the specification.  
 CC The antibiotics are isolated from a novel strain of Microbispora  
 CC corallina designated NRRL 30420. Also included are producing the above  
 CC antibiotic (by cultivating Microbispora corallina NRRL 30420, or an  
 CC antibiotic MF- BA-1768alpal or MF-BA-1768betal -producing mutant,  
 CC variant or its recombinant form, in a culture medium containing  
 CC assimilable sources of carbon, nitrogen and inorganic salts under aerobic  
 CC fermentation conditions until the antibiotic is produced and then  
 CC recovering the antibiotic) and a composition comprising the above  
 CC antibiotic or its salt. The antibiotics are useful for treating a  
 CC bacterial infection caused by Staphylococcus (e.g. S.aureus, S.epidermis  
 CC, S.haemolyticus ), Enterococcus (e.g. E.faecalis, E.faecium ),  
 CC Streptococcus (e.g. S.pneumoniae, S.pyrogenes ), Haemophilus (e.g.  
 CC H.influenzae ) or Escherichia (e.g. E.coli ) in a patient. The present  
 CC sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which  
 CC identifies the strain.  
 XX  
 SQ Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;  
 Query Match 85.5%; Score 18.8; DB 10; Length 1584;  
 Best Local Similarity 90.9%; Pred. No. 22;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GTCGAACGGAAGGCTTTCGG 22  
 Db 128 GTCGAGCGTAAGGCTTTCGG 149  
 RESULT 34  
 AED48445/C  
 ID AED48445 standard; DNA; 84222 BP.  
 XX AED48445;  
 AC 15-DEC-2005 (first entry)  
 XX M. echinospora gentamycin biosynthetic gene cluster DNA.  
 DT ds; gene; antibiotic; virucide; aminoglycoside; bacterial infection;  
 DE viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; genM1; gmrA;  
 KW genS1; genC; genD2; genM2; genD1; genS2; genB1; genB4; genB3; genK;  
 KW genB2; genX; genU; genF; genE; genY; genA; genF; genG; genH; genI; genJ;  
 KW genL; genN; DNA polymerase beta chain; integral membrane protein;  
 KW agglutinin; esterase; Trp-trNA ligase;  
 KW quinine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;  
 KW gentamicin (hexosaminyl-6-)aminotransferase I; gentamicin oxidoreductase;  
 KW (N-acetyl-) hexosaminyltransferase; ribosomal methyltransferase;  
 KW L-glutamine:ketcocylitol; 2-deoxy-scyllo-inosose synthase;  
 KW gentamicin glycosyltransferase II; gentamicin aminotransferase II;  
 KW gentamicin production protein; gentamicin aminotransferase IV;  
 KW aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;  
 KW gentamicin C-methyltransferase; gentamicin aminotransferase II;  
 KW gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;  
 KW gentamicin methyltransferase; two-component system histidine kinase;  
 KW two-component system response regulator; serine protease;  
 KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;  
 KW subtilase; transcriptional regulator; acetyltransferase;  
 KW ATP-binding protein; ABC-transporter, permease component.

```
XX Micromonospora echinospora.
OS
XX
PH Key Location/Qualifiers
FT CDS 191..1264
FT /*tag= a
FT /product= "putative DNA polymerase beta chain"
FT /note= "ORF MecP21.15"
FT complement(1347..2321)
FT CDS
FT /*tag= b
FT /product= "putative integral membrane protein"
FT /note= "ORF MecP21.16c"
FT CDS 2374..2847
FT /*tag= c
FT /product= "hypothetical protein"
FT /note= "ORF MecP21.17"
FT CDS 2847..4517
FT /*tag= d
FT /product= "hypothetical protein"
FT /note= "ORF MecP21.18"
FT complement(4571..5590)
FT CDS
FT /*tag= e
FT /product= "putative plus agglutinin"
FT /note= "ORF MecP21.19c"
FT complement(5628..6206)
FT CDS
FT /*tag= f
FT /product= "hypothetical protein"
FT /note= "ORF MecP21.20c"
FT complement(6297..6899)
FT CDS
FT /*tag= g
FT /product= "putative esterase"
FT /note= "ORF MecP21.21c"
FT CDS 7683..9389
FT /*tag= h
FT /product= "hypothetical protein"
FT /note= "ORF MecP21.22"
FT complement(9518..10144)
FT CDS
FT /*tag= i
FT /product= "hypothetical protein"
FT /note= "ORF MecP21.23c"
FT 16081..16620
FT /*tag= j
FT /product= "hypothetical protein"
FT /note= "ORF MecE04.1"
FT CDS 16711..17790
FT /*tag= k
FT /product= "putative Trp-trNA ligase"
FT /note= "ORF MecE04.2"
FT CDS 17857..19014
FT /*tag= l
FT /product= "queuine/archaeosine tRNA-ribosyltransferase"
FT /gene= "genP"
FT CDS 19121..19939
FT /*tag= m
FT /gene= "gmrb"
FT /product= "putative ribosomal methyltransferase"
FT complement(19953..21206)
FT CDS
FT /*tag= n
FT /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
FT /gene= "genB1"
FT CDS complement(21238..22761)
FT /*tag= o
FT /gene= "genQ"
FT /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
FT complement(22934..23743)
FT CDS
FT /*tag= p
FT /product= "putative gentamicin oxidoreductase"
FT /gene= "genD3"
FT CDS complement(23758..25005)
FT /*tag= q
FT /gene= "genM1"
FT /product= "putative (N-acetyl-) hexosaminyltransferase"
FT complement(25042..25866)
FT CDS
FT /*tag= r
FT /product= "putative ribosomal methyltransferase"
FT /gene= "gmzA"
FT CDS 26161..27423
FT /*tag= s
FT /gene= "genS1"
FT /product= "putative L-glutamine:ketocyclitol"
FT CDS 27558..28751
FT /*tag= t
FT /product= "2-deoxy-scylo-inosose synthase"
FT /gene= "genC"
FT CDS 28744..29769
FT /*tag= u
FT /gene= "genD2"
FT /product= "putative gentamicin oxidoreductase"
FT 29858..31030
FT /*tag= v
FT /product= "putative gentamicin glycosyltransferase II"
FT /gene= "genM2"
FT CDS 31032..33011
FT /*tag= w
FT /gene= "genD1"
FT /product= "putative gentamicin oxidoreductase"
FT 33011..34267
FT /*tag= x
FT /product= "putative gentamicin aminotransferase II"
FT /gene= "genS2"
FT CDS 34275..34646
FT /*tag= y
FT /gene= "genW"
FT /product= "putative gentamicin production protein"
FT complement(34741..36078)
FT CDS
FT /*tag= z
FT /product= "putative gentamicin aminotransferase IV"
FT /gene= "genB4"
FT CDS complement(36137..36943)
FT /*tag= aa
FT /gene= "genJ"
FT /product= "biosynthetic aminoglycoside 3' -
FT phosphotransferase"
FT complement(36981..38453)
FT CDS
FT /*tag= ab
FT /product= "putative gentamicin aminotransferase III"
FT /gene= "genB3"
FT CDS complement(38969..40885)
FT /*tag= ac
FT /gene= "genX"
FT /product= "putative gentamicin C-methyltransferase"
FT 41135..42379
FT /*tag= ad
FT /product= "putative gentamicin aminotransferase II"
FT /gene= "genB2"
FT CDS complement(42465..42977)
FT /*tag= ae
FT /gene= "genX"
FT /product= "putative gentamicin production protein"
FT complement(43032..43967)
FT CDS
FT /*tag= af
FT /product= "putative gentamicin production protein"
FT /gene= "genU"
FT CDS complement(44162..45568)
FT /*tag= ag
FT /gene= "genT"
FT /product= "putative gentamicin exporter"
FT complement(45861..46883)
FT CDS
FT /*tag= ah
FT /product= "putative aminocyclitol 1-dehydrogenase"
FT /gene= "genE"
FT CDS 47364..48878
FT /*tag= ai
FT /gene= "genY"
FT /product= "putative cation antiporter"
FT 49000..49737
FT CDS
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FT      /*tag= aj
FT      /product= "putative gentamicin production protein"
FT      /gene= "genA"
FT      CDS      49734..50381
FT      /*tag= ak
FT      /gene= "genF"
FT      /product= "putative gentamicin production protein"
FT      /gene= "genH"
FT      CDS      50381..50734
FT      /*tag= al
FT      /product= "putative gentamicin production protein"
FT      /gene= "genG"
FT      CDS      complement(50813..54229)
FT      /*tag= am
FT      /product= "putative gentamicin exporter"
FT      /gene= "genH"
FT      CDS      complement(54226..56163)
FT      /*tag= an
FT      /gene= "genI"
FT      /product= "putative gentamicin exporter"
FT      complement(56689..57627)
FT      /*tag= ao
FT      /gene= "genJ"
FT      /product= "putative gentamicin production protein"
FT      58121..58741
FT      /*tag= ap
FT      /product= "putative gentamicin production protein"

Query Match      85.5%; Score 18.8; DB 14; Length 84222;
Best Local Similarity 90.9%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1      GTCGACGGAAAGGCGCTTTCG 22
Db      15392      GTCGACGGAAAGGCGCTTTCG 15371

RESULT 35
ID      AAD57239/c
AC      AAD57239;
XX
XX      06-NOV-2003 (first entry)
XX      Human CGDD-19 cDNA.
XX      Human; cell growth, differentiation and death protein; CGDD; leukaemia;
XX      neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
XX      muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
XX      diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
XX      systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
XX      gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
XX      cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
XX      transgenic animal; gene therapy; neuroprotective; relaxant; cyostatic;
XX      dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
XX      antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
XX      protozoacide; nootropic; gene; ss.
XX      Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      CDS      112..687
XX      /*tag= a
XX      /product= "Human CGDD-19 protein"
XX
XX      WO2003050253-A2.
XX
XX      19-JUN-2003.
XX
XX      04-DEC-2002; 2002WO-US039133.
XX
XX      07-DEC-2001; 2001US-0340747P.
XX      20-DEC-2001; 2001US-0342761P.

```

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PR      15-JAN-2002; 2002US-0349705P.
PR      06-FEB-2002; 2002US-0354764P.
PR      12-FEB-2002; 2002US-0356216P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
XX      Griffin JA, Rankumar J, Emerling BM, Kable AE, Elliott VS,
XX      Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT,
XX      Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B,
XX      Sprague WW, Lee SY, Khate R, Gandhi AR, Gietzen KJ, Bhatia U,
XX      Burriil JD, Blake JJ, Ho A, Zheng W;
XX
XX      WPI; 2003-532903/50.
XX      P-PSDB; AAE37930.
XX
XX      New CGDD polypeptides, useful for diagnosing, preventing, and treating
XX      disorders associated with an abnormal expression or activity of CGDD,
XX      e.g. neuromuscular, immunological, cardiovascular disorders, cancer
XX      and/or infections.
XX
XX      Claim 5; Page 283; 299pp; English.
XX
XX      The present invention relates to novel cell growth, differentiation and
XX      death (CGDD) proteins and polynucleotides encoding them. The sequences of
XX      the invention are useful in diagnosing, preventing and treating disorders
XX      associated with an abnormal expression or activity of CGDD such as
XX      neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
XX      disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
XX      endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
XX      leukaemia, cervical or breast cancers), immunological disorders (e.g.
XX      scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
XX      disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
XX      syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
XX      protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
XX      and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
XX      create humanised animals or transgenic animals to model human diseases.
XX      The invention is also used in gene therapy. The present sequence is human
XX      CGDD-19 cDNA
XX
XX      SQ      Sequence 1137 BP; 317 A; 274 C; 296 G; 250 T; 0 U; 0 Other;

Query Match      81.8%; Score 18; DB 9; Length 1137;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3      CGAACGGAAAGGCGCTTTC 20
Db      1071      CGAACGGAAAGGCGCTTTC 1054

RESULT 36
ADCG1232
ID      ADCG1232 standard; DNA; 1439 BP.
XX
XX      AC      ADCG1232;
XX
XX      DT      18-DEC-2003 (first entry)
XX
XX      DE      Baeyer-Villiger enzyme 16s rDNA gene from Rhodococcus erythropolis AN12.
XX      Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;
XX      16s rDNA; ds.
XX      OS      Rhodococcus erythropolis.
XX      PN      WO2003020890-A2.
XX      PD      13-MAR-2003.
XX      PF      29-AUG-2002; 2002WO-US027549.
XX      PR      29-AUG-2001; 2001US-0315546P.
XX

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CC combination of a magnesium chelator, a nonionic detergent and an anionic  
 CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the  
 CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at  
 CC least one oligonucleotide probe which is capable of selectively  
 CC hybridizing to a region of the pre-rRNA that is not present in a mature  
 CC mycobacterial rRNA. The probes can be used to identify many Mycobacterium  
 CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,  
 CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.  
 CC intracellular. The probes may also be used to measure mycobacterial  
 CC response to inhibitors of RNA and protein synthesis and may therefore be  
 CC used to screen new antimycobacterial drugs. Mycobacteria have a slow  
 CC growth rate. By using the probes, drug developers can now identify  
 CC compounds that are more effective, but less stable than those previously  
 CC identified. (Updated on 17-OCT-2003 to standardise OS field.)  
 XX  
 SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 79.1%; Score 17.4; DB 2; Length 25;  
 Best Local Similarity 80.0%; Pred. No. 74;  
 Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTTCGG 22  
 ||||| ||||| || :|||  
 Db 1 CGAACGGAAGGCTTTTCGG 20

RESULT 39  
 AAS30718  
 ID AAS30718 standard; DNA; 25 BP.  
 XX  
 AC AAS30718;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 04-DEC-2001 (first entry)  
 DE Mycobacterium species-specific probe #24.  
 XX  
 XX Mycobacterium; species-specific bacterial identification; primer; ss.  
 KW Mycobacterium chelonae.  
 OS  
 XX WO200166797-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US006731.  
 XX  
 PR 03-MAR-2000; 2000US-0186840P.  
 XX  
 PA (BECI ) BECKMAN COULTER INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US NAT INST OF HEALTH.  
 XX  
 FI Fischer SH, Rampal JB, Fahle GA, Conville PS;  
 XX  
 DR WPI; 2001-514847/56.  
 XX

Species-specific bacterial identification, used particularly to identify  
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or  
 PT specific primers to a sample.  
 XX  
 PS Claim 28; Page 21; 43pp; English.

CC The invention relates to a method of species-specific bacterial  
 CC identification, comprising hybridising a bacterial genus-selective or  
 CC specific primer to a sample and amplifying nucleic acids. This is  
 CC followed by hybridising the amplified nucleic acid to a solid phase array  
 CC comprising bacterial species specific probe oligonucleotides chemically  
 CC linked to a polymeric support in a predetermined pattern. This method is  
 CC used for species-specific identification of a bacterium, particularly a  
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.  
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid  
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720

CC represent Mycobacterium species-specific primers and probes used in the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;  
 Query Match 79.1%; Score 17.4; DB 4; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 74;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 4 GAACGGAAGGCTTTTCGG 22  
 ||||| ||||| |||||  
 Db 1 GAACGGAAGGCTTTTCGG 19

RESULT 40  
 AAS30716  
 ID AAS30716 standard; DNA; 25 BP.  
 XX  
 AC AAS30716;  
 XX  
 DT 06-AUG-2003 (revised)  
 DT 04-DEC-2001 (first entry)  
 DE Mycobacterium species-specific probe #22.  
 XX  
 XX Mycobacterium; species-specific bacterial identification; primer; ss.  
 KW Mycobacterium chelonae.  
 OS  
 XX WO200166797-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US006731.  
 XX  
 PR 03-MAR-2000; 2000US-0186840P.  
 XX  
 PA (BECI ) BECKMAN COULTER INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US NAT INST OF HEALTH.  
 XX  
 FI Fischer SH, Rampal JB, Fahle GA, Conville PS;  
 XX  
 DR WPI; 2001-514847/56.  
 XX

Species-specific bacterial identification, used particularly to identify  
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or  
 PT specific primers to a sample.  
 XX  
 PS Claim 28; Page 21; 43pp; English.

CC The invention relates to a method of species-specific bacterial  
 CC identification, comprising hybridising a bacterial genus-selective or  
 CC specific primer to a sample and amplifying nucleic acids. This is  
 CC followed by hybridising the amplified nucleic acid to a solid phase array  
 CC comprising bacterial species specific probe oligonucleotides chemically  
 CC linked to a polymeric support in a predetermined pattern. This method is  
 CC used for species-specific identification of a bacterium, particularly a  
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.  
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid  
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720  
 CC represent Mycobacterium species-specific primers and probes used in the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 4; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 74;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCTTTTCGG 22  
 ||||| ||||| |||||  
 Db 1 GAACGGAAGGCTTTTCGG 19

```

RESULT 41
AAD11024/c
ID  AAD11024 standard; DNA; 32 BP.
XX
XX  AAD11024;
AC
XX  24-SEP-2001 (first entry)
DT
XX
DE  Probe #4 to detect amplified MAC 16S rRNA or DNA encoding 16S rRNA.
XX
XX  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW  in vitro amplification; MAC infection; probe; ss.
XX
OS  Mycobacterium sp.
XX
XX  WO200144511-A2.
PN
XX  21-JUN-2001.
PD
XX
PF  15-DEC-2000; 2000WO-US033872.
XX
XX  15-DEC-1999; 99US-0171202P.
PR
XX  (GENP-) GEN-PROBE INC.
PA  (BREN/) BRENTANO S T.
PA  (LANK/) LANKFORD R L.
XX
XX  Brentano ST, Lankford RL;
PI
XX  WPI; 2001-398171/42.
DR
XX
PT  Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT  nucleic acid amplification with amplification oligonucleotides specific
PT  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT  species.
XX
XX  Claim 11; Page 27; 27pp; English.
PS
XX
XX  The present invention relates to a method for detecting Mycobacterium
CC  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC  tuberculosis, M. paratuberculosis) present in a biological sample. The
CC  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC  16S rRNA obtained from a biological sample containing nucleic acid from a
CC  MAC species in an in vitro nucleic acid amplification mixture comprising
CC  a polymerase activity and a pair of primers to produce an amplified
CC  nucleic acid and detecting amplified nucleic acid. The method is useful
CC  for in vitro diagnostic detection of pathogenic bacteria, particularly
CC  detecting infections caused by MAC organisms, distinguished from other
CC  closely-related Mycobacterium species. The present sequence is a probe
CC  used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX  Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;
SQ
    Query Match      79.1%; Score 17.4; DB 4; Length 32;
    Best Local Similarity 94.7%; Pred. No. 76;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GTCGAACGGAAGGCCTTT 19
    |||||
DB  28  GTCGAACGGAAGGCCTCT 10

RESULT 42
AAD11017
ID  AAD11017 standard; DNA; 32 BP.
XX
XX  AAD11017;
AC
XX  24-SEP-2001 (first entry)
DT
XX
DE  PCR primer #4 used for in vitro amplification of MAC rRNA.
XX
XX  Mycobacterium avium complex; MAC; 16S ribosomal RNA; pathogenic bacteria;
KW  in vitro amplification; MAC infection; PCR primer; ss.
XX
OS  Mycobacterium sp.
XX
XX  WO200144511-A2.
PN
XX  21-JUN-2001.
PD
XX
PF  15-DEC-2000; 2000WO-US033872.
XX
XX  15-DEC-1999; 99US-0171202P.
PR
XX  (GENP-) GEN-PROBE INC.
PA  (BREN/) BRENTANO S T.
PA  (LANK/) LANKFORD R L.
XX
XX  Brentano ST, Lankford RL;
PI
XX  WPI; 2001-398171/42.
DR
XX
PT  Detecting Mycobacterium avium complex organisms, comprises using in vitro
PT  nucleic acid amplification with amplification oligonucleotides specific
PT  for 16S ribosomal RNA or DNA encoding 16S rRNA from the bacterial
PT  species.
XX
XX  Claim 11; Page 27; 27pp; English.
PS
XX
XX  The present invention relates to a method for detecting Mycobacterium
CC  avium complex (MAC) organisms (eg. M. avium, M. intracellulare, M.
CC  tuberculosis, M. paratuberculosis) present in a biological sample. The
CC  method comprises amplifying a 16S ribosomal RNA (rRNA) or DNA encoding
CC  16S rRNA obtained from a biological sample containing nucleic acid from a
CC  MAC species in an in vitro nucleic acid amplification mixture comprising
CC  a polymerase activity and a pair of primers to produce an amplified
CC  nucleic acid and detecting amplified nucleic acid. The method is useful
CC  for in vitro diagnostic detection of pathogenic bacteria, particularly
CC  detecting infections caused by MAC organisms, distinguished from other
CC  closely-related Mycobacterium species. The present sequence is a probe
CC  used to detect amplified MAC 16S rRNA sequence or DNA encoding 16S rRNA
XX
XX  Sequence 32 BP; 5 A; 11 C; 7 G; 9 T; 0 U; 0 Other;
SQ
    Query Match      79.1%; Score 17.4; DB 4; Length 32;
    Best Local Similarity 94.7%; Pred. No. 76;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1  GTCGAACGGAAGGCCTTT 19
    |||||
DB  28  GTCGAACGGAAGGCCTCT 10

RESULT 43
AA99195
ID  AA99195 standard; DNA; 50 BP.
XX
XX  AA99195;
AC
XX  28-SEP-1999 (first entry)
DT
XX
DE  M. avium 16S rRNA gene fragment.
XX
KW  Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;
KW  shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.
XX
OS  Mycobacterium avium.
XX
XX  WO9935284-A1.
PN
XX  15-JUL-1999.
PD
XX  30-DEC-1997; 97WO-BR000087.
PF

```

PS Disclosure; Fig 7; 20pp; English.

XX The invention describes a new method for diagnosis, identification and

CC characterisation of Mycobacterium tuberculosis or any other mycobacteria

CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)

CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,

CC DNA amplification and Shift mobility assay. The method is based on

CC divergence in sequences found in 16S rRNA to identify mycobacteria

CC species, since a remarkable shift of heteroduplex bands are obtained

CC between single stranded and homoduplex bands in UPAGE. The method is

CC fast, simple and can produce information not easily obtained when

CC compared with other detection methods. The sensitivity of other assays

CC suffer due to the tendency of the denatured PCR product strands to

CC reassociate and exclude oligonucleotide probes, and steric interference

CC between the bound oligonucleotides and the solid support which impede

CC hybridization to nucleic acids in solution. Sequences AAX99193-237

CC represent 16S rRNA gene regions of some mycobacterial species

XX

SQ Sequence 50 BP; 14 A; 12 C; 14 G; 9 T; 0 U; 1 Other;

Query Match 79.1%; Score 17.4; DB 2; Length 50;

Best Local Similarity 94.7%; Pred. No. 80;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19  
|||||  
Db 13 GTCGAACGGAAGGCCTCT 31

RESULT 45

ADF94050

ID ADF94050 standard; DNA; 50 BP.

XX AC

XX AC ADF94050;

XX XX

DT 11-MAR-2004 (first entry)

XX

DE Microorganism detection probe, SEQ ID 143.

XX

KW Probe; detection; identification; microorganism; food; drug;

KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.

XX

OS Mycobacterium avium.

XX

PN WO2003106676-A1.

XX

PD 24-DEC-2003.

XX

PF 16-JUN-2003; 2003WO-JP007620.

XX

PR 14-JUN-2002; 2002JP-00174564.

XX

PA (HISF ) HITACHI SOFTWARE ENG CO LTD.

PA (MITS-) MITSUBISHI KAGAKU BIO-CLINICAL LAB INC.

XX

PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;

PI Shimadzu M, Kobayashi I, Ishiko H;

XX

DR WPI; 2004-071565/07.

XX

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a

PT microorganism for specific detection and identification of the

PT microorganism in foods and drug compositions.

XX

XX Claim 2; SEQ ID NO 143; 150pp; Japanese.

XX

CC The present invention relates to probes (ADF93908-ADF94059) for the

CC specific detection and identification of harmful microorganisms in

CC samples of foods and drug compositions. The probe sequences are derived

CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,

CC or its complementary sequence. Detection and identification of the

CC microorganism is by amplification of the complete 16S rRNA gene using

CC primers ADF94060 and ADF94061. Labelling the amplification product (a

CC

XX

CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetocornitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguinis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquaticum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella  
 CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
 CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
 CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
 CC gordonae.  
 XX  
 SQ Sequence 50 BP; 12 A; 11 C; 19 G; 8 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 12; Length 50;  
 Best Local Similarity 94.7%; Pred. No. 80;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTT 19  
 |||||  
 Db 5 GTCGAACGGAAGGCTTCT 23

RESULT 46  
 AEB98762  
 ID AEB98762 standard; DNA; 209 BP.  
 AC AEB98762;  
 XX  
 XX 06-OCT-2005 (first entry)  
 XX  
 XX Mycobacterium avium partial 16S rDNA sequence, SEQ ID 4.  
 XX  
 XX microorganism detection; mycobacterium infection; antibacterial; ds.  
 XX  
 XX Mycobacterium avium.  
 XX  
 XX JP2005204582-A.  
 XX  
 XX 04-AUG-2005.  
 XX  
 XX 23-JAN-2004; 2004JP-00015195.  
 XX  
 XX 23-JAN-2004; 2004JP-00015195.  
 XX  
 XX (ASAH ) ASahi KASEI KK.  
 XX  
 XX Oda N;  
 XX  
 XX WPI; 2005-526965/54.  
 XX  
 XX New single-stranded oligonucleotide, useful for amplifying the nucleic  
 XX acid of Mycobacterium avium, Mycobacterium intracellulare, and  
 XX Mycobacterium kansasii.  
 XX  
 XX Example 1; SEQ ID NO 4; 14pp; Japanese.  
 XX  
 XX The invention relates to a novel single-stranded oligonucleotide used in  
 XX a detection method of an atypical mycobacteria group. The invention  
 XX further includes: amplifying the nucleic acid of Mycobacterium avium by a  
 XX loop-mediated isothermal amplification (LAMP) method; amplifying the

CC nucleic acid of M. intracellulare by a LAMP method; amplifying the  
 CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the  
 CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of  
 CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.  
 CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful  
 CC in medical applications. This polynucleotide represents a Mycobacterium  
 CC avium partial 16S rDNA sequence amplified by the LAMP method of the  
 CC invention.  
 XX  
 SQ Sequence 209 BP; 48 A; 48 C; 70 G; 43 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 14; Length 209;  
 Best Local Similarity 94.7%; Pred. No. 93;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTT 19  
 |||||  
 Db 43 GTCGAACGGAAGGCTTCT 61

## RESULT 47

ABT23571  
 ID ABT23571 standard; DNA; 560 BP.

XX AC ABT23571;  
 XX  
 XX 22-MAY-2003 (first entry)  
 XX  
 XX Stabilising reagent method related oligo SEQ ID No 23.  
 XX  
 XX Stabilising reaction reagent; PCR; primer; RNaseH; long-term storage;  
 XX specific amplification; pathogenic microorganism; chimeric;  
 XX genetic engineering; clinical medicine; ss.  
 XX  
 XX Mycobacterium avium.  
 XX  
 XX WO2002101042-A1.  
 XX  
 XX 19-DEC-2002.  
 XX  
 XX 12-JUN-2002; 2002WO-JP005832.  
 XX  
 XX 12-JUN-2001; 2001JP-00177737.  
 XX  
 XX 20-AUG-2001; 2001JP-00249689.  
 XX  
 XX (TAKI ) TAKARA BIO INC.  
 XX  
 XX Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;  
 XX Enoki T, Asada K, Kato I;  
 XX  
 XX WPI; 2003-148805/14.  
 XX  
 XX Method for stabilizing and storing reaction reagents for specific  
 XX amplification and detection of nucleic acids particularly in e.g.  
 XX identifying pathogenic microorganisms or viruses in sample.  
 XX  
 XX Example 15; Page 109; 177pp; Japanese.  
 XX  
 XX The invention relates to a novel stabilising reaction reagent for use in  
 XX the amplification and/or detection of a target nucleic acid comprising:  
 XX preparing a reaction mixture with e.g. a nucleic acid as template, at  
 XX least 1 primer and RNaseH; and incubation of the reaction mixture for a  
 XX defined period of time to form a reaction product during the  
 XX amplification of such target nucleic acid. The method is useful for  
 XX stabilising and long-term storage of reaction reagents for highly  
 XX sensitive and specific amplification and detection of nucleic acids  
 XX particularly in identifying pathogenic microorganisms or viruses in a  
 XX sample using chimeric oligonucleotide primers, which is useful in genetic  
 XX engineering and clinical medicine. This polynucleotide sequence  
 XX represents an oligo relating to the novel stabilising reaction reagent  
 XX method of the invention  
 XX  
 XX Sequence 560 BP; 117 A; 134 C; 198 G; 111 T; 0 U; 0 Other;



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Query Match      79.1%; Score 17.4; DB 10; Length 560;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
   |||||
DB 34 GTCGAACGGAAGGCCTCT 52

RESULT 48
ID AEA22411 standard; DNA; 1421 BP.
XX AC AEA22411;
XX DT 25-AUG-2005 (first entry)
XX DE Mycobacterium lentiflavum 16S rRNA sequence SEQ ID NO:12.
XX KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX OS Mycobacterium lentiflavum.
XX PN US2005130168-A1.
XX PD 16-JUN-2005.
XX PF 31-OCT-2003; 2003US-00697802.
XX PR 31-OCT-2003; 2003US-00697802.
XX (HANX/) HAN X.
XX PA (PHAM/) PHAM A S.
XX PI Han X, Pham AS;
XX DR WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX Disclosure; SEQ ID NO 12; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium lentiflavum 16S rRNA nucleotide

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```

CC sequence, which is used in the exemplification of the present invention.
SQ Sequence 1421 BP; 306 A; 344 C; 487 G; 284 T; 0 U; 0 Other;

Query Match      79.1%; Score 17.4; DB 14; Length 1421;
Best Local Similarity 94.7%; Pred. No. 1.e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
   |||||
DB 24 GTCGAACGGAAGGCCTCT 42

RESULT 49
ID ADK66476
XX ID ADK66476 standard; RNA; 1431 BP.
XX AC ADK66476;
XX DT 06-MAY-2004 (first entry)
XX DE Corynebacterium 16S rRNA sequence.
XX KW ss; 16S rRNA; microorganism detection; clinical sample;
XX PN pharmaceutical composition.
XX OS Corynebacterium sp.
XX PN W02004009839-A2.
XX PD 29-JAN-2004.
XX PF 16-JUL-2003; 2003WO-EP007717.
XX PR 18-JUL-2002; 2002DE-01032776.
XX PR 14-FEB-2003; 2003DE-01007732.
XX (HENK ) HENKEL KGAA.
XX PA (VERM-) VERMICON AG.
XX PI Sattler A, Jaasoy C, Scholtyssek R, Maienschein V, Nieveler S;
XX PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
XX PI Muehlner S, Adomat C, Bergmaier I;
XX DR WPI; 2004-123402/12.
XX
XX New oligonucleotides for specific detection of microorganisms, useful
XX e.g. for detecting or quantifying microbes on the skin, in foods,
XX PT clinical samples or water, by in situ hybridization.
XX PS Disclosure; Page 66-67; 67pp; German.
XX
XX The present invention provides a number of oligonucleotides for the
XX specific detection of microorganisms. The oligonucleotides are used to
XX detect and/or quantify microorganisms, especially on the skin, in foods
XX or the environment (water, soil and air), from waste waters or biofilms,
XX CC in clinical samples (body fluids or tissues), and in pharmaceutical or
XX CC cosmetic compositions. The present sequence is a Corynebacterium 16S rRNA
XX sequence.
SQ Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match      79.1%; Score 17.4; DB 12; Length 1431;
Best Local Similarity 78.9%; Pred. No. 1.e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19
   |||||
DB 34 GUCGAACGGAAGGCCTCU 52

RESULT 50
ADK66445

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ID ADK66445 standard; rRNA; 1431 BP.
XX AC
XX ADK66445;
XX DT
XX 06-MAY-2004 (first entry)
XX DE
XX Corynebacterium 16S rRNA sequence.
XX KW
XX ss; 16S rRNA; microorganism detection; skin; acne.
XX OS
XX Corynebacterium sp.
XX PN
XX WC2004009843-A2.
XX XX
XX 29-JAN-2004.
XX PF
XX 16-JUL-2003; 2003WO-EP007718.
XX PR
XX 18-JUL-2002; 2002DE-01032775.
XX PR
XX 14-FEB-2003; 2003DE-01006616.
XX XX
XX (HENK ) HENKEL KGAA.
XX PI
XX Saettler A, Jassoy C, Scholtyssek R, Maienschein V, Nievelev S;
PI Weiss A, Trebesius K, Beimfohr C, Ludwig W, Bamberg RR, Schleifer K;
PI Mueller S, Adomat C, Bergmaier I;
XX XX
XX WPI; 2004-123405/12.
XX XX
XX Kit for detection of microorganisms on skin, useful e.g. for diagnosis of
PT infection, comprises specific oligonucleotides for in situ hybridization.
XX XX
XX Disclosure; Page 62-63; 63pp; German.
XX CC
XX The present invention relates to a kit for detecting microorganisms that
CC contains at least one oligonucleotide specific for at least one species,
CC or group of species, that is present on the skin. The kit is used to
CC detect and/or quantify microorganisms that are present on the skin; e.g.
CC for early diagnosis of secondary infection in cases of acne. The present
CC sequence is a Corynebacterium 16S rRNA sequence.
XX XX
XX Sequence 1431 BP; 308 A; 327 C; 488 G; 0 T; 307 U; 1 Other;

Query Match 79.1%; Score 17.4; DB 12; Length 1431;
Best Local Similarity 78.9%; Pred. No. 1.1e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 34 GUCGAACGGAAGGCCTT 52

RESULT 51
AAQ37639
ID AAQ37639 standard; rRNA; 1449 BP.
XX AC
XX AAQ37639;
XX DT
XX 25-MAR-2003 (revised)
XX DT
XX 18-JUN-1993 (first entry)
XX XX
XX Mycobacterium genavense 16S rRNA.
XX KW
XX Detection; rapid; immunosuppressed patients; AIDS; ss.
XX OS
XX Mycobacterium genavense.
XX PN
XX EP529985-A1.
XX XX
XX 03-MAR-1993.
XX PD
XX 21-AUG-1992; 92EP-00307690.
XX XX

Query Match 79.1%; Score 17.4; DB 2; Length 1449;
Best Local Similarity 94.7%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
Db 51 GTCGAACGGAAGGCCTCT 69

RESULT 52
AEA22401
ID AEA22401 standard; DNA; 1454 BP.
XX AC
XX AEA22401;
XX DT
XX 25-AUG-2005 (first entry)
XX DE
XX Mycobacterium avium 16S rRNA sequence SEQ ID NO:2.
XX XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX OS
XX Mycobacterium avium.
XX PN
XX US2005130168-A1.
XX PD
XX 16-JUN-2005.
XX PF
XX 31-OCT-2003; 2003US-00697802.
XX XX
XX 31-OCT-2003; 2003US-00697802.
XX PR
XX (HANX/) HAN X.
XX PA
XX (PHAM/) PHAM A S.
XX PI
XX Han X, Pham AS;
XX XX
XX WPI; 2005-424597/43.
XX XX
XX Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX PS
XX Disclosure; SEQ ID NO 2; 74pp; English.
XX CC
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)

```

CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium avium 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.

XX  
 SQ Sequence 1454 BP; 316 A; 348 C; 494 G; 296 T; 0 U; 0 Other;

Query Match 79.1%; Score 17.4; DB 14; Length 1454;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19  
 |||||  
 Db 34 GTCGACGGAAGGCCTCT 52

RESULT 53  
 ADB61680  
 ID ADB61680 standard; DNA; 1465 BP.

XX AC ADB61680;

XX DT 04-DEC-2003 (first entry)

XX DE 16S rRNA of Mycobacterium avium DNA sequence.

XX enriching mRNA; high quality bacterial mRNA; bacterial gene expression;  
 XX poly-A tail; mRNA purification; oligo-dT capture;  
 XX prokaryote mRNA purification; bridging oligonucleotide; targeting region;  
 XX capture oligonucleotide; prokaryotic 16S rRNA; prokaryotic 23S rRNA;  
 XX eukaryotic 17S rRNA; eukaryotic 18S rRNA; eukaryotic 28S rRNA;  
 XX 28S eukaryotic rRNA bridging oligonucleotide; ds.

XX OS Mycobacterium avium.

XX XX WO2003054162-A2.

XX PD 03-JUL-2003.

XX PF 19-DEC-2002; 2002WO-US041014.

XX PR 20-DEC-2001; 2001US-00029397.

XX XX (AMBI-) AMBION INC.

XX PI Murphy GL, Whitley JP;

XX XX WPI; 2003-663255/62.

XX

PT Depleting or isolating targeted nucleic acids e.g. rRNA, involves using a  
 PT bridging oligonucleotide comprising bridging region and a targeting  
 PT region complementary to a targeted nucleic acid, and a capture  
 PT oligonucleotide.

XX Claim 4; Page 168; 209pp; English.

XX This invention relates to a novel method for isolating, depleting or  
 CC separating a targeted nucleic acid, such as rRNA, from a sample  
 CC comprising targeted and non-targeted nucleic acids. It effects a way of  
 CC enriching for non-targeted nucleic acids such as mRNAs. Isolating  
 CC sufficient quantities of high quality bacterial mRNA is a demanding  
 CC process which impedes analysis of bacterial gene expression in the  
 CC presence of host cells. A small percentage of bacterial mRNAs may be poly  
 CC -A tailed, but these are targeted for degradation and tend to be  
 CC unstable. As a result, the commonly employed method for mRNA purification  
 CC with eukaryotic cells, oligo-dT capture, is ineffective. The present  
 CC invention provides an alternative, more suitable method for mRNA  
 CC purification from prokaryotes. The method of the invention comprises the  
 CC incubation of a sample with a bridging oligonucleotide (containing a  
 CC targeting region) and subsequently incubating with a capture  
 CC oligonucleotide allowing the isolation of the target from the sample. The  
 CC method is useful for depleting or isolating targeted nucleic acid, for  
 CC example rRNA such as prokaryotic 16S or prokaryotic 23S, eukaryotic 17S  
 CC or 18S or eukaryotic 28S rRNA, from a sample. The rRNA sequence may  
 CC comprise any one of 64 fully defined sequences as given in the  
 CC specification. The present sequence is that of a DNA sequence which  
 CC represents the sequence of 16S rRNA of Mycobacterium avium related to the  
 CC invention.

XX SQ Sequence 1465 BP; 321 A; 345 C; 496 G; 298 T; 0 U; 5 Other;

Query Match 79.1%; Score 17.4; DB 10; Length 1465;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19  
 |||||  
 Db 24 GTCGACGGAAGGCCTCT 42

RESULT 54

ADR90572

ID ADR90572 standard; DNA; 1472 BP.

XX AC ADR90572;

XX DT 02-DEC-2004 (first entry)

XX DE M avium 16S rRNA gene sequence SeqID1.

XX acid-fast bacterium; differentiation; 16S rRNA; M avium complex; MAC;  
 KW taxonomic-tree analysis; atypical-mycobacteria; gene; ds.

XX OS Mycobacterium avium.

XX FH Key Location/Qualifiers

FT variation 893

FT /\*tag= a

FT variation 1312

FT /\*tag= b

FT variation 1393

FT /\*tag= c

XX JP2004254591-A.

XX PD 16-SEP-2004.

XX PF 26-FEB-2003; 2003JP-00048654.

XX PR 26-FEB-2003; 2003JP-00048654.

XX XX (MITP ) MITSUBISHI YUKA BCL KK.

XX WPI; 2004-664464/65.  
XX  
XX  
PT Differentiating acid-fast bacterium e.g., *Mycobacterium avium* complex,  
PT useful for detecting mutant of *M. avium* complex, and for grouping strains  
PT of *M. kansasii*, involves detecting mutation in 16S rRNA gene of acid-fast  
PT bacterium.  
XX  
XX Claim 3; SEQ ID NO 1; 23pp; Japanese.  
XX  
XX This invention relates to a novel method of differentiating acid-fast  
CC bacterium, which involves detecting a mutation in the 16S rRNA gene of  
CC the acid-fast bacterium. The method is useful for differentiating acid-  
CC fast bacterium such as *M. avium* complex (MAC) or *M. kansasii*, in particular  
CC for detecting mutants of MAC, and for grouping strains of *M. kansasii*. The  
CC method is also useful for carrying out taxonomic-tree analysis of  
CC atypical-mycobacteria and enables detection of MAC accurately and  
CC reliably. The present sequence is that of a *Mycobacterium* 16S rRNA gene  
CC which may be used in the method of the invention.  
XX  
XX Sequence 1472 BP; 323 A; 348 C; 500 G; 298 T; 0 U; 3 Other;  
SQ  
Query Match 79.1%; Score 17.4; DB 13; Length 1472;  
Best Local Similarity 94.7%; Pred. No. 1.1e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GTCGACGGGAAGGCCTTT 19  
Db 34 GTCGACGGGAAGGCCTCT 52  
RESULT 55  
AD875567  
ID ADS75567 standard; DNA; 535 BP.  
XX  
XX ADS75567;  
AC  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE *Rhodococcus equi* TB-60 16S rDNA sequence, SEQ ID 1.  
XX  
XX Urethane; polyurethane; 16S rDNA; ds.  
XX  
XX *Rhodococcus equi*; TB-60.  
OS  
XX  
XX WO2004078952-A1.  
PN  
XX  
PD 16-SEP-2004.  
XX  
XX 03-MAR-2004; 2004WO-JP002691.  
XX  
XX 03-MAR-2003; 2003JP-00055421.  
XX  
XX (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.  
PA  
XX  
XX Kambe T, Shigeno Y;  
PI  
XX  
XX WPI; 2004-728402/71.  
DR  
XX  
XX Novel microorganism or its mutant belonging to *Rhodococcus* genus and  
PT having ability to cleave urethane bond, useful for plastic disposal and  
PT recycling of urethane compounds.  
PT  
XX  
XX Example 2; SEQ ID NO 1; 26pp; Japanese.  
PS  
XX  
XX The present invention relates to a novel *Rhodococcus equi* TB-60 strain  
CC microorganism (I) or its mutant, which can cleave urethane bonds. (I) is  
CC useful for decomposing urethane compounds which involves contacting (I)  
CC with urethane compound. The urethane compound is a raw material of  
CC polyurethane or is polyurethane. (I) is useful in plastic disposal and  
CC recycling of urethane compounds by decomposing urethane compounds. The  
CC present sequence is a 16S rDNA sequence from the microorganism of the  
CC invention.

XX  
SQ Sequence 535 BP; 118 A; 131 C; 191 G; 95 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 13; Length 535;  
Best Local Similarity 86.4%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GTCGACGGGAAGGCCTTTTCGG 22  
Db 55 GTCGACGGGAAGGCCTTCGG 76  
RESULT 56  
AAC33114  
ID AAC33114 standard; DNA; 788 BP.  
XX  
AC AAC33114;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
XX *Arabidopsis thaliana* DNA fragment SEQ ID NO: 1832.  
DE  
XX  
XX Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
XX *Arabidopsis thaliana*.  
OS  
XX  
PN EP1033405-A2.  
XX  
XX 06-SEP-2000.  
XX  
XX 25-FEB-2000; 2000EP-00301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.  
PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130077P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
PR 06-MAY-1999; 99US-0132485P.  
PR 06-MAY-1999; 99US-0132486P.  
PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 03-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.

PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 05-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.

PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0149368P.  
PR 16-AUG-1999; 99US-0149175P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 13-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 78.2%; Score 17.2; DB 3; Length 788;  
Best Local Similarity 86.4%; Pred. No. 1.3e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 333 GTCGACGTTAAGGCTTTTCGG 354

RESULT 57
ADFS6670
ID ADF56670 standard; DNA; 1437 BP.
XX
XX ADF56670;
AC
XX
XX 12-FEB-2004 (first entry)
XX
XX DE
XX YS-44442 16S rDNA, SEQ ID 1.
XX
XX Pravastatin; HMG-CoA reductase inhibitor;
KW 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.
XX
XX Saccharothrix sp.
XX
XX JP2003250532-A.
PN
XX
XX 09-SEP-2003.
PD
XX
XX 22-FEB-2002; 2002JP-00046750.
PF
XX
XX 22-FEB-2002; 2002JP-00046750.
PR
XX
XX (YUNG-) YUNG SHIN PHARM IND CO LTD.
PA
XX
XX WPI; 2004-046768/05.
DR
XX
XX Microorganisms Saccharothrix genus YS-44442 and YS-45494 and their
PT mutants useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 18pp; Japanese.
PS
XX
XX The present invention relates to microorganisms (I) Saccharothrix genus
CC YS-44442 and YS-45494 strains and their mutants. Also claimed is a method
CC (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-
CC 3-methyl glutaryl (HMG)-CoA reductase inhibitors.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;
SQ

Query Match 78.2%; Score 17.2; DB 12; Length 1437;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 34 GTCGACGTTAAGGCTTTTCGG 55

RESULT 58
ADG64519
ID ADG64519 standard; DNA; 1437 BP.
XX
XX ADG64519;
AC
XX
XX 11-MAR-2004 (first entry)
XX
XX Saccharothrix strain YS-44442 16S rDNA sequence.
DE
XX
XX Microorganism; Saccharothrix; YS-44442; YS-45494;
KW 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;
KW pravastatin; fermentation; compactin; lovastatin;
KW blood cholesterol level; antilipemic; 16S rDNA; ds.
XX
XX Saccharothrix sp.
OS
XX
XX US2003199047-A1.
PN
XX
XX 23-OCT-2003.
PD

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```

XX 27-FEB-2002; 2002US-00085871.
PF
XX 27-FEB-2002; 2002US-00085871.
PR
XX
XX (LEEF/) LEE F.
PA (LEEM/) LEE M.
PA (HONG/) HONG A C.
PA (CHIU/) CHIU S.
XX
XX Lee F, Lee M, Hong AC, Chiu S;
PI
XX WPI; 2004-041353/04.
DR
XX
XX Novel microorganism strains YS-44442 and YS-45494 of Saccharothrix,
PT useful for producing pravastatin.
XX
XX Example 1; SEQ ID NO 1; 16pp; English.
PS
XX
XX The present invention relates to the isolation of novel microorganism
CC strains of Saccharothrix designated YS-44442 and YS-45494. Also disclosed
CC is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase
CC inhibitors such as pravastatin. The Saccharothrix strains YS-44442 and YS
CC -45494 are useful for producing pravastatin. The method involves
CC cultivating the strains at a suitable condition to generate a
CC fermentation broth, feeding compactin into the broth, fermenting the
CC broth for a period of time to convert the compactin to pravastatin, and
CC isolating the pravastatin from the broth. The fermentation broth is
CC cultivated for less than 2 days, preferably for 18 hours. The
CC fermentation broth is derived from a seed culture of the microorganism
CC which is cultivated at a suitable condition for 18-48 hours before
CC inoculation into the broth. The broth is fermented for less than 5 days,
CC preferably 3 days, most preferably less than 24 hours. The method of the
CC invention is useful for isolating HMG-CoA reductase inhibitor. Such as
CC pravastatin, compactin or lovastatin, preferably pravastatin. The
CC pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood
CC cholesterol levels. The present sequence represents Saccharothrix strain
CC YS-44442 16S rDNA sequence.
XX
XX Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;
SQ

Query Match 78.2%; Score 17.2; DB 12; Length 1437;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22
Db 34 GTCGACGTTAAGGCTTTTCGG 55

RESULT 59
ADY86147
ID ADY86147 standard; DNA; 1437 BP.
XX
XX ADY86147;
AC
XX
XX 02-JUN-2005 (first entry)
DT
XX
XX Saccharothrix YS-44442 16S rDNA, SEQ ID NO: 1.
DE
XX
XX Microorganism; fermentation; hypercholesterolemia; 16S rDNA; antilipemic;
KW metabolic disorder; ds.
KW
XX
XX Saccharothrix; YS-44442.
OS
XX
XX US2005064566-A1.
PN
XX
XX 24-MAR-2005.
PD
XX
XX 03-DEC-2003; 2003US-00727643.
PF
XX
XX 27-FEB-2002; 2002US-00085871.
PR
XX

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```
PA (LEEF/) LEE F.  
PA (LEEM/) LEE M.  
PA (HONG/) HONG A C.  
PA (CHIU/) CHIU S.  
XX  
XX  
PI Lee F, Lee M, Hong AC, Chiu S;  
XX  
XX WPI; 2005-252680/26.  
DR  
XX  
XX  
XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises  
XX adding ammonium sulfate into a first solution to form precipitate, and  
XX isolating and dissolving the precipitate to form a second solution and  
XX followed by extracting.  
XX  
XX Example 1; SEQ ID NO 1; 19pp; English.  
XX  
XX The present invention relates to two new microorganism strains of  
XX Saccharothrix, designated as YS-4442 and YS-45494. The invention also  
XX provides a method of isolating pravastatin from Saccharothrix sp and an  
XX improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A  
XX (HMG CoA) reductase inhibitor. The invention is useful for the  
XX preparation of pravastatin which is useful in the treatment of  
XX hypercholesterolemia. The present sequence is the Saccharothrix YS-4442  
XX 16S rDNA.  
XX  
SQ Sequence 1437 BP; 320 A; 362 C; 495 G; 260 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 14; Length 1437;  
Best Local Similarity 86.4%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 GTCGAACGGAAAGCGCTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55  
RESULT 60  
ADFS6671  
ID ADFS6671 standard; DNA; 1471 BP.  
AC ADFS6671;  
XX  
XX 12-FEB-2004 (first entry)  
XX  
XX  
XX YS-45494 16S rDNA, SEQ ID 2.  
XX  
XX Pravastatin; HMG-CoA reductase inhibitor;  
XX 3-hydroxy-3-methyl glutaryl-CoA reductase inhibitor; 16S rDNA; ds.  
XX  
XX Saccharothrix sp.  
XX  
XX JP2003250532-A.  
XX  
XX PD 09-SEP-2003.  
XX  
XX 22-FEB-2002; 2002JP-00046750.  
XX  
XX 22-FEB-2002; 2002JP-00046750.  
XX  
XX (YUNG-) YUNG SHIN PHARM IND CO LTD.  
XX  
XX WPI; 2004-046768/05.  
XX  
XX Microorganisms Saccharothrix genus YS-4442 and YS-45494 and their  
XX mutants useful for producing pravastatin.  
XX  
XX Example 1; SEQ ID NO 2; 18pp; Japanese.  
XX  
XX The present invention relates to microorganisms (I) Saccharothrix genus  
XX YS-4442 and YS-45494 strains and their mutants. Also claimed is a method  
XX (M1) for producing pravastatin by using (I) and isolating (M2) 3-hydroxy-  
XX 3-methyl glutaryl (HMG)-CoA reductase inhibitors.  
SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 12; Length 1471;  
Best Local Similarity 86.4%; Pred. No. 1.4e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 GTCGAACGGAAAGCGCTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55  
RESULT 61  
ADG64520  
ID ADG64520 standard; DNA; 1471 BP.  
XX  
XX AC ADG64520;  
XX  
XX DT 11-MAR-2004 (first entry)  
XX  
XX DE Saccharothrix strain YS-45494 16S rDNA sequence.  
XX  
XX KW Microorganism; Saccharothrix; YS-4442; YS-45494;  
XX 3-hydroxy-3-methylglutaryl-CoA reductase inhibitor; HMG-CoA reductase;  
XX pravastatin; fermentation; compactin; lovastatin;  
XX blood cholesterol level; antilipemic; 16S rDNA; ds.  
XX  
XX OS Saccharothrix sp.  
XX  
XX PN US2003199047-A1.  
XX  
XX PD 23-OCT-2003.  
XX  
XX PF 27-FEB-2002; 2002US-00085871.  
XX  
XX PR 27-FEB-2002; 2002US-00085871.  
XX  
XX PA (LEEF/) LEE F.  
XX PA (LEEM/) LEE M.  
XX PA (HONG/) HONG A C.  
XX PA (CHIU/) CHIU S.  
XX  
XX PI Lee F, Lee M, Hong AC, Chiu S;  
XX  
XX WPI; 2004-041353/04.  
XX  
XX Novel microorganism strains YS-4442 and YS-45494 of Saccharothrix,  
XX useful for producing pravastatin.  
XX  
XX Example 1; SEQ ID NO 2; 16pp; English.  
XX  
XX The present invention relates to the isolation of novel microorganism  
XX strains of Saccharothrix designated YS-4442 and YS-45494. Also disclosed  
XX is a method for isolating 3-hydroxy-3-methylglutaryl (HMG)-CoA reductase  
XX inhibitors such as pravastatin. The Saccharothrix strains YS-4442 and YS  
XX -45494 are useful for producing pravastatin. The method involves  
XX cultivating the strains at a suitable condition to generate a  
XX fermentation broth, feeding compactin into the broth, fermenting the  
XX broth for a period of time to convert the compactin to pravastatin, and  
XX isolating the pravastatin from the broth. The fermentation broth is  
XX cultivated for less than 2 days, preferably for 18 hours. The  
XX fermentation broth is derived from a seed culture of the microorganism  
XX which is cultivated at a suitable condition for 18-48 hours before  
XX inoculation into the broth. The broth is fermented for less than 5 days,  
XX preferably 3 days, most preferably less than 24 hours. The method of the  
XX invention is useful for isolating HMG-CoA reductase inhibitor such as  
XX pravastatin, compactin or lovastatin, preferably pravastatin. The  
XX pravastatin or HMG-CoA reductase inhibitors are useful for reducing blood  
XX cholesterol levels. The present sequence represents Saccharothrix strain  
XX YS-45494 16S rDNA sequence.  
SQ Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;  
Query Match 78.2%; Score 17.2; DB 12; Length 1471;
```

```
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCTTTCGG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 62
ADY86148
ID ADY86148 standard; DNA; 1471 BP.
XX AC
XX ADY86148;
DT 02-JUN-2005 (first entry)
XX DE
XX Saccharothrix YS-45494 16s rDNA, SEQ ID NO: 2.
DE DE
XX Microorganism; fermentation; hypercholesterolemia; 16s rDNA; antilipemic;
KW metabolic disorder; ds.
XX KW
XX Saccharothrix; YS-45494.
OS OS
XX US2005064566-A1.
XX PN
XX 24-MAR-2005.
XX PD
XX 03-DEC-2003; 2003US-00727643.
XX PF
XX 27-FEB-2002; 2002US-00085871.
XX PR
XX (LEEF/) LEE F.
XX PA
XX (LEEM/) LEE M.
XX PA
XX (HONG/) HONG A. C.
XX PA
XX (CHIU/) CHIU S.
XX PI
XX Lee F, Lee M, Hong AC, Chiu S;
XX WPI; 2005-252680/26.
XX DR
XX Isolation of pravastatin, used to treat hypercholesterolemia, comprises
PT adding ammonium sulfate into a first solution to form precipitate,
PT isolating and dissolving the precipitate to form a second solution and
PT followed by extracting.
XX PT
XX Example 1; SEQ ID NO 2; 19pp; English.
XX PS
XX The present invention relates to two new microorganism strains of
CC Saccharothrix, designated as YS-4442 and YS-45494. The invention also
CC provides a method of isolating pravastatin from Saccharothrix sp and an
CC improved process for isolation of 3-hydroxy-3-methylglutaryl-Coenzyme A
CC (HMG CoA) reductase inhibitor. The invention is useful for the
CC preparation of pravastatin which is useful in the treatment of
CC hypercholesterolemia. The present sequence is the Saccharothrix YS-45494
CC 16s rDNA.
XX CC
XX Sequence 1471 BP; 331 A; 369 C; 506 G; 265 T; 0 U; 0 Other;
SQ

Query Match 78.2%; Score 17.2; DB 14; Length 1471;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCTTTCGG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 63
AED47485
ID AED47485 standard; DNA; 1477 BP.
XX AC
XX AED47485;
XX XX

Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCTTTCGG 22
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 64
ADS17269
ID ADS17269 standard; DNA; 1488 BP.
XX AC
XX ADS17269;
XX AC
XX 02-DEC-2004 (first entry)
DT DT
XX Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
DE DE
XX Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;
KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX KW
XX Lechevalieria aerocolonigenes.
OS OS
XX US2004180960-A1.
XX PN
XX 16-SEP-2004.
XX PD

15-DEC-2005 (first entry)
XX DE
XX Nocardia sp. TP-A0674 16S ribosomal DNA, SEQ ID 1.
XX XX
XX Analgesic; Nootropic; Antiparkinsonian; Antiasthmatic; Respiratory-Gen.;
KW Uropathic; binding inhibitor; muscarinic acetylcholine receptor;
KW analgesic; Parkinsons disease; asthma;
KW chronic obstructive pulmonary disease; bladder disease;
KW micturition disorder; 16S ribosomal RNA; 16S rRNA; gene; ds.
XX KW
XX Nocardia sp.
OS OS
XX JP2005289890-A.
XX PN
XX 20-OCT-2005.
XX PD
XX 31-MAR-2004; 2004JP-00107929.
XX XX
XX 31-MAR-2004; 2004JP-00107929.
XX PR
XX (YOSH ) YOSHITOMI PHARM IND KK.
XX PA
XX Furumai T, Igarashi Y, Onaka H, Ikeda Y, Nonaka H;
XX PI
XX WPI; 2005-738172/76.
XX XX
XX Binding inhibitor of muscarinic acetylcholine receptor subtype 4 or 3
PT useful for treating diseases e.g. asthma, contains chelate having TPU
PT 0052A-F compound derived from Nocardia species TP-A0674 and metal ion.
XX PT
XX Disclosure; SEQ ID NO 1; 22pp; Japanese.
XX PS
XX The invention relates to a novel binding inhibitor of muscarinic
CC acetylcholine receptor subtype 4 or 3, comprising a chelate having a TPU
CC 0052A-F compound or its salt and a metal ion. The invention further
CC comprises a method and a microorganism for producing the novel binding
CC inhibitor. The binding inhibitor and compound are useful as central
CC analgesics and memory improving drugs, for treating Parkinson's disease,
CC asthma, chronic obstructive pulmonary disease, overactive bladder,
CC frequent urination and urinary incontinence. This polynucleotide sequence
CC represents the 16S ribosomal DNA of a Nocardia sp. TP-A0674
CC microorganism, useful in producing a muscarinic acetylcholine receptor
CC binding inhibitor compound of the invention.
XX CC
XX Sequence 1477 BP; 341 A; 357 C; 494 G; 285 T; 0 U; 0 Other;
SQ

Query Match 78.2%; Score 17.2; DB 14; Length 1477;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCTTTCGG 22
Db 51 GTCGAGCGGTAAGGCCCTTCGG 72

RESULT 64
ADS17269
ID ADS17269 standard; DNA; 1488 BP.
XX AC
XX ADS17269;
XX AC
XX 02-DEC-2004 (first entry)
DT DT
XX Lechevalieria aerocolonigenes strain VK-A9 16S rDNA.
DE DE
XX Plant protectant; antibiotic; thiobutacin; antifungal; antioomycete;
KW phytophthora blight; gene; ds; ribosomal DNA; rDNA.
XX KW
XX Lechevalieria aerocolonigenes.
OS OS
XX US2004180960-A1.
XX PN
XX 16-SEP-2004.
XX PD
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XX 13-JAN-2004; 2004US-00756683.
XX
XX
XX 13-MAR-2003; 2003KR-00015628.
XX
XX 13-MAR-2003; 2003KR-00015629.
XX
XX (HWAN/) HWANG B K.
XX (LBEJ/) LEE J Y.
XX
XX Hwang BK, Lee JY;
XX
XX WPI; 2004-661528/64.
XX
XX EMBL; AY196703.
XX
XX New antibiotic compound, thiobutacin, is used to treat plant disease e.g.
XX phytophthora blight and to control plant diseases caused by pathogens
XX e.g. Phytophthora capsici and Botrytis cinerea.
XX
XX Example 2; SEQ ID NO 1; 17pp; English.
XX
XX The invention relates to an antibiotic compound thiobutacin and
XX antifungal and antioomycete compositions comprising thiobutacin.
XX Thiobutacin is used to treat plant disease such as phytophthora blight
XX and to control plant diseases caused by pathogens e.g. Phytophthora
XX capsici and Botrytis cinerea. The present sequence is the Lechevalieria
XX aerocolonigenes strain VK-A9 16S ribosomal DNA (rDNA). L. aerocolonigenes
XX strain VK-A9 has strong antifungal and antimicrobial activity and it can
XX inhibit the growth of Phytophthora capsici.
XX
XX Sequence 1488 BP; 339 A; 369 C; 508 G; 272 T; 0 U; 0 Other;
SQ
Query Match 78.2%; Score 17.2; DB 13; Length 1488;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTCGAACGGGAAGCCCTTCGG 22
Db 46 GTCGAGCGGTAAGGCCCTTCGG 67
RESULT 65
ADW12667
ID ADW12667 standard; DNA; 1514 BP.
XX
XX AC ADW12667;
XX
XX 07-APR-2005 (first entry)
XX
XX Rhodococcus opacus 16S rDNA, SEQ ID NO:2.
XX
XX Stereoselective synthesis; enantiomeric enrichment;
XX beta-amino acid synthesis; cell culture; 16S ribosomal RNA; 16S rRNA; ds.
XX
XX Rhodococcus opacus.
XX
XX US2005009151-A1.
XX
XX 13-JAN-2005.
XX
XX 22-JUN-2004; 2004US-00875161.
XX
XX 10-JUL-2003; 2003US-0486032P.
XX
XX 02-SEP-2003; 2003US-0499622P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Chase M, Clayton R, Landis B, Banerjee A;
XX
XX WPI; 2005-110890/12.
XX
XX Stereoselective synthesis of beta-amino acid such as D-beta- or L-beta-
XX phenylalanine, by contacting amino donor and amino acceptor in presence
XX of beta-amino acid transaminase to form beta-amino acid enantiomer, from
PT
PT amino acceptor.
XX
XX Claim 78; SEQ ID NO 2; 44pp; English.
XX
XX The invention relates to methods for the stereoselective synthesis and
XX for the enantiomeric enrichment of a beta-amino acid or its salt. The
XX methods involve contacting an amino donor and an amino acceptor in the
XX presence of a stereoselective beta-amino acid transaminase to form a beta
XX -amino acid enantiomer (or its salt) from the amino acceptor. The
XX invention also relates to purified stereoselective D-beta-transaminases
XX derived from a microorganism of the genera Variovorax, Nocardia,
XX Comamonas, Rhodococcus or Pseudomonas; purified stereoselective L-beta-
XX transaminases derived from a microorganism of the genus Alcaligenes;
XX methods of selecting and culturing microorganisms which express a beta-
XX transaminase; purified cultures of Variovorax paradoxus or Rhodococcus
XX opacus; the 16S ribosomal RNA gene (rDNA) of Variovorax paradoxus or
XX Rhodococcus opacus (ADW12666 and ADW12667, respectively); and a method of
XX detecting these 16S rDNA sequences. The methods of the invention are
XX useful for stereoselectively synthesizing a beta-amino acid such as D-
XX beta-phenylalanine or L-beta-phenylalanine, or for enriching one or the
XX other enantiomer in a racemic mixture. In the examples of the invention,
XX microorganisms from soil samples from two different environments were
XX screened transaminase activity on DL-beta-phenylalanine. Ribosomal DNA
XX sequencing was used to facilitate the taxonomic identification of two
XX purified microorganisms from the environmental samples. The present
XX sequence represents the specifically claimed 16S rDNA sequence which was
XX identified as originating from Rhodococcus opacus.
XX
XX Sequence 1514 BP; 339 A; 368 C; 509 G; 286 T; 0 U; 12 Other;
SQ
Query Match 78.2%; Score 17.2; DB 14; Length 1514;
Best Local Similarity 86.4%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GTCGAACGGGAAGCCCTTCGG 22
Db 57 GTCGAGCGGTAAGGCCCTTCGG 78
RESULT 66
AEB98771
ID AEB98771 standard; DNA; 39 BP.
XX
XX AC AEB98771;
XX
XX 06-OCT-2005 (first entry)
XX
XX Mycobacterium avium identification LAMP primer, SEQ ID 13.
XX
XX microorganism detection; mycobacterium infection; antibacterial; primer;
XX PCR; ss; LAMP.
XX
XX Mycobacterium avium.
XX
XX Synthetic.
XX
XX JF2005204582-A.
XX
XX 04-AUG-2005.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX 23-JAN-2004; 2004JP-00015195.
XX
XX (ASAH ) ASahi KASEI KK.
XX
XX Oda N;
XX
XX WPI; 2005-526965/54.
XX
XX New single-stranded oligonucleotide, useful for amplifying the nucleic
XX acid of Mycobacterium avium, Mycobacterium intracellulare, and
XX Mycobacterium kansasii.
XX

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PS Claim 1; SEQ ID NO 13; 14pp; Japanese.
XX
XX The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; and a kit for detecting the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This oligo sequence represents a loop-mediated
CC isothermal amplification (LAMP) primer used in the exemplification of the
CC invention.
XX
SQ Sequence 39 BP; 10 A; 11 C; 10 G; 8 T; 0 U; 0 Other;

Query Match 77.3%; Score 17; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCCT 17
   |||||
DB 23 GTCGAACGGAAAGGCCT 39

RESULT 67
AAT45276
ID AAT45276 standard; rRNA; 1391 BP.
XX
AC AAT45276;
XX
DT 12-SEP-1997 (first entry)
XX
DE Corynebacterium diphtheriae 16S rRNA.
XX
KW Ribosomal RNA; species specific; detection; reverse transcription;
KW primer; hybridisation probe; identification; ss.
XX
OS Corynebacterium diphtheriae.
XX
FH Key Location/Qualifiers
FT misc_feature 38..59
FT /*tag= a
FT /notes= "Defined as nucleotides 72-100"
FT misc_feature 153..170
FT /*tag= b
FT /notes= "Defined as nucleotides 195-215"
FT misc_feature 415..431
FT /*tag= c
FT /notes= "Defined as nucleotides 466-494"
FT misc_feature 544..567
FT /*tag= d
FT /notes= "Defined as nucleotides 544-567"
FT misc_feature 773..787
FT /*tag= e
FT /notes= "Defined as nucleotides 838-853"
FT misc_feature 793..808
FT /*tag= f
FT /notes= "Defined as nucleotides 859-875"
FT misc_feature 946..965
FT /*tag= g
FT /notes= "Defined as nucleotides 1013-1032"
XX
PN FR2733755-A1.
XX
PD 08-NOV-1996.
XX
PF 03-MAY-1995; 95PR-00005494.
XX
PR 03-MAY-1995; 95FR-00005494.
XX
PA (INMR ) BIO MERIEUX.

XX Mabilat C, Ruimy R;
XX WPI; 1997-001738/01.
XX
XX Fragments of Corynebacterium 16S RNA - useful as probes and primers for
XX identifying Corynebacterium spp.
XX
XX Claim 1; Fig 1; 60pp; French.
XX
XX Fragments covering 90 % of the sequence of 16S ribosomal RNA were
XX amplified from 28 strains of 25 different species of Corynebacterium by
XX PCR using primers specific for eubacteria. The amplification products
XX were sequenced and the sequences were aligned for comparison. It was
XX found that certain regions, i.e. those corresponding to nucleotides 72-
XX 100, 195-215, 466-494, 608-631, 838-853, 859-875 and 1013-1033 in the 16S
XX ribosomal RNA of C. diphtheriae (refer to features table for the present
XX sequence), vary considerably between different species. Probes and
XX primers comprising at least 5 nucleotides from one of these species-
XX specific sequences, including the present sequence, or their complements,
XX are useful to distinguish between different Corynebacterium species. DNA
XX versions of the probes and primers are also included
XX
SQ Sequence 1391 BP; 309 A; 317 C; 464 G; 1 T; 295 U; 5 Other;

Query Match 77.3%; Score 17; DB 2; Length 1391;
Best Local Similarity 88.2%; Pred. No. 1.8e+02;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCCT 17
   |||||
DB 33 GUCGAACGGAAAGCCU 49

RESULT 68
ABN86276
ID ABN86276 standard; DNA; 1457 BP.
XX
AC ABN86276;
XX
DT 08-OCT-2002 (first entry)
XX
DE G. polyisoprenivorans P8219 16S rDNA sequence #2.
XX
KW Microorganism; environmental; hormone; phthalic acid; alkyl ester; ds.
XX
OS Gordonia polyisoprenivorans.
XX
PN JP2002142754-A.
XX
PD 21-MAY-2002.
XX
PF 08-NOV-2000; 2000JP-00341214.
XX
PR 08-NOV-2000; 2000JP-00341214.
XX
PA (IMBI-) IMB KK.
XX
DR WPI; 2002-561124/60.
XX
XX A Gordonia sp. microorganism, useful in the eradication of the
XX environmental hormone of phthalic acid esters for environmental
XX protection.
XX
PS Disclosure; Fig 2A-D; 21pp; Japanese.
XX
XX The invention relates to a Gordonia sp. microorganism, capable of
XX eradication of the environmental hormone of phthalic acid alkyl esters.
XX The microorganism is used in the eradication of phthalic acid esters for
XX environmental protection. The present sequence represents an alternate G.
XX polyisoprenivorans P8219 16S rDNA sequence
XX
XX Sequence 1457 BP; 323 A; 348 C; 493 G; 291 T; 0 U; 2 Other;

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Query Match 76.4%; Score 16.8; DB 6; Length 1457;  
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTC 20  
 |||||  
 Db 44 GTCGAACGGAAGGCCCTGTC 63

RESULT 69  
 AAS59540/c  
 ID AAS59540 standard; DNA; 1457 BP.  
 XX AC AAS59540;  
 XX DT 13-FEB-2002 (first entry)  
 XX DE Propionibacterium acnes immunogenic protein encoding DNA #35.  
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant; ds.

Query Match 76.4%; Score 16.8; DB 6; Length 1457;  
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTC 20  
 |||||  
 Db 44 GTCGAACGGAAGGCCCTGTC 63

RESULT 70  
 AAS59540/c  
 ID AAS59540 standard; DNA; 2743 BP.  
 XX AC AAS59540;  
 XX DT 13-FEB-2002 (first entry)  
 XX DE Propionibacterium acnes immunogenic protein encoding DNA #35.  
 XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant; ds.

Query Match 76.4%; Score 16.8; DB 6; Length 1457;  
 Best Local Similarity 90.0%; Pred. No. 2.3e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTC 20  
 |||||  
 Db 44 GTCGAACGGAAGGCCCTGTC 63

RESULT 71  
 ACF64469/c  
 ID ACF64469 standard; DNA; 2743 BP.  
 XX AC ACF64469;  
 XX DT 17-OCT-2003 (first entry)  
 XX DE Propionibacterium acnes DNA contig sequence #35.  
 XX KW Acne vulgaris; antiseborrheic; dermatological; antibacterial;  
 KW immunostimulant; immune response; vaccine; ds.  
 OS Propionibacterium acnes.

Query Match 76.4%; Score 16.8; DB 4; Length 2743;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTTC 20  
 |||||  
 Db 2589 GTCGAACGGAAGGCCCTGTC 2570

Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;

XX OS Propionibacterium acnes.  
 XX PN WO200181581-A2.  
 XX PD 01-NOV-2001.  
 XX PF 20-APR-2001; 2001WO-US012865.  
 XX PR 21-APR-2000; 2000US-0199047P.  
 XX PR 02-JUN-2000; 2000US-0208841P.  
 XX PR 07-JUL-2000; 2000US-0216747P.  
 XX PA (CORI-) CORIXA CORP.  
 XX PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;  
 XX DR WPI; 2001-616774/71.  
 XX PT Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris.  
 XX PS Claim 1; SEQ ID NO 35; 1069pp; English.

Sequences AAS59506-AAS59804 represent DNA molecules encoding  
 Propionibacterium acnes immunogenic polypeptides. The proteins and their  
 associated DNA sequences are used in the treatment, prevention and  
 diagnosis of medical conditions caused by P. acnes. The disorders include  
 SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and  
 osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in  
 infections of bone, joints and the central nervous system, however it is  
 particularly involved in the inflammatory lesions associated with acne  
 vulgaris. A method for detecting the presence or absence of P. acnes in a  
 patient comprises contacting a sample with a binding agent that binds to  
 the proteins of the invention and determining the amount of bound protein  
 in the sample. The polypeptides may be used as antigens in the production  
 of antibodies specific for P. acnes proteins. These antibodies can be  
 used to downregulate expression and activity of P. acnes polypeptides and  
 therefore treat P. acnes infections. The antibodies may also be used as  
 diagnostic agents for determining P. acnes presence, for example, by  
 enzyme linked immunosorbent assay (ELISA). This sequence encodes the  
 polypeptides shown in AAU47822-AAU47846. Note: The sequence data for this  
 patent did not form part of the printed specification, but was obtained  
 in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences

XX WO2003033515-A1.  
 PN 24-APR-2003.  
 PD 11-OCT-2002; 2002WO-US032727.  
 XX 15-OCT-2001; 2001US-00978825.  
 PR (CORI-) CORIXA CORP.  
 XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;  
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;  
 PI Barth B, Vallie-Douglas J;  
 XX WPI; 2003-381789/36.  
 DR  
 XX New Propionibacterium acnes polypeptides and polynucleotides encoding the  
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,  
 PT or for stimulating an immune response specific for a P. acnes protein.  
 PT  
 XX Claim 1; SEQ ID NO 35; 1491pp; English.  
 PS  
 XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)  
 CC encoding a Propionibacterium acnes protein. The invention also relates to  
 CC polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to  
 CC immunogenic fragments of P. acnes polypeptides. The invention  
 CC additionally encompasses expression vectors and host cells comprising a  
 CC polynucleotide of the invention; antibodies against polypeptides of the  
 CC invention; fusion proteins comprising a polypeptide of the invention; a  
 CC method for stimulating an immune response specific for a P. acnes  
 CC polypeptide and an isolated T cell population comprising T cells prepared  
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,  
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or  
 CC antigen-presenting cells that express the polypeptide); a method and kit  
 CC for detecting or determining the presence or absence of P. acnes in a  
 CC patient; and a method for inhibiting the development of P. acnes in a  
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion  
 CC proteins, T cell populations or antigen-presenting cells that express the  
 CC polypeptides are useful for diagnosing, preventing or treating acne  
 CC vulgaris, or for stimulating an immune response specific for a P. acnes  
 CC protein. The polynucleotides can also be used as probes or primers for  
 CC nucleic acid hybridisation. The vaccine composition is useful for the  
 CC stimulation of an immune response against P. acnes, or for treating acne,  
 CC and the kit is useful for performing a diagnostic assay. The present  
 CC sequence represents a P. acnes DNA contig which is specifically claimed  
 CC in the invention. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 2743 BP; 645 A; 999 C; 546 G; 551 T; 0 U; 2 Other;  
 Query Match 76.4%; Score 16.8; DB 8; Length 2743;  
 Best Local Similarity 90.0%; Pred. No. 2.5e+02;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GTCGACGGAAAGCCCTTC 20  
 Db 2589 GTCGACGGAAAGCCCTGC 2570  
 RESULT 72  
 ABV75558  
 ID ABV75558 standard; DNA; 36538 BP.  
 XX AC ABV75558;  
 XX  
 DT 22-JAN-2003 (first entry)  
 XX  
 DE Saccharopolyspora butenyl-spinosyn biosynthetic gene cluster 2.  
 XX Butenyl; biosynthetic enzyme; PKS; polyketide synthetase; macrolide;  
 KW metabolite; spinosyn; gene; ds.  
 KW

XX Saccharopolyspora sp.  
 OS  
 XX  
 FH Location/Qualifiers  
 CDS complement(114..938)  
 FT /\*tag= a  
 FT /product= "busp"  
 FT /note= "No start codon given"  
 FT 1389..2561  
 FT /\*tag= b  
 FT /product= "busG"  
 FT 2601..3353  
 FT /\*tag= c  
 FT /product= "bush"  
 FT complement(3359..4546)  
 FT /\*tag= d  
 FT /product= "busI"  
 FT 4684..6303  
 FT /\*tag= e  
 FT /product= "busJ"  
 FT 6317..7510  
 FT /\*tag= f  
 FT /product= "busK"  
 FT 7555..8406  
 FT /\*tag= g  
 FT /product= "busL"  
 FT complement(8407..9572)  
 FT /\*tag= h  
 FT /product= "busM"  
 FT /note= "No start codon given"  
 FT complement(9668..10666)  
 FT /\*tag= i  
 FT /product= "busN"  
 FT complement(10675..12135)  
 FT /\*tag= j  
 FT /product= "busO"  
 FT complement(12864..14177)  
 FT /\*tag= k  
 FT /product= "busP"  
 FT 14627..15970  
 FT /\*tag= l  
 FT /product= "busQ"  
 FT /note= "No start codon given"  
 FT 16008..17144  
 FT /\*tag= m  
 FT /product= "busR"  
 FT /note= "No start codon given"  
 FT 17168..17917  
 FT /\*tag= n  
 FT /product= "busS"  
 FT complement(18520..19932)  
 FT /\*tag= o  
 FT /product= "ORF LI"  
 FT complement(19978..20488)  
 FT /\*tag= p  
 FT /product= "ORF LII"  
 FT /note= "No start codon given"  
 FT complement(20536..21033)  
 FT /\*tag= q  
 FT /product= "ORF LIII"  
 FT /note= "No start codon given"  
 FT 21179..21925  
 FT /\*tag= r  
 FT /product= "ORF LIV"  
 FT complement(22671..23453)  
 FT /\*tag= s  
 FT /product= "ORF LVI"  
 FT complement(23687..24886)  
 FT /\*tag= t  
 FT /product= "ORF LVII"  
 FT complement(26177..26923)  
 FT /\*tag= u  
 FT

```

FT FT /product= "ORF LVIII"
FT FT /note= "No start codon given"
FT CDS 27646. .28476
FT FT /*tag= v
FT FT /product= "ORF LIX"
FT FT /note= "No start codon given"
XX
XX
XX WO200279477-A2.
XX
XX 10-OCT-2002.
XX
XX 28-MAR-2002; 2002WO-US009968.
XX
XX 30-MAR-2001; 2001US-0280175P.
XX
XX (DOWC ) DOW AGROSCIENCES LLC.
XX
XX Hahn DR, Jackson JD, Bullard BS, Gustafson GD, Waldron C;
XX Mitchell JC;
XX
XX WPI; 2003-058434/05.
XX P-PSDB; ABP57683, ABP57684, ABP57685, ABP57686, ABP57687, ABP57688,
XX ABP57689, ABP57690, ABP57691, ABP57692, ABP57693, ABP57694, ABP57695,
XX ABP57696, ABP57697, ABP57698, ABP57699, ABP57700, ABP57701, ABP57702,
XX ABP57703, ABP57704.
XX
XX New butenyl-spinosyn biosynthetic genes, useful for increasing the
XX production of butenyl-spinosyn insecticidal macrolides, or for changing
XX the metabolites or products produced by spinosyn-producing
XX microorganisms.
XX
XX Claim 2; Page 99-119; 218pp; English.
XX
XX The invention relates to a novel DNA molecule comprising a DNA sequence
XX that encodes a butenyl-spinosyn biosynthetic enzyme, a butenyl-spinosyn
XX PKS (polyketide synthetase) domain, or a spinosyn PKS module. The butenyl-
XX spinosyn biosynthetic genes are useful for increasing the production of
XX butenyl-spinosyn insecticidal macrolides. The genes are also useful for
XX changing the metabolites or products produced by spinosyn-producing
XX microorganisms. The present sequence represents a DNA molecule encoding
XX butenyl-spinosyn biosynthetic enzymes
XX
XX SQ Sequence 36538 BP; 6867 A; 12266 C; 11182 G; 6223 T; 0 U; 0 Other;
XX
XX Query Match 76.4%; Score 16.8; DB 10; Length 36538;
XX Best Local Similarity 90.0%; Pred. No. 3.2e+02;
XX Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 1 GTCGAACGGAAGGCCTTTC 20
XX ||||| |||||
XX 7521 GTCGAACGCACAGGCTTTC 7540
XX
XX RESULT 73
XX AAV24413
XX ID AAV24413 standard; preRNA; 23 BP.
XX
XX AC AAV24413;
XX
XX 24-AUG-1998 (first entry)
XX
XX Target sequence #2 for M. intracellulare specific probe.
XX
XX Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
XX antimicrobial agent; pre-rRNA detection; ss.
XX
XX Synthetic.
XX OS Mycobacterium intracellulare.
XX
XX US5770373-A.
XX
XX 23-JUN-1998.
XX

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```

PF 08-NOV-1996; 96US-00745638.
XX
XX 16-JUN-1994; 94US-00261068.
XX 07-JUN-1995; 95US-00485602.
XX
XX (BECT ) BECTON DICKINSON & CO.
XX
XX Cangelosi GA, Britschgi TB;
XX WPI; 1998-376792/32.
XX
XX Mycobacterial sensitivity and drug screening assays - involving release
XX of pre-rRNA by lysis.
XX
XX Example 4; Col 17-18; 50pp; English.
XX
XX This sequence represents a target sequence for mycobacterial probes. This
XX sequence represents a precursor RNA fragment that is released during the
XX method of the invention. The method is for the determination of
XX mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
XX (a) culturing the cells in the presence of the antimicrobial agent; (b)
XX treating the cells by enzymatic or mechanical means to expose the cell
XX membrane to lysis reagents, and contacting the cells with a lysis reagent
XX under conditions such that pre-rRNA is released from the cells but not
XX degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
XX capable of hybridising to a region of the pre-rRNA that is not present in
XX mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
XX is indicated by an increase or decrease in pre-rRNA levels for cells
XX exposed to the antimicrobial agent compared with mycobacterial cells not
XX exposed to the antimicrobial agent. The lysis method, unlike known
XX methods, results in detectable levels of pre-rRNA
XX
XX SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
XX
XX Query Match 74.5%; Score 16.4; DB 2; Length 23;
XX Best Local Similarity 78.9%; Pred. No. 2.4e+02;
XX Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 4 GAACGGAAGGCCTTTCGG 22
XX ||||| |||||
XX 1 GAACGGAAGNCCUUCGG 19
XX
XX Db
XX
XX RESULT 74
XX AAV13021
XX ID AAV13021 standard; rRNA; 23 BP.
XX
XX AC AAV13021;
XX
XX 18-MAY-1998 (first entry)
XX
XX Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.
XX
XX Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
XX hybridisation; antibiotic resistance; cell lysis; ss.
XX
XX OS Mycobacterium intracellulare.
XX
XX US5712095-A.
XX
XX 27-JAN-1998.
XX
XX 07-JUN-1995; 95US-00485602.
XX
XX 16-JUN-1994; 94US-00261068.
XX
XX (BECT ) BECTON DICKINSON CO.
XX
XX Cangelosi GA, Britschgi TB;
XX WPI; 1998-119975/11.
XX
XX Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX

```

PT with specific probes after cell lysis.  
 XX Disclosure; Col 18; 54pp; English.  
 XX  
 CC The present sequence represents a mycobacterial mature ribosomal RNA  
 CC target sequence. The present invention describes a method for detecting  
 CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)  
 CC treating the cells to release pre-rRNA by: (i) pretreating the cells by  
 CC enzymatic degradation using both lysozyme and protease until their cell  
 CC walls are rendered porous to expose their cell membranes, making the  
 CC cells susceptible to lysis; (ii) contacting the pretreated cells with a  
 CC combination of a magnesium chelator, a nonionic detergent and an anionic  
 CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the  
 CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at  
 CC least one oligonucleotide probe which is capable of selectively  
 CC hybridizing to a region of the pre-rRNA that is not present in a mature  
 CC mycobacterial RNA. The probes can be used to identify many Mycobacterium  
 CC spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,  
 CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.  
 CC intracellulare. The probes may also be used to measure mycobacterial  
 CC response to inhibitors of RNA and protein synthesis and may therefore be  
 CC used to screen new antimycobacterial drugs. Mycobacteria have a slow  
 CC growth rate. By using the probes, drug developers can now identify  
 CC compounds that are more effective, but less stable than those previously  
 CC identified  
 XX  
 SQ Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;  
 Query Match 74.5%; Score 16.4; DB 2; Length 23;  
 Best Local Similarity 78.9%; Pred. No. 2.4e+02;  
 Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GAACGGAAAGCCCTTCGG 22  
 ||||| :|||  
 Db 1 GAACGGAAAGCCCUCCG 19  
 RESULT 75  
 AAX99198  
 ID AAX99198 standard; DNA; 50 BP.  
 AC AAX99198;  
 XX  
 DT 28-SEP-1999 (first entry)  
 XX  
 DE M. smegmatis 16S rRNA gene fragment.  
 XX  
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.  
 XX  
 OS Mycobacterium smegmatis.  
 XX  
 PN WO9935284-A1.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 30-DEC-1997; 97WO-BR000087.  
 XX  
 PR 30-DEC-1997; 97WO-BR000087.  
 XX  
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.  
 XX  
 PI Peregrino Ferreira PC, Geessien Kroon E;  
 PI Bernardes Margutti Pinto ME, Aleixo AW;  
 XX  
 DR WPI; 1999-444201/37.  
 XX  
 PT Detection of mycobacteria by shift mobility assay.  
 XX  
 PS Disclosure; Fig 7; 20pp; English.  
 XX  
 CC The invention describes a new method for diagnosis, identification and  
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
 CC DNA amplification and shift mobility assay. The method is based on  
 CC divergence in sequences found in 16S rRNA to identify mycobacteria  
 CC species, since a remarkable shift of heteroduplex bands are obtained  
 CC between single stranded and homoduplex bands in UPAGE. The method is  
 CC fast, simple and can produce information not easily obtained when  
 CC compared with other detection methods. The sensitivity of other assays  
 CC suffer due to the tendency of the denatured PCR product strands to  
 CC reassociate and exclude oligonucleotide probes, and stearic interference  
 CC between the bound oligonucleotides and the solid support which impede  
 CC reassociation to nucleic acids in solution. Sequences AAX99193-237  
 CC represent 16S rRNA gene regions of some mycobacterial species  
 XX  
 SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;  
 Query Match 74.5%; Score 16.4; DB 2; Length 50;  
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GTCGAACGGAAGGCCTTT 19  
 ||||| :|||  
 Db 13 GTCGAACGGAAGNCCCTT 31

CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
 CC DNA amplification and shift mobility assay. The method is based on  
 CC divergence in sequences found in 16S rRNA to identify mycobacteria  
 CC species, since a remarkable shift of heteroduplex bands are obtained  
 CC between single stranded and homoduplex bands in UPAGE. The method is  
 CC fast, simple and can produce information not easily obtained when  
 CC compared with other detection methods. The sensitivity of other assays  
 CC suffer due to the tendency of the denatured PCR product strands to  
 CC reassociate and exclude oligonucleotide probes, and stearic interference  
 CC between the bound oligonucleotides and the solid support which impede  
 CC reassociation to nucleic acids in solution. Sequences AAX99193-237  
 CC represent 16S rRNA gene regions of some mycobacterial species  
 XX  
 SQ Sequence 50 BP; 13 A; 12 C; 15 G; 9 T; 0 U; 1 Other;  
 Query Match 74.5%; Score 16.4; DB 2; Length 50;  
 Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GTCGAACGGAAGGCCTTT 19  
 ||||| :|||  
 Db 13 GTCGAACGGAAGNCCCTT 31  
 RESULT 76  
 AAX99201  
 ID AAX99201 standard; DNA; 50 BP.  
 AC AAX99201;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 28-SEP-1999 (first entry)  
 XX  
 DE M. simium 16S rRNA gene fragment.  
 XX  
 KW Mycobacterium tuberculosis; polymerase chain reaction; PCR; SMA;  
 KW shift mobility assay; urea-polyacrylamide gel; UPAGE; 16S rRNA; ss.  
 XX  
 OS Mycobacterium simiae.  
 XX  
 PN WO9935284-A1.  
 XX  
 PD 15-JUL-1999.  
 XX  
 PF 30-DEC-1997; 97WO-BR000087.  
 XX  
 PR 30-DEC-1997; 97WO-BR000087.  
 XX  
 PA (UYMI-) UNIV FEDERAL MINAS GERAIS.  
 XX  
 PI Peregrino Ferreira PC, Geessien Kroon E;  
 PI Bernardes Margutti Pinto ME, Aleixo AW;  
 XX  
 DR WPI; 1999-444201/37.  
 XX  
 PT Detection of mycobacteria by shift mobility assay.  
 XX  
 PS Disclosure; Fig 7; 20pp; English.  
 XX  
 CC The invention describes a new method for diagnosis, identification and  
 CC characterisation of Mycobacterium tuberculosis or any other mycobacteria  
 CC by using polymerase chain reaction (PCR) and shift mobility assay (SMA)  
 CC in urea-polyacrylamide gel (UPAGE) comprises culturing, DNA extraction,  
 CC DNA amplification and shift mobility assay. The method is based on  
 CC divergence in sequences found in 16S rRNA to identify mycobacteria  
 CC species, since a remarkable shift of heteroduplex bands are obtained  
 CC between single stranded and homoduplex bands in UPAGE. The method is  
 CC fast, simple and can produce information not easily obtained when  
 CC compared with other detection methods. The sensitivity of other assays  
 CC suffer due to the tendency of the denatured PCR product strands to  
 CC reassociate and exclude oligonucleotide probes, and stearic interference  
 CC between the bound oligonucleotides and the solid support which impede

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CC hybridization to nucleic acids in solution. Sequences AAX99193-237
CC represent 16S rRNA gene regions of some mycobacterial species. (Updated
CC on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 50 BP; 14 A; 11 C; 13 G; 9 T; 0 U; 3 Other;

Query Match      74.5%; Score 16.4; DB 2; Length 50;
Best Local Similarity 89.5%; Pred. NO. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCTTT 19
    |||||
Db 13 GTCGAACGGAAGNCCTT 31
    |||||

RESULT 77
ADA68711/c
ID ADA68711 standard; DNA; 765 BP.
XX
AC ADA68711;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 2034.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Karagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 2034; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present invention was used to
CC illustrate the invention.
SQ Sequence 765 BP; 207 A; 171 C; 153 G; 216 T; 0 U; 18 Other;

Query Match      73.6%; Score 16.2; DB 8; Length 765;
Best Local Similarity 78.9%; Pred. NO. 4.3e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAACGGAAGGCTTTCCG 22
    |||:|||||
Db 725 GAAYGGAARGCTTTCGR 707
    |||:|||||
```

```
RESULT 78
ADW16249
ID ADW16249 standard; DNA; 1158 BP.
XX
AC ADW16249;
XX
DT 07-APR-2005 (first entry)
XX
DE DNA copy of the Microbispora 16s ribosomal RNA EN2 isolate Seq 1.
XX
KW 16s ribosomal RNA; ds; 16s rRNA; medicinal plant; plant breeding;
KW disease resistance; insect resistance; crop improvement;
KW plant growth factor; antibacterial; antimicrobial; fungicide;
KW insecticide; nematocide.
XX
OS Microbispora.
XX
PN WO2005003328-A1.
XX
PD 13-JAN-2005.
XX
PF 07-JUL-2004; 2004WO-AU000914.
XX
PR 07-JUL-2003; 2003US-0485241P.
PR 22-SEP-2003; 2003US-0504703P.
XX
PA (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.
XX
PI Franco CHM, Coombs JT;
XX
DR WPI; 2005-091806/10.
XX
PT Improving plant productivity comprises introducing into the plant or
PT propagation material an endophytic actinomycete that facilitates
PT induction of at least one characteristic related to improved
PT productivity.
XX
PS Claim 1; SEQ ID NO 1; 235pp; English.
XX
CC This invention relates to a novel method for improving plant
CC productivity. Specifically, it refers to introducing into the plant or
CC propagation material an endophytic actinomycetes or variant thereof,
CC where the actinomycetes facilitate induction of a characteristic related
CC to improved productivity. The present invention further describes
CC metabolites of the actinomycetes microorganism such as auxin, gibberellin
CC or cytokinin that are able to induce disease resistance in plants i.e.
CC provide disease bio-control capabilities against pathogen infection.
CC Accordingly, the method facilitates the improvement of cereal crop
CC productivity including increasing germination by up-regulating plant
CC growth promoting activities, as well as improving plant vigor or flower
CC and fruit yield. Furthermore, the new actinomycete or metabolite is
CC useful in the manufacture of a medicament for the therapeutic and/or
CC prophylactic treatment of a mammalian or non-mammalian subject i.e.
CC plant. As such, this method provides plant protectants and plant growth
CC stimulants that exhibit antibacterial, antimicrobial, fungicide,
CC insecticide and nematocide activities. This polynucleotide is the DNA
CC sequence of an actinomycetes 16s ribosomal RNA sequence of the invention.
XX
SQ Sequence 1158 BP; 247 A; 265 C; 379 G; 234 T; 0 U; 33 Other;

Query Match      73.6%; Score 16.2; DB 14; Length 1158;
Best Local Similarity 85.7%; Pred. NO. 4.5e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TCGNACGGAAGGCTTTCG 22
    |||:|||||
Db 16 TCAAGCGGAAGGCTTTCG 36
    |||:|||||

RESULT 79
AAD11277
ID AAD11277 standard; DNA; 23 BP.
```

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XX AAD11277;
AC
XX
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #21.
DE
XX DE
XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
XX Mycobacterium sp.
XX
XX WO200144510-A2.
XX
XX 21-JUN-2001.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
XX 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 37; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
XX Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAAGGCC 16
Db |||||
4 GTCGAACGGAAAGGCC 19

RESULT 80
ADG88358
ID ADG88358 standard; DNA; 23 BP.
XX
AC ADG88358;
XX
XX 11-MAR-2004 (first entry)
DT
XX Mycobacterium amplifying PCR primer #27.
DE
XX In vitro amplification; PCR; primer; ss.
KW
XX Mycobacterium xenopi.
OS
XX US2003165824-A1.
FN
XX 04-SEP-2003.
PD

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XX 15-DEC-2000; 2000US-00738274.
PF
XX 17-DEC-1999; 99US-0172190P.
PR
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 27; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
XX Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAAGGCC 16
Db |||||
4 GTCGAACGGAAAGGCC 19

RESULT 81
AEA08233
ID AEA08233 standard; DNA; 23 BP.
XX
AC AEA08233;
XX
XX 14-JUL-2005 (first entry)
DT
XX Mycobacterium xenopi 16SrRNA amplifying non-T7 primer, SEQ ID NO: 27.
DE
XX Microorganism detection; DNA amplification; 16S ribosomal RNA; 16S rRNA;
KW PCR; primer; ss.
XX
XX Mycobacterium xenopi; ATCC 19250.
OS
XX US2005100915-A1.
FN
XX 12-MAY-2005.
PD
XX 18-SEP-2003; 2003US-00665708.
PF
XX 17-DEC-1999; 99US-0172190P.
PR
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT

```



PT in a biological sample, comprises using in vitro nucleic acid  
XX amplification and detection of amplified products.

PS Example 3; SEQ ID NO 27; 21pp; English.

CC The present invention relates to a method of detecting Mycobacterium  
CC species present in a biological sample. The method involves using in  
CC vitro nucleic acid amplification and detection of amplified products. The  
CC invention is useful for diagnostic detection of pathogenic bacteria such  
CC as Mycobacterium species. The present sequence is the Mycobacterium  
CC xenopi (ATCC 19250) 16S ribosomal RNA (16SrRNA) amplifying non-T7 PCR  
CC primer.

XX Sequence 23 BP; 7 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
Db 4 GTCGAACGGAAGGCC 19  
|||||

## RESULT 82

ID AAD11278 standard; DNA; 26 BP.

XX AAD11278;

DT 24-SEP-2001 (first entry)

XX Mycobacterium 16S rRNA amplifying primer #22.

XX Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.

XX Mycobacterium sp.

OS WO200144510-A2.

XX 21-JUN-2001.

XX 17-DEC-1999; 99WO-US030346.

XX 17-DEC-1999; 99WO-US030346.

XX (GENP-) GEN-PROBE INC.  
PA (INNR ) BIOMERIEUX SA.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2001-398170/42.

XX Detecting Mycobacterium species, involves in vitro amplification of 16S  
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
PT specific primers, and detecting the amplified nucleic acid.

PS Claim 1; Page 37; 44pp; English.

XX The invention relates to a method of detecting Mycobacterium species,  
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
CC comprising a polymerase, and at least two primers, and then detecting the  
CC amplified nucleic acid. The method is relatively simple and useful for  
CC detecting the presence of various Mycobacterium species in a biological  
CC sample, and thus important for diagnosis of infections resulting from  
CC them. The method is especially important for screening opportunistic  
CC infections caused by M. tuberculosis or a Mycobacterium other than  
CC tuberculosis (MOTT). The present sequence is a PCR primer used for  
CC amplifying Mycobacterium 16S rRNA

XX Sequence 26 BP; 5 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 4; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
Db 1 GTCGAACGGAAGGCC 16  
|||||

## RESULT 83

ADG88359  
ID ADG88359 standard; DNA; 26 BP.

XX AC ADG88359;

DT 11-MAR-2004 (first entry)

XX Mycobacterium amplifying PCR primer #28.

DE In vitro amplification; PCR; primer; ss.

XX Mycobacterium xenopi.

XX US2003165824-A1.

XX 04-SEP-2003.

XX 15-DEC-2000; 2000US-00738274.

XX 17-DEC-1999; 99US-0172190P.

XX (BREN/) BRENTANO S T.

XX (JUCK/) JUCKER M T.

XX (DELG/) DELGADO F D.

XX (CLEU/) CLEUZIAZ P.

XX (RODR/) RODRIGUE M.

XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;

XX WPI; 2003-898044/82.

XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
PT in a biological sample comprises performing in vitro nucleic acid  
PT amplification and detection of amplified products.

XX Claim 1; SEQ ID NO 28; 20pp; English.

XX The present invention relates to a method of detecting Mycobacterium  
CC species present in a biological sample comprises performing an in vitro  
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and  
CC detecting the amplified Mycobacterium nucleic acid. The present sequence  
CC is Mycobacterium amplifying PCR primer.

XX Sequence 26 BP; 5 A; 6 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
Db 1 GTCGAACGGAAGGCC 16  
|||||

## RESULT 84

AEA08234  
ID AEA08234 standard; DNA; 26 BP.

XX AC AEA08234;

XX 14-JUL-2005 (first entry).

XX DT XX



XX The present invention relates to probes (ADP93908-ADP94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism,  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADP94060 and ADP94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from *Actinobacillus actinomycetemcomitans*,  
 CC *Acinetobacter calcoaceticus*, *Haemophilus influenzae*, *Stenotrophomonas*  
 CC *malophilia*, *Proteus mirabilis*, *Streptococcus pneumoniae*, *Pseudomonas*  
 CC *aeruginosa*, *Citrobacter freundii*, *Veillonella parvula*, *Providencia*  
 CC *stuartii*, *Neisseria gonorrhoeae*, *Streptococcus agalactiae*, *Morganella*  
 CC *morganii*, *Bacteroides fragilis*, *Staphylococcus hominis*, *Staphylococcus*  
 CC *warneri*, *Staphylococcus haemolyticus*, *Enterobacter cloacae*, *Enterobacter*  
 CC *aerogenes*, *Staphylococcus epidermidis*, *Streptococcus constellatus*,  
 CC *Serratia marcescens*, *Streptococcus anginosus*, *Escherichia coli*,  
 CC *Klebsiella pneumoniae*, *Enterococcus faecalis*, *Enterococcus faecium*,  
 CC *Streptococcus sanguis*, *Streptococcus mitis*, *Streptococcus intermedius*,  
 CC *Listeria monocytogenes*, *Clostridium perfringens*, *Corynebacterium*  
 CC *aquaticum*, *Streptococcus oxalis*, *Staphylococcus aureus*, *Neisseria*  
 CC *meningitidis*, *Campylobacter fetus*, *Enterococcus gallinarum*, *Enterococcus*  
 CC *caseloflavus*, *Aeromonas hydrophila*, *Salmonella paratyphi*, *Salmonella*  
 CC *typhi*, *Streptococcus equisimilis*, *Streptococcus canis*, *Klebsiella*  
 CC *oxytoca*, *Staphylococcus saprophyticus*, *Pasteurella multocida*, *Eikenella*  
 CC *corrodens*, *Streptococcus pyogenes*, *Moraxella catarrhalis*, *Legionella*  
 CC *pneumophila*, *Mycobacterium tuberculosis*, *Mycobacterium avium*,  
 CC *Mycobacterium intracellulare*, *Mycobacterium kansasii* or *Mycobacterium*  
 CC *gordonae*.

XX Sequence 50 BP; 11 A; 12 C; 20 G; 7 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 12; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGACGGAAAGGCC 16  
 |||||  
 Db 5 GTCGACGGAAAGGCC 20

RESULT 87  
 ADU66542  
 ID ADU66542 standard; DNA; 80 BP.

XX AC ADU66542;

XX 27-JAN-2005 (first entry)

XX Cut base A amplicon fragment.

XX ds; mass spectroscopy; DNA cleavage; DNA sequencing; sequencing.

XX Unidentified.

XX W02004097369-A2.

XX 11-NOV-2004.

XX 22-APR-2004; 2004WO-US012520.

XX 25-APR-2003; 2003US-0466006P.

XX (SEQU-) SEQUENOM INC.

XX (BOEC/) BOECKER S.

XX Boecker S, Van Den Boom D;

XX WPI; 2005-012656/01.

XX Obtaining sequence information from target biomolecule, by fragmenting

PT target biomolecule by partial cleavage, performing mass spectrometry,  
 PT extracting information from mass spectra, constructing sequencing graph  
 PT and traversing graphs.

XX Disclosure; SEQ ID NO 11; 133pp; English.

XX This invention describes a novel method for obtaining sequence  
 CC information from a target biomolecule and involves fragmenting the target  
 CC biomolecule into several fragments by partial cleavage, performing mass  
 CC spectrometry on fragments to produce mass spectra, extracting peak  
 CC information from the produced mass spectra, constructing sequencing graph  
 CC using the extracted peak information and traversing the sequencing graph  
 CC to reconstruct sequence information of the target biomolecule. The target  
 CC biomolecule is nucleic acid molecule such as DNA or RNA, or is a protein  
 CC and the compositions of the two fragments are the base compositions or  
 CC amino acid compositions. This method preferably involves subjecting the  
 CC nucleic acid molecule to partial cleavage reactions with one or more  
 CC specific cleavage reagents, thus generating two or more fragments that  
 CC are specific cleavage products, determining the molecular weights of the  
 CC two or more fragments, determining the possible base compositions of the  
 CC two or more fragments, ordering the possible base compositions of the two  
 CC or more fragments according to the number of specific cleavage sites that  
 CC are not cleaved in each fragment, constructing one or more sequencing  
 CC graphs that are a graph theoretical representation of the ordered base  
 CC compositions for the two or more fragments, and traversing the one or  
 CC more sequencing graph to reconstruct one or more underlying sequence  
 CC candidates, where each sequencing graph corresponds to the ordered base  
 CC compositions derived from a partial cleavage reaction with one base-  
 CC specific cleavage reagent. This method further involves scoring the one  
 CC or more underlying sequence candidates and determining the rank order of  
 CC fitness, where the scoring is done by statistical analysis or maximum  
 CC likelihood statistical analysis. This method determines epigenetic  
 CC changes in a target nucleic acid molecule relative to reference nucleic  
 CC acid molecule and allows the sequencing of large biomolecules. The  
 CC invention also describes a method of producing a candidate sequence of a  
 CC biomolecule which involves receiving several sequencing graphs having  
 CC several vertices and edges, where each vertex represents a compomer of  
 CC the biomolecule and each edge represents a cut base of the sequencing  
 CC graph and generating the candidate sequence by traversing several  
 CC sequencing graphs. This second method further involves traversing several  
 CC sequencing graphs by tracing through each sequencing graph, starting at a  
 CC source vertex. The results of each method can be read by a program  
 CC product for use in a computer that executes program instructions recorded  
 CC in a computer-readable media to produce a candidate sequence of a  
 CC biomolecule or to obtain sequence information in a target biomolecule.  
 CC The target biomolecule contains a sequence variation, which is a mutation  
 CC or a polymorphism. The target is a target nucleic acid molecule from an  
 CC organism chosen from eukaryotes, prokaryotes and viruses, preferably a  
 CC bacterium. The specific cleavage reagent is an RNase chosen from RNase  
 CC T1, RNase U2, RNase Phym, RNase A, chicken liver RNase (RNase CL3) and  
 CC cusavirin, or a glycosylase. The sequence variations in the target  
 CC biomolecule permit genotyping a subject, forensic analysis, disease  
 CC diagnosis or disease prognosis. The novel methods are useful for de novo  
 CC sequencing, to identify genetic disease or chromosome abnormality,  
 CC identifying a predisposition to a disease, or condition including  
 CC obesity, atherosclerosis, or cancer, to identify an infection by an  
 CC infectious agent, to identify a pathogen, determine haplotypes, analyze  
 CC microsatellite sequences, and short tandem repeat (STR) loci, determine  
 CC allelic variation and/or frequency, and analyze cellular methylation  
 CC patterns. This sequence represents an amplicon used to illustrate the  
 CC sequencing technique described in the invention.

XX Sequence 80 BP; 18 A; 20 C; 27 G; 15 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 80;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTCGACGGAAAGGCC 16

Db 54 GTCGACGGAAAGGCC 69

```

RESULT 88
AEB98763
ID AEB98763 standard; DNA; 209 BP.
XX
AC AEB98763;
XX
DT 06-OCT-2005 (first entry)
XX
DE Mycobacterium intracellulare partial 16S rDNA sequence, SEQ ID 5.
XX
KW microorganism detection; mycobacterium infection; antibacterial; ds.
XX
OS Mycobacterium intracellulare.
XX
PN JP2005204582-A.
XX
PD 04-AUG-2005.
XX
PF 23-JAN-2004; 2004JP-00015195.
XX
PR 23-JAN-2004; 2004JP-00015195.
XX
PA (ASAH ) ASahi KASEI KK.
XX
PI Oda N;
XX
DR WPI; 2005-526965/54.
XX
PT New single-stranded oligonucleotide, useful for amplifying the nucleic
PT acid of Mycobacterium avium, Mycobacterium intracellulare, and
PT Mycobacterium kansasii.
XX
PS Example 1; SEQ ID NO 5; 14pp; Japanese.
XX
CC The invention relates to a novel single-stranded oligonucleotide used in
CC a detection method of an atypical mycobacteria group. The invention
CC further includes: amplifying the nucleic acid of Mycobacterium avium by a
CC loop-mediated isothermal amplification (LAMP) method; amplifying the
CC nucleic acid of M. intracellulare by a LAMP method; amplifying the
CC nucleic acid of M. kansasii by a LAMP method; and a kit for detecting the
CC nucleic acid of M. avium by a LAMP method; detecting the nucleic acid of
CC M. intracellulare by a LAMP method; or detecting the nucleic acid of M.
CC kansasii by a LAMP method. The single-stranded oligonucleotide is useful
CC in medical applications. This polynucleotide represents a Mycobacterium
CC intracellulare partial 16S rDNA sequence amplified by the LAMP method of
CC the invention.
XX
SQ Sequence 209 BP; 45 A; 47 C; 73 G; 44 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 14; Length 209;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCC 16
Db 43 GTCGAACGGAAGGCC 58
RESULT 89
ABT23572
ID ABT23572 standard; DNA; 560 BP.
XX
AC ABT23572;
XX
DT 22-MAY-2003 (first entry)
XX
DE Stabilising reagent method related oligo SEQ ID No 24.
XX
KW Stabilising reagent; PCR; primer; RNaseH; long-term storage;
KW specific amplification; pathogenic microorganism; chimeric;
KW genetic engineering; clinical medicine; ss.
XX
OS Mycobacterium avium.

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XX WO2002101042-A1.
PN
XX 19-DEC-2002.
PD
XX
PF 12-JUN-2002; 2002WO-JP005832.
XX
PR 12-JUN-2001; 2001JP-0017737.
PR 20-AUG-2001; 2001JP-00249689.
XX
PA (TAKI ) TAKARA BIO INC.
XX
PI Sagawa H, Uemori T, Mukai H, Yamamoto J, Tomono J, Kobayashi E;
PI Enoki T, Asada K, Kato I;
XX
DR WPI; 2003-148805/14.
XX
PT Method for stabilizing and storing reaction reagents for specific
PT amplification and detection of nucleic acids particularly in e.g.
PT identifying pathogenic microorganisms or viruses in sample.
XX
PS Example 15; Page 110; 177pp; Japanese.
XX
CC The invention relates to a novel stabilising reaction reagent for use in
CC the amplification and/or detection of a target nucleic acid comprising:
CC preparing a reaction mixture with e.g. a nucleic acid as template, at
CC least 1 primer and RNaseH; and incubation of the reaction mixture for a
CC defined period of time to form a reaction product during the
CC amplification of such target nucleic acid. The method is useful for
CC stabilising and long-term storage of reaction reagents for highly
CC sensitive and specific amplification and detection of nucleic acids
CC particularly in identifying pathogenic microorganisms or viruses in a
CC sample using chimeric oligonucleotide primers, which is useful in genetic
CC engineering and clinical medicine. This polynucleotide sequence
CC represents an oligo relating to the novel stabilising reaction reagent
CC method of the invention
XX
SQ Sequence 560 BP; 117 A; 134 C; 199 G; 110 T; 0 U; 0 Other;
Query Match 72.7%; Score 16; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTCGAACGGAAGGCC 16
Db 46 GTCGAACGGAAGGCC 61
RESULT 90
AAA02278
ID AAA02278 standard; cDNA; 935 BP.
XX
AC AAA02278;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2269.
XX
KW Human; colon cancer; tumour; diagnosis; gene expression product; probe;
KW detection; cancerous state; metastasis; identification; breast cancer;
KW oestrogen receptor-positive breast cancer; therapy;
KW oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS Homo sapiens.
XX
PN WO9958675-A2.
XX
PD 18-NOV-1999.
XX
PF 13-MAY-1999; 99WO-US010602.
XX
PR 14-MAY-1998; 98US-0085426P.
PR 15-MAY-1998; 98US-0085537P.

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PR 15-MAY-1998; 98US-0085696P.
PR 21-OCT-1998; 98US-0105234P.
PR 27-OCT-1998; 98US-0105877P.
XX
PA (CHIR ) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
XX
PI Williams LT, Escobedo J, Innis MA, Garcia PD, Sudduth-Klinger J;
PI Reinhard C, Giese K, Randazzo F, Kennedy GC, Pot D, Kassam A;
PI Lamson G, Drmanac R, Crkvenjakov R, Dickson M, Drmanac S, Labat I;
PI Leshkowitz D, Kita D, Garcia V, Jones LW, Stache-Crain B;
XX
XX WPI; 2000-126369/11.
XX
XX Polynucleotide library used to determine cancerous states of mammalian
XX cells.
XX
XX Claim 1; Page 892; 1097pp; English.
XX
XX AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
XX libraries constructed from human colon cancer cell lines. The present
XX invention also describes a method of detecting differentially expressed
XX genes correlated with a cancerous state of a mammalian cell, comprising
XX detecting at least one differentially expressed gene product in a test
XX sample derived from a cell suspected of being cancerous, where detection
XX of the differentially expressed gene product is correlated with a
XX cancerous state of the cell from which the test sample was derived. The
XX polynucleotides sequences can be used in a method for detecting
XX differentially expressed genes correlated with a cancerous state of a
XX mammalian cell. The polynucleotides can also be used as probes for
XX detecting and mapping related genes. They can be used in diagnosis and
XX prognosis of diseases and disorders (e.g. identification of pre-
XX metastatic or metastatic cancerous states, stages of cancer, or
XX responsiveness of cancer to therapy). This is particularly for breast
XX cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
XX negative breast cancer, lung cancer, and colon cancer
XX
XX Sequence 935 BP; 300 A; 234 C; 227 G; 44 T; 0 U; 130 Other;
XX
XX Query Match 72.7%; Score 16; DB 3; Length 935;
XX Best Local Similarity 84.2%; Pred. No. 5.6e+02;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
Oy 4 GAACGGAAAGCCTTTCGG 22
Db ||| ||| ||| ||| ||| |||
452 GAANGGAANGGCCTTTNGG 470

RESULT 91
AEA22410
XX ID AEA22410 standard; DNA; 1321 BP.
XX AC AEA22410;
XX
XX 25-AUG-2005 (first entry)
XX
XX Mycobacterium kubicae 16S rRNA sequence SEQ ID NO:11.
XX
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
XX
XX Mycobacterium kubicae.
XX
XX US2005130168-A1.
XX
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX 31-OCT-2003; 2003US-00697802.
XX
XX (HANX/) HAN X.
XX (PHAM/) PHAM A S.
XX

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PI Han X, Pham AS;
XX
XX WPI; 2005-424597/43.
XX
XX Determining a bacterium species comprises providing oligonucleotide
XX primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 11; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
XX species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
XX extracting a genomic nucleotide from the bacterium to provide a
XX nucleotide template; (c) annealing a region of a nucleotide template to a
XX specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
XX complimentary fashion, the primer set designed to provide a product
XX having a predetermined size dictated by a complementary primer set; (d)
XX amplifying the region of the nucleotide template to produce the product;
XX and (e) determining a species of a bacterium in a nucleotide sequence of
XX the product. Also described is an alternative method (M2) for determining
XX a bacterium species comprising: (a) providing a specimen or a sample
XX having a template; (b) providing a pair of primers selected from: (i) a
XX first forward primer having consecutive bases of an AFB-f comprising any
XX of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
XX or variations and a first reverse primer having consecutive bases of an
XX AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
XX or their fragments or variations, (ii) a second forward primer having
XX consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
XX bp (AEA22489-AEA22516) or their fragments or variations and a second
XX reverse primer having consecutive bases of an UB-r comprising any of the
XX 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
XX variations, or (iii) a first forward primer having consecutive bases of
XX an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
XX second reverse primer having consecutive bases of an UB-r of AEA22517-
XX AEA22544 or their fragments or variations; (c) the specimen; and (d)
XX comparing the product from the specimen with a nucleotide sequence from a
XX database to determine the bacterium species present in the specimen. The
XX methods are useful for determining a bacterium species. The present
XX sequence represents a Mycobacterium kubicae 16S rRNA nucleotide sequence,
XX which is used in the exemplification of the present invention.
XX
XX Sequence 1321 BP; 287 A; 314 C; 457 G; 263 T; 0 U; 0 Other;
XX
XX Query Match 72.7%; Score 16; DB 14; Length 1321;
XX Best Local Similarity 100.0%; Pred. No. 5.9e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1 GTCGACGGAAGGCC 16
Db ||| ||| ||| ||| ||| |||
18 GTCGACGGAAGGCC 33

RESULT 92
ADO85868/c
XX ID ADO85868 standard; DNA; 1344 BP.
XX AC ADO85868;
XX
XX 29-JUL-2004 (first entry)
XX
XX Gordonia sp. bacterium 16S rDNA.
XX
XX microorganism; Gordonia genus; gram-positive bacillus; catalase;
XX nitrate reduction; alkali phosphatase; beta-galactosidase;
XX pyrazinamidase; pyrolidonyl allyl amidase; beta-glucuronidase;
XX alpha-glucosidase; urease; gelatin-liquefaction; esculin; glucose;
XX ribose; GR-004 strain; FERM P-18806;
XX cyclic hydrocarbon degradation agent; waste engine oil; 16S rDNA; ds.
XX
XX Gordonia sp.
XX
XX JP2004121068-A.
XX
XX 22-APR-2004.
XX

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XX 01-OCT-2002; 2002JP-00288714.
XX
XX
PR 01-OCT-2002; 2002JP-00288714.
XX
XX (GEIT-) GEITO KK.
XX
XX WPI; 2004-322761/30.
XX
XX Novel microorganism of Gordonia genus having biochemical properties
PT positive for catalase, approximatelyb-galactosidase, nitrate reduction
PT ability, is useful as cyclic hydrocarbon degradation agent in waste-oil
PT treatment.
XX
XX Claim 2; SEQ ID NO 1; 12pp; Japanese.
XX
XX The invention relates to a novel microorganism belonging to the Gordonia
CC genus, a gram-positive bacillus. The novel microorganism having
CC biochemical properties positive for catalase, nitrate reduction ability,
CC alkali phosphatase, and beta-galactosidase, and negative for
CC pyrazinamidase, pyrolidonyl allyl amidase, beta-glucuronidase, alpha-
CC glucosidase, urease, gelatin-liquefaction ability, and esculin, glucose
CC and ribose utilisation ability. The invention further comprises: a GR-004
CC strain of Gordonia sp. having the accession number FERM P-18806; and a
CC cyclic hydrocarbon degradation agent containing the novel microorganism.
CC The Gordonia genus microorganism is useful for processing a cyclic
CC hydrocarbon-containing substance, which involves using the cyclic
CC hydrocarbon degradation agent, where the cyclic hydrocarbon-containing
CC substance is a waste engine oil. The Gordonia genus microorganism is
CC useful as a cyclic hydrocarbon degradation agent for waste-oil treatment.
CC This polynucleotide sequence represents the Gordonia sp. bacterium 16S
CC rDNA of the invention.
XX
XX Sequence 1344 BP; 276 A; 447 C; 315 G; 306 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 12; Length 1344;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGACGGGAAGGCC 16
Db 1295 GTCGACGGGAAGGCC 1280
RESULT 93
AEA22413
ID AEA22413 standard; DNA; 1415 BP.
XX
XX AEA22413;
AC
XX 25-AUG-2005 (first entry)
DT
XX
XX Mycobacterium paraffinicum 16S rRNA sequence SEQ ID NO:14.
DE
XX microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.
KW
XX Mycobacterium paraffinicum.
OS
XX US2005130168-A1.
PN
XX 16-JUN-2005.
XX
XX 31-OCT-2003; 2003US-00697802.
PF
XX 31-OCT-2003; 2003US-00697802.
PR
XX (HANX/) HAN X.
PA (PHAM/) PHAM A S.
XX
XX Han X, Pham AS;
PI
XX WPI; 2005-424597/43.
DR
XX
XX

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PT Determining a bacterium species comprises providing oligonucleotide
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.
XX
XX Disclosure; SEQ ID NO 14; 74pp; English.
XX
XX The invention relates to a method (M1) for determining a bacterium
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)
CC extracting a genomic nucleotide from the bacterium to provide a
CC nucleotide template; (c) annealing a region of a nucleotide template to a
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a
CC complimentary fashion, the primer set designed to provide a product
CC having a predetermined size dictated by a complimentary primer set; (d)
CC amplifying the region of the nucleotide template to produce the product;
CC and (e) determining a species of a bacterium in a nucleotide sequence of
CC the product. Also described is an alternative method (M2) for determining
CC a bacterium species comprising: (a) providing a specimen or a sample
CC having a template; (b) providing a pair of primers selected from: (i) a
CC first forward primer having consecutive bases of an AFB-f comprising any
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments
CC or variations and a first reverse primer having consecutive bases of an
CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)
CC or their fragments or variations, (ii) a second forward primer having
CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21
CC bp (AEA22489-AEA22516) or their fragments or variations and a second
CC reverse primer having consecutive bases of an UB-r comprising any of the
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or
CC variations or (iii) a first forward primer having consecutive bases of
CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a
CC second reverse primer having consecutive bases of an UB-r of AEA22517-
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)
CC comparing the product from the specimen with a nucleotide sequence from a
CC database to determine the bacterium species present in the specimen. The
CC methods are useful for determining a bacterium species. The present
CC sequence represents a Mycobacterium paraffinicum 16S rRNA nucleotide
CC sequence, which is used in the exemplification of the present invention.
XX
XX Sequence 1415 BP; 307 A; 343 C; 480 G; 285 T; 0 U; 0 Other;
SQ
Query Match 72.7%; Score 16; DB 14; Length 1415;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTCGAACGGGAAGGCC 16
Db 19 GTCGAACGGGAAGGCC 34
RESULT 94
AAZ22765
ID AAZ22765 standard; DNA; 1460 BP.
XX
XX AAZ22765;
AC
XX 15-MAR-2000 (first entry)
DT
XX
XX Corynebacterium sp. NK-1 16S rRNA gene.
DE
XX
XX Corynebacterium sp.
KW Seasoning liquor; flavour; vegetable; pickling; salted rice bran paste;
KW microorganism; gamma-dodecalactone; gamma-dodecelactone; lactic acid;
KW propionic acid; 16S rRNA; pickle; ss.
XX
XX Corynebacterium sp.
OS
XX WO9962347-A1.
PN
XX 09-DEC-1999.
PD
XX 28-MAY-1999; 99WO-JP002854.
PF
XX 29-MAY-1998; 98JP-00166226.
PR
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX
XX

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PI Saitoh C, Yashiro A, Tokunaga C, Ozawa K, Yokoi A, Ogata N;  
 XX Ochiai K, Ando K, Katahira H;  
 DR WPI; 2000-062809/05.  
 XX Production of seasoning liquors with the flavor of vegetables pickled in  
 PT salted rice bran.  
 XX  
 XX Disclosure; Page 41-43; 45pp; Japanese.  
 XX The invention relates to a method of producing seasoning liquors with the  
 CC flavour of vegetables pickled in salted rice bran paste by culturing a  
 CC microorganism in a rice bran dispersion to produce gamma-dodecalactone  
 CC and/or gamma-dodecalactone. The microorganism produces lactic acid,  
 CC propionic acid, gamma-dodecalactone and/or gamma-dodecalactone. The  
 CC microorganism is especially a novel strain of *Corynebacterium* (strain NK-  
 CC 1, FERM BP-6329) with properties defined in the specification. This  
 CC sequence represents the 16S rRNA gene from the novel *Corynebacterium*  
 CC strain. The seasoning liquor is used for preparing a salted rice bran  
 CC pickle bed which provides pickles  
 XX  
 SQ Sequence 1460 BP; 320 A; 342 C; 492 G; 305 T; 0 U; 1 Other;  
 Query Match 72.7%; Score 16; DB 3; Length 1460;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCGAACGGAAGGCC 16  
 Db 42 GTCGAACGGAAGGCC 57  
 RESULT 95  
 AEA22415  
 ID AEA22415 standard; DNA; 1462 BP.  
 XX AEA22415;  
 XX 25-AUG-2005 (first entry)  
 DT Mycobacterium szulgai 16S rRNA sequence SEQ ID NO:16.  
 DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX Mycobacterium szulgai.  
 OS US2005130168-A1.  
 PN 16-JUN-2005.  
 PD 31-OCT-2003; 2003US-00697802.  
 PF 31-OCT-2003; 2003US-00697802.  
 PR (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX Han X, Pham AS;  
 XX WPI; 2005-424597/43.  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX Disclosure; SEQ ID NO 16; 74pp; English.  
 XX The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)

CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a *Mycobacterium szulgai* 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1462 BP; 314 A; 350 C; 507 G; 291 T; 0 U; 0 Other;  
 Query Match 72.7%; Score 16; DB 14; Length 1462;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCGAACGGAAGGCC 16  
 Db 24 GTCGAACGGAAGGCC 39  
 RESULT 96  
 AEA22414  
 ID AEA22414 standard; DNA; 1484 BP.  
 XX AEA22414;  
 XX 25-AUG-2005 (first entry)  
 DT Mycobacterium simiae 16S rRNA sequence SEQ ID NO:15.  
 DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX Mycobacterium simiae.  
 OS US2005130168-A1.  
 PN 16-JUN-2005.  
 PD 31-OCT-2003; 2003US-00697802.  
 PF 31-OCT-2003; 2003US-00697802.  
 PR (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX Han X, Pham AS;  
 XX WPI; 2005-424597/43.  
 XX Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX Disclosure; SEQ ID NO 15; 74pp; English.  
 XX The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)

CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complementary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium simiae 16S rRNA nucleotide sequence,  
 CC which is used in the exemplification of the present invention.

XX  
 SQ Sequence 1484 BP; 320 A; 362 C; 509 G; 293 T; 0 U; 0 Other;

Query Match 72.7%; Score 16; DB 14; Length 1484;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCC 16  
 |||||  
 DB 24 GTCGAACGGAAAGGCC 39

## RESULT 97

ADW92517  
 ID ADM92517 standard; DNA; 1517 BP.

XX AC ADM92517;

XX DT 03-JUN-2004 (first entry)

XX DE Gordonia genus Actinomyces DNA sequence SeqID1.

XX KW Gordonia genus; Actinomyces; ammonia; nitrous acid oxidation;  
 KW purifying fresh water; purifying seawater; ayu fish; flatfish; blowfish;  
 KW gold fish; ds.

XX OS Gordonia.

XX PN JP2004081109-A.

XX PD 18-MAR-2004.

XX PF 27-AUG-2002; 2002JP-00247166.

XX PR 27-AUG-2002; 2002JP-00247166.

XX PA (KANM-) KANMONKAI KK.

XX DR WPI; 2004-233309/22.

XX PT Gordonia genus Actinomyces for purifying fresh water and seawater useful  
 PT in raising ayu fish, flatfish, blowfish and gold fish, has ammonia  
 PT utilizing ability and nitrous acid oxidation ability.

XX PS Disclosure; SEQ ID NO 1; 16pp; Japanese.

XX CC This invention relates to a novel Gordonia genus Actinomyces which has

CC ammonia utilizing ability and nitrous acid oxidation ability. The  
 CC invention may be useful for purifying fresh water and seawater, of  
 CC particular use in raising ayu fish, flatfish, blowfish and gold fish. The  
 CC Gordonia genus actinomyces effectively suppresses concentration of  
 CC ammonia and nitrous acid in fresh water and seawater, and provides  
 CC purified water that is favourable for raising fishes.

SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;

Query Match 72.7%; Score 16; DB 12; Length 1517;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCC 16  
 |||||  
 DB 57 GTCGAACGGAAAGGCC 72

## RESULT 98

AD071823  
 ID AD071823 standard; DNA; 1517 BP.

XX AC AD071823;

XX DT 15-JUL-2004 (first entry)

XX DE DNA of RNA isolated from Gordonia sp. Kammonkai-1129 SeqID 1.

XX KW astaxanthin; canthaxanthine; microbial; livestock fodder; fish breeding;  
 KW ds.

XX OS Gordonia sp.

XX PN JP2004089015-A.

XX PD 25-MAR-2004.

XX PF 29-AUG-2002; 2002JP-00251165.

XX PR 29-AUG-2002; 2002JP-00251165.

XX PA (KANM-) KANMONKAI KK.

XX DR WPI; 2004-253025/24.

XX PT Production of astaxanthin and canthaxanthine useful as fodder and feed  
 PT for livestock, domestic fowl and fish, involves cultivating Actinomyces  
 PT belonging to Gordonia genus.

XX PS Disclosure; SEQ ID NO 1; 13pp; Japanese.

XX CC This invention relates to a novel method for producing astaxanthin and  
 CC canthaxanthine. Specifically, it refers to the cultivation of Actinomyces  
 CC microbial cells belonging to the Gordonia genus using a fresh water or  
 CC sea water mineral nutrition containing culture medium. The present  
 CC invention describes producing astaxanthin and canthaxanthine for use as a  
 CC fodder for livestock and domestic fowl, as well as a feed for fish  
 CC breeding. The production method uses natural products and is efficient at  
 CC a low cost. This polynucleotide sequence is a DNA copy of RNA isolated  
 CC from the Gordonia sp. Kammonkai-1129 microorganism of the invention.

SQ Sequence 1517 BP; 334 A; 363 C; 515 G; 304 T; 0 U; 1 Other;

Query Match 72.7%; Score 16; DB 12; Length 1517;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCC 16  
 |||||  
 DB 57 GTCGAACGGAAAGGCC 72

## RESULT 99



AEA22407  
 ID AEA22407 standard; DNA; 1527 BP.  
 XX AEA22407;  
 AC AEA22407;  
 XX 25-AUG-2005 (first entry)  
 DT  
 DE Mycobacterium heckeshornense 16S rRNA sequence SEQ ID NO:8.  
 KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX Mycobacterium heckeshornense.  
 OS  
 XX US2005130168-A1.  
 PN  
 XX 16-JUN-2005.  
 PD  
 XX 31-OCT-2003; 2003US-00697802.  
 PF  
 XX 31-OCT-2003; 2003US-00697802.  
 PR  
 XX (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 XX Han X, Pham AS;  
 PI  
 XX WPI; 2005-424597/43.  
 DR  
 XX  
 PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 PT  
 PS Disclosure; SEQ ID NO 8; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complementary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations; and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations; (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations; and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC variations; or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations; and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium heckeshornense 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1527 BP; 325 A; 365 C; 534 G; 303 T; 0 U; 0 Other;  
 Query Match 72.7%; Score 16; DB 14; Length 1527;  
 Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTCGACGGAAGGCC 16  
 Db 48 GTCGACGGAAGGCC 63

RESULT 100  
 AAD11264  
 ID AAD11264 standard; DNA; 32 BP.  
 XX AAD11264;  
 AC AAD11264;  
 XX 24-SEP-2001 (first entry)  
 DT  
 DE Mycobacterium 16S rRNA amplifying primer #8.  
 KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;  
 XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.  
 OS  
 XX Mycobacterium sp.  
 PN WO200144510-A2.  
 XX 21-JUN-2001.  
 PD  
 XX 17-DEC-1999; 99WO-US030346.  
 PF  
 XX 17-DEC-1999; 99WO-US030346.  
 PR  
 XX (GENP-) GEN-PROBE INC.  
 PA (INMR ) BIOMERIEUX SA.  
 XX  
 XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 PI  
 XX WPI; 2001-398170/42.  
 DR  
 XX  
 PT Detecting Mycobacterium species, involves in vitro amplification of 16S  
 PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using  
 PT specific primers, and detecting the amplified nucleic acid.  
 XX  
 PS Claim 1; Page 35; 44pp; English.  
 XX  
 CC The invention relates to a method of detecting Mycobacterium species,  
 CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA  
 CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture  
 CC comprising a polymerase, and at least two primers, and then detecting the  
 CC amplified nucleic acid. The method is relatively simple and useful for  
 CC detecting the presence of various Mycobacterium species in a biological  
 CC sample, and thus important for diagnosis of infections resulting from  
 CC them. The method is especially important for screening opportunistic  
 CC infections caused by M. tuberculosis or a Mycobacterium other than  
 CC tuberculosis (MOTT). The present sequence is a PCR primer used for  
 CC amplifying Mycobacterium 16S rRNA  
 XX  
 SQ Sequence 32 BP; 10 A; 6 C; 10 G; 6 T; 0 U; 0 Other;  
 Query Match 71.8%; Score 15.8; DB 4; Length 32;  
 Best Local Similarity 89.5%; Pred. No. 5e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GTCGACGGAAGGCCCTTT 19  
 Db 5 GTCGACGGAAGGCTCTCT 23

Search completed: May 19, 2006, 04:19:01  
 Job time : 266.361 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1471.35 Seconds  
(without alignments)  
836.120 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacggaaggccttcgg 22

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 48236798 segs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

EST.\*

1: gb\_est1.\*

2: gb\_est3.\*

3: gb\_est4.\*

4: gb\_est5.\*

5: gb\_est6.\*

6: gb\_est7.\*

7: gb\_est8.\*

8: gb\_est9.\*

9: gb\_est10.\*

10: gb\_est11.\*

11: gb\_est12.\*

12: gb\_est13.\*

13: gb\_est14.\*

14: gb\_est15.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	18.8	85.5	312	7	BB241896
c 2	18.8	85.5	657	8	BB241896
c 3	18.4	83.6	735	5	CF882404
c 4	18.4	83.6	788	4	CB908942
c 5	17.8	80.9	452	4	BY275654
c 6	17.8	80.9	910	9	DN561788
c 7	17.8	80.9	967	13	CL447050
c 8	17.8	80.9	1205	11	BZ552660
c 9	17.8	80.9	1242	11	BZ559026
c 10	17.4	79.1	316	4	CB603496
c 11	17.4	79.1	828	7	BF240426
c 12	17.2	78.2	247	1	AV314699
c 13	17.2	78.2	305	7	BF172476
c 14	17.2	78.2	446	5	CK234849
c 15	17.2	78.2	451	6	CNS0096P
c 16	17.2	78.2	461	9	DR323178
c 17	17.2	78.2	515	3	BM649944
c 18	17.2	78.2	538	1	AL910651
c 19	17.2	78.2	563	3	BU609865

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DY61640 ZO\_E8000  
CF722314 CCAGS66TR  
CR077081 Reverse S  
DT758502 EST119235  
CZ520644 GWW2-67J1  
DT803768 127434557  
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AL287640 Tetraodon  
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BF982698 602305084  
BE195630 HVSMBA008  
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AL186707 Tetraodon  
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14 BG538412  
15 CC939630  
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17 DT685074  
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19 BX542565  
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38 BF257478  
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45 BH794488  
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74 BW530083

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727 8  
803 3  
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625 11  
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822 5  
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927 10  
927 10  
930 13  
946 10  
958 14  
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305 8  
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747 2  
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883 14  
944 8  
1124 12  
1173 9  
1330 11  
1370 10  
1462 9  
182 2  
267 5  
288 5  
294 4  
298 3  
315 2  
339 8  
346 10  
370 13  
379 1  
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399 7  
431 12  
431 4

93	16.2	73.6	492	1	AA640643	AA640643 nr22c11.r	166	16.2	73.6	922	3	BQ888316	BQ888316
	16.2	73.6	498	14	DU596062	DU596062 OO_Ba009	c 167	16.2	73.6	924	5	CK290199	CK290199
c 95	16.2	73.6	520	1	AA798556	AA798556 vx75H03.r	c 169	16.2	73.6	925	12	CC620929	CC620929
c 96	16.2	73.6	521	11	BZ543563	BZ543563 OGAD15TC	c 168	16.2	73.6	927	14	DU793027	DU793027
c 97	16.2	73.6	537	9	CK608591	CK608591 ANR1_39_B	c 170	16.2	73.6	935	5	CK282064	CK282064
c 98	16.2	73.6	548	4	CB826166	CB826166 rw22a03.Y	c 171	16.2	73.6	938	5	CK282065	CK282065
c 99	16.2	73.6	565	7	AV822903	AV822903 AV822903	c 172	16.2	73.6	940	12	CG145299	CG145299
c 100	16.2	73.6	569	13	CW966724	CW966724 ATAA-aab2	c 173	16.2	73.6	942	5	CK296945	CK296945
c 101	16.2	73.6	594	8	CN061365	CN061365 Ag2_P30.P	c 174	16.2	73.6	945	12	CC712360	CC712360
c 102	16.2	73.6	605	3	BM622761	BM622761 170006874	c 175	16.2	73.6	949	12	CC678267	CC678267
c 103	16.2	73.6	622	2	BM327318	BM327318 PIC1_12_A	c 176	16.2	73.6	954	7	BE727405	BE727405
c 104	16.2	73.6	625	4	BX620074	BX620074 BX620074	c 177	16.2	73.6	955	12	CG142098	CG142098
c 105	16.2	73.6	627	5	CK282937	CK282937 EST745659	c 178	16.2	73.6	962	5	CK294576	CK294576
c 106	16.2	73.6	630	5	CK282063	CK282063 EST744785	c 179	16.2	73.6	969	5	CK293763	CK293763
c 107	16.2	73.6	632	2	BG927981	BG927981 HNC67-1-B	c 180	16.2	73.6	971	3	BQ713233	BQ713233
c 108	16.2	73.6	640	13	CW074031	CW074031 104_342.1	c 181	16.2	73.6	978	5	CK298679	CK298679
c 109	16.2	73.6	643	14	AG078845	AG078845 Pan_crogl	c 182	16.2	73.6	994	12	CC620945	CC620945
c 110	16.2	73.6	654	12	CE016451	CE016451 tigr-gss-	c 183	16.2	73.6	1003	5	CK282938	CK282938
c 111	16.2	73.6	659	1	AA543680	AA543680 v183c06.r	c 184	16.2	73.6	1006	9	DR139593	DR139593
c 112	16.2	73.6	659	4	CA590992	CA590992 hab333510.r	c 185	16.2	73.6	1009	12	CC712366	CC712366
c 113	16.2	73.6	661	12	BZ688362	BZ688362 OGAD75TC	c 186	16.2	73.6	1018	14	DU741222	DU741222
c 114	16.2	73.6	665	4	BG747224	BG747224 BY747224	c 187	16.2	73.6	1039	7	BE036789	BE036789
c 115	16.2	73.6	679	2	BG498953	BG498953 602544616	c 188	16.2	73.6	1115	2	BF0716050	BF0716050
c 116	16.2	73.6	681	13	CZ139111	CZ139111 OA_BBa003	c 189	16.2	73.6	1132	9	DR141636	DR141636
c 117	16.2	73.6	686	5	CK752412	CK752412 atr02-11m	c 190	16.2	73.6	1160	14	CNS06785	CNS06785
c 118	16.2	73.6	695	3	BM620783	BM620783 170006874	c 191	16.2	73.6	1242	13	CL645653	CL645653
c 119	16.2	73.6	698	4	CB426182	CB426182 601338_MA	c 192	16.2	73.6	1289	14	AG393690	AG393690
c 120	16.2	73.6	698	12	CC518953	CC518953 CH240_365	c 193	16.2	73.6	1360	10	DU782232	DU782232
c 121	16.2	73.6	702	5	CF896860	CF896860 EST761394	c 194	16.2	73.6	1414	10	DT967460	DT967460
c 122	16.2	73.6	708	5	CF868740	CF868740 tric016xe	c 195	16.2	73.6	1421	10	DT967242	DT967242
c 123	16.2	73.6	710	12	CG693604	CG693604 OGAA065TH	c 196	16	72.7	268	2	BF851999	BF851999
c 124	16.2	73.6	722	5	CK290200	CK290200 EST752922	c 197	16	72.7	360	12	CG153371	CG153371
c 125	16.2	73.6	726	8	CK312674	CK312674 JGI_XZT86	c 198	16	72.7	476	11	AZ737267	AZ737267
c 126	16.2	73.6	727	12	CG078011	CG078011 PU1D25TD	c 199	16	72.7	590	7	AW850543	AW850543
c 127	16.2	73.6	728	14	CT146916	CT146916 Sus_scriof	c 200	16	72.7	650	8	CN204419	CN204419
c 128	16.2	73.6	743	1	AV384319	AV384319 AV384319	c 201	16	72.7	663	10	DR891379	DR891379
c 129	16.2	73.6	751	5	CK282940	CK282940 EST745662	c 202	16	72.7	711	9	CK793255	CK793255
c 130	16.2	73.6	759	5	CK282066	CK282066 EST744788	c 203	16	72.7	736	9	CK798411	CK798411
c 131	16.2	73.6	760	5	CK282066	CK282066 EST744788	c 204	16	72.7	802	7	BE532564	BE532564
c 132	16.2	73.6	763	12	CC684169	CC684169 OGWD19TV	c 205	16	72.7	803	9	CK797048	CK797048
c 133	16.2	73.6	764	4	CB898835	CB898835 tric016xe	c 206	16	72.7	829	9	CK815303	CK815303
c 134	16.2	73.6	769	5	CF714016	CF714016 CCAB383TR	c 207	16	72.7	853	9	CK815302	CK815302
c 135	16.2	73.6	770	3	BP157969	BP157969 BP157969	c 208	16	72.7	874	8	CO365133	CO365133
c 136	16.2	73.6	771	13	CL208387	CL208387 ZMMBB056	c 209	16	72.7	885	8	CN201712	CN201712
c 137	16.2	73.6	781	11	BZ411392	BZ411392 OGAA7272M	c 210	16	72.7	1112	9	DR146839	DR146839
c 138	16.2	73.6	784	12	CC579325	CC579325 CH240_458	c 211	16	72.7	1136	9	DN695496	DN695496
c 139	16.2	73.6	787	12	CG240876	CG240876 OG2BE70TV	c 212	16	72.7	1390	10	DT995972	DT995972
c 140	16.2	73.6	791	5	CF712651	CF712651 CCAA575TR	c 213	15.8	71.8	137	12	CG617366	CG617366
c 141	16.2	73.6	802	5	CF681782	CF681782 CCAI622TR	c 214	15.8	71.8	169	3	BM633199	BM633199
c 142	16.2	73.6	813	11	BZ408304	BZ408304 OGAAW94TM	c 215	15.8	71.8	172	4	CA330592	CA330592
c 143	16.2	73.6	822	11	BZ513472	BZ513472 BOMQ437F	c 216	15.8	71.8	184	9	DN102120	DN102120
c 144	16.2	73.6	825	12	CC848875	CC848875 NDL_12167	c 217	15.8	71.8	225	10	DT929107	DT929107
c 145	16.2	73.6	835	12	CG191642	CG191642 PUFMR44TB	c 218	15.8	71.8	255	8	CV341801	CV341801
c 146	16.2	73.6	843	11	BH899332	BH899332 Cts00399	c 219	15.8	71.8	256	8	CV341780	CV341780
c 147	16.2	73.6	845	4	BM979961	BM979961 BM979961	c 220	15.8	71.8	262	1	AA642644	AA642644
c 148	16.2	73.6	855	3	BU239599	BU239599 603321930	c 221	15.8	71.8	263	7	BB276884	BB276884
c 149	16.2	73.6	858	12	CG240871	CG240871 OG2BE70TH	c 222	15.8	71.8	268	7	BB586302	BB586302
c 150	16.2	73.6	861	5	CK291891	CK291891 EST754605	c 223	15.8	71.8	273	13	CL211057	CL211057
c 151	16.2	73.6	861	12	CG191643	CG191643 PUFMR44TD	c 224	15.8	71.8	279	7	BB528177	BB528177
c 152	16.2	73.6	863	5	CK298397	CK298397 EST751119	c 225	15.8	71.8	292	4	CB710003	CB710003
c 153	16.2	73.6	870	13	CZ248423	CZ248423 ATAA-aad1	c 226	15.8	71.8	302	12	BZ866870	BZ866870
c 154	16.2	73.6	876	10	DV607221	DV607221 EST121021	c 227	15.8	71.8	308	7	BF451770	BF451770
c 155	16.2	73.6	882	3	BQ223234	BQ223234 AGENCOURT	c 228	15.8	71.8	316	1	AV304782	AV304782
c 156	16.2	73.6	882	5	CK285697	CK285697 EST748419	c 229	15.8	71.8	325	11	AZ773748	AZ773748
c 157	16.2	73.6	889	5	CF709327	CF709327 CCAI838TR	c 230	15.8	71.8	331	4	BY343361	BY343361
c 158	16.2	73.6	898	7	BF570603	BF570603 602075547	c 231	15.8	71.8	335	4	BY335795	BY335795
c 159	16.2	73.6	906	14	DU746898	DU746898 ASNC3551.	c 232	15.8	71.8	335	10	DT901979	DT901979
c 160	16.2	73.6	912	14	DU790219	DU790219 APK33518.	c 233	15.8	71.8	337	7	BB846888	BB846888
c 161	16.2	73.6	913	12	CG222182	CG222182 OG3AS75TV	c 234	15.8	71.8	338	4	BY103528	BY103528
c 162	16.2	73.6	914	12	CG222182	CG222182 OGLBS14TH	c 235	15.8	71.8	342	4	BY193164	BY193164
c 163	16.2	73.6	915	5	CK295834	CK295834 EST758548	c 236	15.8	71.8	363	4	BY202264	BY202264
c 164	16.2	73.6	919	5	CD379805	CD379805 PTWM04974	c 237	15.8	71.8	369	4	BY212596	BY212596
c 165	16.2	73.6	919	5	CK282939	CK282939 EST745661	c 238	15.8	71.8	370	4	BY222901	BY222901

BB241896.1	GI:8934642	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 312)	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Konno,H., et al.)	Unpublished (2000)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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BB241896.1	GI:8934642	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 312)	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Konno,H., et al.)	Unpublished (2000)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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BB241896.1	GI:8934642	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 312)	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Konno,H., et al.)	Unpublished (2000)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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BB241896.1	GI:8934642	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 312)	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Konno,H., et al.)	Unpublished (2000)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT		
BB241896.1	GI:8934642	EST.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 312)	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayateu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watanishi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.	RIKEN Mouse ESTs (Konno,H., et al.)	Unpublished (2000)	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsuunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.rtc.riken.go

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ORIGIN
Query Match      85.5%; Score 18.8; DB 7; Length 312;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2
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LOCUS Tor9226 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
DEFINITION
ACCESSION CN208729.1 GI:46905460
VERSION /mol_type="mRNA"
KEYWORDS /strain="QM6a"
SOURCE /db_xref="taxon:51453"
ORGANISM /clone="tric086xml6"
/dev_stage="mycelia"
/clone_lib="T:reesei mycelial culture, Version 6 October 2003"

REFERENCE
1 (bases 1 to 657)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Dicranidae; Pottiaceae; Tortula.
AUTHORS Oliver,M.J., Dowd,S.E., Zaragosa,J., Mauget,S.A. and Payton,P.R.
TITLE The rehydration transcriptome of the desiccation-tolerant bryophyte
Tortula ruralis: transcript classification and analysis
JOURNAL BMC Genomics 5 (1), 89 (2004)
PUBMED 15346486
COMMENT Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St. Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbf.ars.usda.gov
PCR Primers
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BACKWARD: CAGGAACAGCTATGAC.
Location/Qualifiers
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FEATURES
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Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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243 GTCGACGGAAGGCCTTTCGG 264

RESULT 3
CF882404      735 bp mRNA linear EST 31-OCT-2003
LOCUS triC086xml6.b1 T.reesei mycelial culture, Version 6 October 2003
DEFINITION Hypocrea jecorina cDNA clone tric086xml6, mRNA sequence.
ACCESSION CF882404.1 GI:38137086
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SOURCE /db_xref="taxon:51453"
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REFERENCE
1 (bases 1 to 735)
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
AUTHORS Diener,S.E., Dunn-Coleman,N., Foreman,P., Houfek,T.D.,
Teunissen,P.J.M., van Solingen,P., Dankmeyer,L., Mitchell,T.K.,
Ward,M. and Dean,R.A.
TITLE Characterization of the protein processing and secretion pathways
in a comprehensive set of expressed sequence tags from Trichoderma
reesei
JOURNAL FEMS Microbiol. Lett. 230 (2), 275-282 (2004)
PUBMED 14757250
COMMENT Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: LT-F1 primer.
Location/Qualifiers
1..735
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58 GTCGAACGGAACGCTTTC 77

RESULT 4
CB908942      788 bp mRNA linear EST 02-JUL-2003
LOCUS triC086xml6 T.reesei mycelial culture, Version 3 april Hypocrea
DEFINITION jecorina cDNA clone tric086xml6, mRNA sequence.
ACCESSION CB908942
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REFERENCE
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
AUTHORS Foreman,P.K., Brown,D.E., Dankmeyer,L., Dean,R., Diener,S.,
Dunn-Coleman,N.S., Goedegebuur,F., Houfek,T.D., England,G.J.,
Kelley,A.S., Meerman,H.J., Mitchell,T., Mitchinson,C.,
Olivares,H.A., Teunissen,P.J., Yao,J. and Ward,M.
TITLE Transcriptional regulation of biomass-degrading enzymes in the
filamentous fungus Trichoderma reesei
J. Biol. Chem. 278 (34), 31988-31997 (2003)
PUBMED 12788920
COMMENT Contact: Pamela K. Foreman
Genencor Intl.
925 Page Mill Road, Palo Alto, CA 94304, USA
Tel: (650) 846-7635
Fax: (650) 621-7817
Email: pforeman@genencor.com
Seq primer: LT-F1 primer.
Location/Qualifiers
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Best Local Similarity 95.0%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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  cDNA clone K430314L24 5', mRNA sequence.
ACCESSION
  BY275654
VERSION
  BY275654.1 GI:26465991
KEYWORDS
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SOURCE
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ORGANISM
  Mus musculus
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muroidea; Muridae; Murinae; Mus.
  1 (bases 1 to 452)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, R., Saito, R., Suzuki, H., Yananaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Buit, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawai, J., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
12466851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Laboratory for Neuronal Circuit Development Brain Science Institute
RIKEN 2-1 Hiroseawa, Wako-shi, Saitama 351-0198 Japan ) whose
assistance we gratefully acknowledge. Please visit our web site
(http://genome.gsc.riken.go.jp) for further details.
FEATURES
source
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RESULT 6
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ACCESSION
  DN561788
VERSION
  DN561788.1 GI:61120827
KEYWORDS
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SOURCE
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ORGANISM
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  Echinoidea; Euechinoidea; Echinacea; Echinoida;
  Strongylocentrotidae; Strongylocentrotus.
  1 (bases 1 to 910)
Zhu, X., Mahairas, G., Illies, M.R., Cameron, R.A., Davidson, E.H. and
Ettensohn, C.A.
A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
Development 128 (13), 2615-2627 (2001)
11493577
Contact: Erica Sodergren
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-7676
Fax: 713-798-6977
Email: ericas@bcm.tmc.edu
NCBI Trace Archive: 486682679

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CL447050
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CL447050
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VERSION
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade: Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 967)
REFERENCE
AUTHORS
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE
Sequencing of the maize genome at PGIR (2003c)
JOURNAL
Unpublished (2003)
COMMENT
Contact: Bharti.A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 83.
FEATURES
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Query Match      80.9%;   Score 17.8;   DB 13;   Length 967;
Best Local Similarity 90.5%;   Pred. No. 6.8e+02;
Matches 19;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      2  TCGAACGGAAGGCCTTTCG 22
      | ||||| ||||| |||||
Db      791  GGCGAAGCGAAAGCCTTTCG 811

Insert Length: 1750   Std Error: 0.25
Plate: 102   row: A   column: 16.
FEATURES
    source
        1..910
            /organism="Strongylocentrotus purpuratus"
            /mol_type="mRNA"
            /db_xref="taxon:7668"
            /clone="PMCSRP2-102A16"
            /tissue_type="embryo"
            /cell_type="primary mesenchyme cells"
            /lab_host="E.coli"
            /clone_lib="Sea Urchin primary mesenchyme cell cDNA
            library"
            /notes="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
            dt priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match      80.9%;   Score 17.8;   DB 9;   Length 910;
Best Local Similarity 90.5%;   Pred. No. 6.8e+02;
Matches 19;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      1  GTCGACGGAAAGCCTTTCG 21
      | ||||| ||||| |||||
Db      791  GGCGAAGCGAAAGCCTTTCG 811

RESULT 8
BZ552660
LOCUS
DEFINITION
pacal-60_3757.x1 pacal-60 Pseudomonas aeruginosa genomic clone
pacal-60_3757, genomic survey sequence.
ACCESSION
BZ552660
VERSION
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1205)
REFERENCE
AUTHORS
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL
J. Bacteriol. (2002) In press
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.
FEATURES
    source
        1..1205
            /organism="Pseudomonas aeruginosa"
            /mol_type="genomic DNA"
            /strain="1-60"
            /db_xref="taxon:287"
            /clone="pacal-60_3757"
            /clone_lib="pacal-60"
            /notes="clinical isolate 1-60 Whole genomic shotgun
            library."

ORIGIN
Query Match      80.9%;   Score 17.8;   DB 11;   Length 1205;
Best Local Similarity 90.5%;   Pred. No. 7.1e+02;
Matches 19;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

QY      2  TCGAACGGAAGCCTTTCG 22
      | ||||| ||||| |||||
Db      741  TCGACCGGAAGACCTTTCG 761

RESULT 9
BZ559026
LOCUS
DEFINITION
pacs2-164_1210.s2 pacs2-164 Pseudomonas aeruginosa genomic clone
pacs2-164_1210, genomic survey sequence.
ACCESSION
BZ559026
VERSION
KEYWORDS
SOURCE
ORGANISM
Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1242)
REFERENCE
AUTHORS
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
JOURNAL
J. Bacteriol. (2002) In press
COMMENT
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954

```



Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.

# FEATURES

source  
Location/Qualifiers  
1. 1242  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="2-164"  
/db\_xref="taxon:287"  
/clone="pacs2-164 1210"  
/clone\_lib="pacs2-164"  
/note="Clinical isolate 2-164 whole genomic shotgun library."

## ORIGIN

Query Match 80.9%; Score 17.8; DB 11; Length 1242;  
Best Local Similarity 90.5%; Pred. No. 7.1e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCCG 22  
||||| ||||| ||||| ||||| |||||  
Db 910 TCGAACGGAAGGCGCTTTCCG 930

## RESULT 10

CB603496 316 bp mRNA linear EST 16-MAY-2003  
LOCUS L843 Late-oocyst subtraction library Anopheles stephensi/Plasmodium  
DEFINITION berghei mixed EST library cDNA clone L843, mRNA sequence.

ACCESSION CB603496  
VERSION CB603496.1 GI:29543286

## KEYWORDS

SOURCE Anopheles stephensi/Plasmodium berghei mixed EST library

## ORGANISM

Eukaryota; mixed EST libraries.

## REFERENCE

1 (bases 1 to 316)  
Srinivasan, P., Eappen, A.G., Ghosh, A.K., Valenzuela, J.,  
Ribeiro, J.M.C., Dimopoulos, G., Kafatos, F., Adams, J., Fujioka, H. and  
Jacobs-Lorena, M.

## AUTHORS

Analysis of the Plasmodium and Anopheles transcriptomes during  
oocyst differentiation

## JOURNAL

PUBMED J. Biol. Chem. 279 (7), 5581-5587 (2004)

## COMMENT

Contact: Srinivasan, P., Jacobs-Lorena, M  
Case Western Reserve University  
10900 Euclid Ave., 647 B., Biomedical Research Building., Dept of  
Genetics., Cleveland, OH 44106, USA

Tel: 216-368-2790

Fax: 216-368-3432

Email: sxp82@cwru.edu.

Location/Qualifiers

## FEATURES

source  
1. 316  
/organism="Anopheles stephensi/Plasmodium berghei mixed  
EST library"

/mol\_type="mRNA"

/db\_xref="taxon:224741"

/clone="L843"

/tissue\_type="Midgut"

/dev\_stage="Oocyst"

/clone\_lib="Late-oocyst subtraction library"

/note="Vector: pGEMT-easy; Site 1: EcoRI; Site 2: EcoRI;  
P.berghei ANKA 2.34; Enrichment for differentially  
expressed genes during parasite development by subtractive  
hybridization. The library represents A. stephensi and  
P.berghei genes expressed specifically during oocyst  
development (4-6 days after infectious blood meal)."

## ORIGIN

Query Match 79.1%; Score 17.4; DB 4; Length 316;  
Best Local Similarity 94.7%; Pred. No. 9.2e+02;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTT 19

Db 192 GTCGAACGGAAGGCGCTTT 210

## RESULT 11

### LOCUS

### DEFINITION

BF240426 828 bp mRNA linear EST 14-NOV-2000

601905978F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:413899 5',  
mRNA sequence.

### ACCESSION

BF240426

### VERSION

BF240426.1 GI:11154350

### KEYWORDS

EST.

### SOURCE

Homo sapiens (human)

### ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

1 (bases 1 to 828)

### REFERENCE

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straubeberg, Ph.D.

Email: csaps@remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONETECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LUCM1035 row: k column: 20

High quality sequence stop: 497.

## FEATURES

source  
1. 828  
Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:413899"

/tissue\_type="from chronic myelogenous leukemia"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_54"

/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI  
(ggccattatggcc); Double-stranded cDNA was prepared from  
cell line RNA. 5' and 3' adaptors were used in cloning as  
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and  
3' adaptor sequence:  
5'-ATTCTAGCGCGGCGGCACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size  
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA)."

## ORIGIN

Query Match 79.1%; Score 17.4; DB 7; Length 828;

Best Local Similarity 94.7%; Pred. No. 1.1e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTCCG 22

||||| ||||| ||||| ||||| |||||

Db 708 GAACGGAAGGCGCTTTCCG 690

## RESULT 12

### LOCUS

### DEFINITION

AV314699 247 bp mRNA linear EST 08-NOV-1999

AV314699 RIKEN full-length enriched, adult male thymus muscle

cDNA clone 5830420018 3', mRNA sequence.

### ACCESSION

AV314699

### VERSION

AV314699.1 GI:6280117

### KEYWORDS

EST.

### SOURCE

Mus musculus (house mouse)



QY	1	GTCTGAACGGAAAGGCCTTTTCGG	22	ORGANISM
				Phycocystis, Endiandra
				Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 461)  
Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T., Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.  
Features of Arabidopsis genes and genome discovered using full-length cDNAs  
Plant Mol. Biol. 60 (1), 71-87 (2006)  
Contact: Alexandrov NN  
Ceres, Inc  
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA  
Tel: (805) 376-6539  
Fax: (805) 498-1002  
Email: nalexandrov@ceres-inc.com.  
Location/Qualifiers  
1. .461  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/strain="Mixed, WS and Landsberg erecta"  
/db\_xref="taxon:3702"  
/clone="4267"  
/tissue\_type="Mixed floral buds, roots (9:1)"  
/clone\_lib="CERES-148"

ORIGIN  
Query Match 78.2%; Score 17.2; DB 9; Length 461;  
Best Local Similarity 86.4%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
|||||  
Db 333 GTCGACGGTAAAGCGCTTTTCGG 354

RESULT 17  
BM649944/c  
LOCUS  
DEFINITION 17000687370162 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449640428 5', mRNA sequence.  
ACCESSION BM649944  
VERSION BM649944.1 GI:18949455  
SOURCE EST.  
ORGANISM Anopheles gambiae (African malaria mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anophelinae; Anopheles.  
1 (bases 1 to 515)  
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
Celera Anopheles gambiae EST project  
Unpublished (2002)  
Contact: Holt R.A.  
Celera Genomics  
45 W. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: HoltR@celera.com  
Plate: NU01003CY0 row: G column: 18  
Seq primer: M13 Reverse.  
Location/Qualifiers  
1. .515  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449640428"  
/dev\_stage="Adult"  
/lab\_host="DH10b"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="vector: pSport1; Site\_1: SalI; Site\_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen.

FEATURES  
source

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

ORIGIN  
Query Match 78.2%; Score 17.2; DB 9; Length 461;  
Best Local Similarity 86.4%; Pred. No. 1.2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
|||||  
Db 333 GTCGACGGTAAAGCGCTTTTCGG 354

RESULT 18  
AL910651  
LOCUS  
DEFINITION AL910651 PJR-Z1+Z2 Danio rerio cDNA clone 187-C09-2, mRNA sequence.  
ACCESSION AL910651  
VERSION AL910651.1 GI:23175763  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 538)  
Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,J.  
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis  
Genome Res. 13 (3), 455-466 (2003)  
12618376  
Contact: Peng J  
Lab of Functional Genomics  
Institute of Molecular and Cell Biology  
30 Medical Drive, Singapore, 117609, Singapore  
Email: pengjr@imcb.a-star.edu.sg  
Clone requests: info@openbiosystems.com  
Open Biosystems,  
6705 Odyssey Drive, Huntsville, AL 35806.  
Location/Qualifiers  
1. .538  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local wildtype"  
/db\_xref="taxon:7955"  
/clone="187-C09-2"  
/tissue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_lib="PJR-Z1+Z2"

FEATURES  
source

ORIGIN  
Query Match 78.2%; Score 17.2; DB 1; Length 538;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
|||||  
Db 343 GTCGAACGGACAGCGCTTTTCGG 364

RESULT 19  
BU609865/c  
LOCUS  
DEFINITION BU609865 UI-M-DJ2-bwb-b-23-0-UI.r1 NIH BMAP DJ2 Mus musculus cDNA clone  
UI-M-DJ2-bwb-b-23-0-UI 5', mRNA sequence.  
ACCESSION BU609865  
VERSION BU609865.1 GI:23276080  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

ORIGIN  
Query Match 78.2%; Score 17.2; DB 3; Length 515;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
|||||  
Db 95 GTCGAACGGGAGGCCGATCGG 74

RESULT 18  
AL910651  
LOCUS  
DEFINITION AL910651 PJR-Z1+Z2 Danio rerio cDNA clone 187-C09-2, mRNA sequence.  
ACCESSION AL910651  
VERSION AL910651.1 GI:23175763  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 538)  
Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W., Wang,W., Wen,Z. and Peng,J.  
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis  
Genome Res. 13 (3), 455-466 (2003)  
12618376  
Contact: Peng J  
Lab of Functional Genomics  
Institute of Molecular and Cell Biology  
30 Medical Drive, Singapore, 117609, Singapore  
Email: pengjr@imcb.a-star.edu.sg  
Clone requests: info@openbiosystems.com  
Open Biosystems,  
6705 Odyssey Drive, Huntsville, AL 35806.  
Location/Qualifiers  
1. .538  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local wildtype"  
/db\_xref="taxon:7955"  
/clone="187-C09-2"  
/tissue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_lib="PJR-Z1+Z2"

FEATURES  
source

ORIGIN  
Query Match 78.2%; Score 17.2; DB 1; Length 538;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCGCTTTTCGG 22  
|||||  
Db 343 GTCGAACGGACAGCGCTTTTCGG 364

RESULT 19  
BU609865/c  
LOCUS  
DEFINITION BU609865 UI-M-DJ2-bwb-b-23-0-UI.r1 NIH BMAP DJ2 Mus musculus cDNA clone  
UI-M-DJ2-bwb-b-23-0-UI 5', mRNA sequence.  
ACCESSION BU609865  
VERSION BU609865.1 GI:23276080  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 563)  
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
PUBMED 8889548  
COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mst@mail.nih.gov  
Tissue Procurement: Dr. Robin Davison  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
The following repetitive elements were found in this cDNA sequence: 49-84, >AT-richlow\_complexity  
Seq primer: M13 REVERSE.

FEATURES source  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clones="UI-M-DJ2-bwb-b-23-0-UI"  
/tissue\_type="subfornical organ and postrema"  
/dev\_stage="Adult"  
/lab\_hosts="DH10B (Life Technologies) (T1 phage resistant)"  
/clone\_libs="NIH-BMAP\_DJ2"  
/notes="Organ: Brain; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-M-DJ2 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is: GCTACATGAT, subfornical organ and area postrema."

ORIGIN  
Query Match 78.2%; Score 17.2; DB 3; Length 563;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCCG 22  
|||||  
Db 525 GTCAAAAGGAAGGCGCTTTCCG 504

RESULT 20  
AM154744/c  
LOCUS AM154744 Oryzias latipes CAB gastrula Oryzias latipes cDNA clone  
DEFINITION MCF0029J13-MGRbd1, mRNA sequence.  
ACCESSION AM154744  
VERSION AM154744.1 GI:81517022  
KEYWORDS EST.  
SOURCE Oryzias latipes (Japanese medaka)  
ORGANISM Oryzias latipes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE 1 (bases 1 to 618)  
AUTHORS Berger, A., Dohm, J.C., Hennig, S., Sasaki, T., Furutani-Seiki, M., Mitani, H., Shima, A., Lehrach, H., Wittbrodt, J., Kondoh, H., Shimizu, N. and Himmelbauer, H.  
TITLE A UniGene cDNA set for the medaka Oryzias latipes obtained by normalization of embryonic and adult cDNA libraries  
JOURNAL Unpublished (2005)  
COMMENT Contact: Himmelbauer, H  
Department of Vertebrate Genomics  
Max Planck Institute of Molecular Genetics  
Innesstrasse 73, 14195 Berlin, GERMANY  
Genome Center  
Center: Max Planck Institute for Molecular Genetics Center code:  
MPIMG  
Web site: http://www.molgen.mpg.de/  
rodent  
Genome Center  
Center: Keio University, School of Medicine  
Center code: Keio  
Web site: http://www.dmb.med.keio.ac.jp/.

FEATURES source  
Location/Qualifiers  
1..618  
/organism="Oryzias latipes"  
/mol\_type="mRNA"  
/strain="CAB"  
/db\_xref="taxon:8090"  
/clone="McF0029J13-MGRbd1"  
/dev\_stage="gastrula"  
/clone\_libs="Oryzias latipes CAB gastrula"

ORIGIN  
Query Match 78.2%; Score 17.2; DB 1; Length 618;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCCG 22  
|||||  
Db 483 GTCAAAAGGACAGGCGCTTTCCG 462

RESULT 21  
AA754068  
LOCUS AA754068 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa  
DEFINITION (indica cultivar-group) cDNA clone 97GS0781, mRNA sequence.  
ACCESSION AA754068  
VERSION AA754068.1 GI:2800774  
KEYWORDS EST.  
SOURCE Oryza sativa (indica cultivar-group)  
ORGANISM Oryza sativa (indica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 620)  
AUTHORS Nahm, B.H., Kim, J.K., Cheong, J.J., Kim, S.I., Hahn, T.R., Moon, E.P., Kim, W.T., Kim, W.Y., Yang, M.S., Park, R.D., Sohn, U.I., Kang, K.Y., Lee, M.C. and Eun, M.Y.  
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed  
JOURNAL Unpublished (1998)  
COMMENT Contact: Eun M.Y.  
Department of Cytogenetics  
National Inst. of Agri. Sci. and Tech, RDA  
Suwon, Kyunggi-do, Korea  
Tel: 82 331 290 0301  
Fax: 82 331 290 0307  
Email: myeun@sun20.asti.re.kr  
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr  
Seq primer: M13 Reverse Primer.  
Location/Qualifiers  
1..620

/organisms="Oryza sativa (indica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Milyang 23"

/db\_xref="taxon:39946"

/clone="97GS0781"

/tissue\_type="Immature Seed"

/dev\_stage="5 days after pollination"

/lab\_host="E. coli SOLR"

/clone\_lib="Rice Immature Seed Lambda ZAPII cDNA Library"

/notes="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:

XhoI; Directional cDNA library inserted into lambda ZAPII

vector at 5' end with EcoRI and 3' end with Xho I site."

# ORIGIN

Query Match 78.2%; Score 17.2; DB 1; Length 620;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCGG 22

Db 298 GTCGAACGGAAGGCCTTTCGG 319

# RESULT 22

CR532627/c

LOCUS

DEFINITION CR532627 Normalized Anopheles Head (NAH) Library Anopheles gambiae

cDNA clone AGAGL07TR, mRNA sequence.

ACCESSION CR532627

VERSION CR532627.1

SOURCE GI:49931744

KEYWORDS EST.

ORGANISM Anopheles gambiae (African malaria mosquito)

ANopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 646)

REFERENCE Lobo.N.L., Gardner.M., Romans.P. and Collins.F.H.

ANopheles gambiae EST, Center for Tropical Disease Research and

Training

JOURNAL Unpublished (2003)

COMMENT

Contact: Frank H. Collins

Center for Tropical Disease Research and Training

University of Notre Dame

Notre Dame, IN 46556, USA

Tel: 574-631-9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu

Center for Tropical Disease Research and Training

University of Notre Dame, Notre Dame, IN 46556, USA. Tel: 574-631-

9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

# FEATURES

source

1. .646

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/db\_xref="taxon:7165"

/clone="AGAGL07TR"

/lab\_host="E. coli DH10B"

/notes="Vector: p7T3D-PacI; Site\_1: EcoRI (5'end); Site\_2:

NotI (3'end); a directionally cloned and normalized, 4arr

oligo-T primed cDNA library constructed from strain 4arr

adult mosquito heads. Equal numbers of sugar fed males,

sugar fed females and 6, 24 and 48 hr post blood meal

females were used: Bonaldo, Lennon & Soares (1996):

Normalization and Subtraction: Two Approaches To

Facilitate Gene Discovery, Genome Research 6, 791-806.

ESTs sequenced from the M13 reverse priming site reading

from the 5' ends of the cDNAs are indicated by 'R' in the

clone name. ESTs sequenced from the M13 forward priming

site reading from the 3' ends of the cDNAs are indicated  
by 'F' in the clone name."

# ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 646;

Best Local Similarity 86.4%; Pred. No. 1.3e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCGG 22

Db 289 GTCGAACGGAAGGCCTTTCGG 268

# RESULT 23

EX618313/c

LOCUS

DEFINITION EX618313 Normalized Anopheles Head (NAH) Library Anopheles gambiae

cDNA clone AGAE426TR, mRNA sequence.

ACCESSION EX618313

VERSION EX618313.1

KEYWORDS GI:33536740

SOURCE EST.

ORGANISM Anopheles gambiae (African malaria mosquito)

ANopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 649)

REFERENCE Lobo.N.L., Gardner.M., Romans.P. and Collins.F.H.

ANopheles gambiae EST, Center for Tropical Disease Research and

Training

JOURNAL Unpublished (2003)

COMMENT

Contact: Frank H. Collins

Center for Tropical Disease Research and Training

University of Notre Dame

Notre Dame, IN 46556, USA

Tel: 574-631-9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

source

1. .649

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/db\_xref="taxon:7165"

/clone="AGAE426TR"

/lab\_host="E. coli DH10B"

/notes="Vector: p7T3D-PacI; Site\_1: EcoRI (5'end); Site\_2:

NotI (3'end); a directionally cloned and normalized, 4arr

oligo-T primed cDNA library constructed from strain 4arr

adult mosquito heads. Equal numbers of sugar fed males,

sugar fed females and 6, 24 and 48 hr post blood meal

females were used: Bonaldo, Lennon & Soares (1996):

Normalization and Subtraction: Two Approaches To

Facilitate Gene Discovery, Genome Research 6, 791-806.

ESTs sequenced from the M13 reverse priming site reading

from the 5' ends of the cDNAs are indicated by 'R' in the

clone name. ESTs sequenced from the M13 forward priming

site reading from the 3' ends of the cDNAs are indicated

by 'F' in the clone name."

# ORIGIN

Query Match 78.2%; Score 17.2; DB 4; Length 649;

Best Local Similarity 86.4%; Pred. No. 1.3e+03;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTCGG 22

Db 211 GTCGAACGGAAGGCCTTTCGG 190

# RESULT 24

DU818647

LOCUS

DU818647 683 bp DNA linear GSS 13-DEC-2005

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DEFINITION OG_ABa0092L10.r OG_ABa Oryza granulata genomic clone OG_ABa0092L10
3', genomic survey sequence.
ACCESSION DUB18647
VERSION DUB18647.1 GI:83614306
KEYWORDS GSS.
SOURCE Oryza granulata
ORGANISM Oryza granulata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 683)
AUTHORS SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wiersotski,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.
WPAP (Oryza Map Alignment Project) - Purdue University
Unpublished (2004)
JOURNAL
COMMENT Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu
Baecalling by phred version 0.020425.c. This sequence was derived
from the raw sequence read by clipping with Lucy version 1.198.
Bases 111-793 of the raw sequence (length 1048) were retained after
clipping.
Plate: 0092 row: L column: 10
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
FEATURES             Location/Qualifiers
     source           1..683
                     /organism="Oryza granulata"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:110450"
                     /clone="OG_ABa0092L10"
                     /tissue_type="young leaves"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="OG_ABa"
                     /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      78.2%; Score 17.2; DB 14; Length 683;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22
Db 241 GTCGAGCGGTAGGCGCTTCGG 262

RESULT 25
DR370688          684 bp mRNA linear EST 29-JAN-2006
LOCUS 103424 CERES-148 Arabidopsis thaliana cDNA clone 4267 3', mRNA
DEFINITION
sequence.
ACCESSION DR370688
VERSION DR370688.1 GI:86074931
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 684)
REFERENCE 1
AUTHORS Alexandrov,N.N., Troukhan,M.E., Brover,V.V., Tatarinova,T.,
Lu,Y.-P., Flavell,R.B. and Feldmann,K.A.
Features of Arabidopsis genes and genome discovered using
full-length cDNAs
Plant Mol. Biol. 60 (1), 71-87 (2006)
JOURNAL
COMMENT Contact: Alexandrov NN
Ceres, Inc
1535 Rancho Conejo Blvd., Thousand Oaks, CA 91320, USA

```

```

Tel: (805) 376-6539
Fax: (805) 498-1002
Email: nalexandrov@ceres-inc.com.
Location/Qualifiers
FEATURES             source
     source           1..684
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /strain="Mixed, WS and Landsberg erecta"
                     /db_xref="taxon:3702"
                     /clone="4267"
                     /tissue_type="Mixed floral buds, roots (9:1)"
                     /clone_lib="CERES-148"

ORIGIN
Query Match      78.2%; Score 17.2; DB 10; Length 684;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22
Db 224 GTCGACGGAAGGCGCTTCGG 245

RESULT 26
BM622387/c
LOCUS 17000687476225 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449666435 5', mRNA sequence.
ACCESSION BM622387
VERSION BM622387.1 GI:18921898
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 709)
REFERENCE Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,
AUTHORS Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celerix Anopheles gambiae EST project
JOURNAL Unpublished (2002)
COMMENT Contact: Holt R.A.
Celerix Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU01004HMD row: C column: 09
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES             source
     source           1..709
                     /organism="Anopheles gambiae"
                     /mol_type="mRNA"
                     /strain="RSP-ST (Reduced susc. to Permethrin - std.
                     chromosome)"
                     /db_xref="taxon:7165"
                     /clone="19600449666435"
                     /dev_stage="Adult"
                     /lab_host="DH10b"
                     /clone_lib="A.Gam.ad.cDNA1"
                     /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
                     adult mosquitoes (mixed sex) frozen on liquid nitrogen.
                     cDNA inserts >500 bp cloned directionally into pSport 1.
                     Not 1 site is 3'. Clones available through the Malaria
                     Research and Reference Reagent Resource Center
                     (www.malaria.mr4.org)."
```

## ORIGIN

```

Query Match      78.2%; Score 17.2; DB 3; Length 709;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTCGG 22
```

```

Db      290  GTCCAGCGGAGGCCGATCGG 269
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CC605085      724 bp      DNA      linear      GSS 18-JUN-2003
OCWFF25TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZNMBMa0564F02,
genomic_survey_sequence.
ACCESSION      CC605085
VERSION         CC605085.1  GI:31966506
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 724)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWFF25TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
FEATURES             source
    Location/Qualifiers
        1..724
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZNMBMa0564F02"
            /clone_lib="ZM_0.7_1.5_KB"
            /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
            methylation filtered genomic DNA library"

ORIGIN
Query Match      78.2%; Score 17.2; DB 12; Length 724;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GTCCAGCGGAGGCCCTTTCGG 22
      |||||
Db      692  GTCCAGCGGAGGCCATTCGG 713

RESULT 28
Query Match      78.2%; Score 17.2; DB 12; Length 724;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

LOCUS      CR532626
DEFINITION      CR532626 Normalized Anopheles Head (NAH) Library Anopheles gambiae
                cDNA clone AGAGL07TF, mRNA sequence.
ACCESSION      CR532626
VERSION         CR532626.1  GI:49931743
KEYWORDS        EST.
SOURCE          Anopheles gambiae (African malaria mosquito)
ORGANISM        Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Culicidae; Anophelinae; Anopheles.
1 (bases 1 to 727)
Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.
Anopheles gambiae EST, Center for Tropical Disease Research and
Training
Unpublished (2003)
Contact: Frank H. Collins
Center for Tropical Disease Research and Training

Db      290  GTCCAGCGGAGGCCGATCGG 269
|||||
CC605085      724 bp      DNA      linear      GSS 18-JUN-2003
OCWFF25TH_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZNMBMa0564F02,
genomic_survey_sequence.
ACCESSION      CC605085
VERSION         CC605085.1  GI:31966506
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 724)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWFF25TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
FEATURES             source
    Location/Qualifiers
        1..724
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZNMBMa0564F02"
            /clone_lib="ZM_0.7_1.5_KB"
            /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
            methylation filtered genomic DNA library"

ORIGIN
Query Match      78.2%; Score 17.2; DB 8; Length 727;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1  GTCCAGCGGAGGCCCTTTCGG 22
      |||||
Db      439  GTCCAGCGGAGGCCGATCGG 460

RESULT 29
Query Match      78.2%; Score 17.2; DB 8; Length 727;
Best Local Similarity 86.4%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

LOCUS      BU365226
DEFINITION      BU365226 803 bp mRNA linear EST 28-NOV-2002
                603567944F1 CSEQCHN72 Gallus gallus cDNA clone CHEST523g12 5', mRNA
                sequence.
ACCESSION      BU365226
VERSION         BU365226.1  GI:25873227
KEYWORDS        EST.
SOURCE          Gallus gallus (chicken)
ORGANISM        Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 803)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
        1..803
            /organism="Gallus gallus"

FEATURES             source
    Location/Qualifiers

```

University of Notre Dame  
Notre Dame, IN 46556, USA  
Tel: 574-631-9245  
Fax: 574-631-3996  
Email: frank.h.collins.75@nd.edu  
Contact: Frank H. Collins  
Center for Tropical Disease Research and Training  
University of Notre Dame, Notre Dame, IN 46556, USA. Tel: 574-631-9245  
Fax: 574-631-3996  
Email: frank.h.collins.75@nd.edu.  
Location/Qualifiers  
1..727  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7165"  
/clone="AGAGL07TF"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Normalized Anopheles Head (NAH) Library"  
/notes="Vector: pT7T3D-PacI; Site 1: EcoRI (5'end); Site 2:  
NotI (3'end); a directionally cloned and normalized, 4arr  
oligo-T primed cDNA library constructed from strain 4arr  
adult mosquito heads. Equal numbers of sugar fed males,  
sugar fed females and 6, 24 and 48 hr post blood meal  
females were used: Bonaldo, Lennon & Soares (1996):  
Normalization and Subtraction: Two Approaches To  
Facilitate Gene Discovery, Genome Research 6, 791-806.  
ESTs sequenced from the M13 reverse priming site reading  
from the 5' ends of the cDNAs are indicated by 'R' in the  
clone name. ESTs sequenced from the M13 forward priming  
site reading from the 3' ends of the cDNAs are indicated  
by 'F' in the clone name."

FEATURES  
source

ORIGIN

Query Match 78.2%; Score 17.2; DB 8; Length 727;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GTCCAGCGGAGGCCCTTTCGG 22  
|||||  
Db 439 GTCCAGCGGAGGCCGATCGG 460

RESULT 29

Query Match 78.2%; Score 17.2; DB 8; Length 727;  
Best Local Similarity 86.4%; Pred. No. 1.3e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

LOCUS BU365226  
DEFINITION BU365226 803 bp mRNA linear EST 28-NOV-2002  
603567944F1 CSEQCHN72 Gallus gallus cDNA clone CHEST523g12 5', mRNA  
sequence.  
ACCESSION BU365226  
VERSION BU365226.1 GI:25873227  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 803)

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
1..803  
/organism="Gallus gallus"

COMMENT

FEATURES  
source





```

KEYWORDS
SOURCE  Xenopus tropicalis (western clawed frog)
ORGANISM
REFERENCE 1 (bases 1 to 952)
AUTHORS  Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,
Mardis, E. and Wilson, R.
TITLE  A physical map of the xenopus tropicalis genome
JOURNAL  Unpublished (2003)
COMMENT  Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGTGACACTATAG
Class: BAC ends
High quality sequence start: 39
High quality sequence stop: 785.
FEATURES
source
1..952
/organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-104C12"
/sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/notes="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
ORIGIN
Query Match 78.2%; Score 17.2; DB 12; Length 952;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTCGAACGGGAAGGCTTTTCGG 22
|||||
Db 501 GTCCAGGGAATGCTTTTCGG 480
|||||
RESULT 33
BG538412/c
LOCUS BG538412 979 bp mRNA linear EST 03-APR-2001
DEFINITION 602567112F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4691739 5',
mRNA sequence.
ACCESSION BG538412
VERSION BG538412.1 GI:13530645
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE 1 (bases 1 to 979)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC1511 row: 9 column: 04
High quality sequence stop: 658.
FEATURES
source
1..979
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4691739"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/notes="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgcctggcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCGGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
ORIGIN
Query Match 78.2%; Score 17.2; DB 2; Length 979;
Best Local Similarity 86.4%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTCGAACGGGAAGGCTTTTCGG 22
|||||
Db 745 GTCGACGGGAACGCTTTTCGG 724
|||||
RESULT 34
CC939630/c
LOCUS CC939630 299 bp DNA linear GSS 13-AUG-2003
DEFINITION ZMMBBb0239D20.r ZMMBBb Zea mays genomic clone ZMMBBb0239D20 3',
genomic survey sequence.
ACCESSION CC939630
VERSION CC939630.1 GI:33625477
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 299)
AUTHORS Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
and Wing, R.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0239 row: D column: 20
Seq primer: M13r
Class: BAC ends.
FEATURES
source
1..299
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0239D20"
/lab_host="DH10B"
/clone_lib="ZMMBBb"
/notes="Vector: pBelobAC11; Site 1: HindIII; Site 2:
HindIII; Zea mays L. ssp. mays"
ORIGIN
Query Match 76.4%; Score 16.8; DB 12; Length 299;

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Best Local Similarity 90.0%; Pred. No. 1.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTCGG 22
Db 46 CGACGGAAGGCGCTTCGG 27

RESULT 35
CD122074/c
LOCUS
DEFINITION
MEI-0071G-Al60-E04-1.B MEI-0071 Schistosoma mansoni CDNA clone
MEI-0071G-Al60-E04.B, mRNA sequence.
ACCESSION
CD122074
KEYWORDS
CD122074.1 GI:34660126
SOURCE
EST.
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 356)
Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
TITLE
Nat. Genet. 35 (2), 148-157 (2003)
JOURNAL
12973350
PUBMED
Other ESTs: MEI-0071G-Al60-E04-2.B
COMMENT
Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquímica
Instituto de Química - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MEI-0071G-Al60 Row: 4 column: E.
FEATURES
Location/Qualifiers
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/db_xref="taxon:6183"
/clone="MEI-0071G-Al60-E04.B"
/dev_stages="egg"
/lab_host="Mus musculus"
/clone_lib="MEI-0071"
/note="Vector: pGEM T-easy"

ORIGIN
Query Match 76.4%; Score 16.8; DB 4; Length 356;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTC 20
Db 291 GTCGACGGAAGGCGCTGC 272

RESULT 36
DT685074
LOCUS
DEFINITION
MEI-0071G-Al60-E04-1.B MEI-0071 Schistosoma mansoni CDNA clone
MEI-0071G-Al60-E04.B, mRNA sequence.
ACCESSION
CD122074
KEYWORDS
CD122074.1 GI:34660126
SOURCE
EST.
ORGANISM
Schistosoma mansoni
Schistosoma mansoni
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 356)
Verjovski-Almeida,S., DeMarco,R., Martins,E.A.L., Guimaraes,P.E.M.,
Ojopi,E.P.B., Paquola,A.C.M., Piazza,J.P., Nishiyama,M.Y. Jr.,
Coulson,P.S., Dillon,G.P., Farias,L.P., Gregorio,S.P., Ho,P.L.,
Leite,R.A., Malaquias,L.C.C., Marques,R.C.P., Miyasato,P.A.,
Nascimento,A.L.T.O., Ohlweiler,F.P., Reis,E.M., Ribeiro,M.A.,
Sa,R.G., Stukart,G.C., Soares,M.B., Gargioni,C., Kawano,T.,
Rodrigues,V., Madeira,A.M.B.N., Wilson,R.A., Menck,C.F.M.,
Setubal,J.C., Leite,L.C.C. and Dias-Neto,E.
Transcriptome analysis of the acelomate human parasite Schistosoma
mansoni
TITLE
Nat. Genet. 35 (2), 148-157 (2003)
JOURNAL
12973350
PUBMED
Other ESTs: MEI-0071G-Al60-E04-2.B
COMMENT
Contact: Dr. Sergio Verjovski-Almeida
Departamento de Bioquímica
Instituto de Química - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,
Brasil
Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Email: verjo@iq.usp.br
This sequence was derived from the FAPESP Schistosoma mansoni EST
Genome Project. All sequences in the project were assembled and
annotated. This entry and all the assembled sequences can be seen
in the following URL http://bioinfo.iq.usp.br/schisto/
Plate: MEI-0071G-Al60 Row: 4 column: E.
FEATURES
Location/Qualifiers
source
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/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone="MEI-0071G-Al60-E04.B"
/dev_stages="egg"
/lab_host="Mus musculus"
/clone_lib="MEI-0071"
/note="Vector: pGEM T-easy"

ORIGIN
Query Match 76.4%; Score 16.8; DB 4; Length 356;
Best Local Similarity 90.0%; Pred. No. 1.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCGCTTTC 20
Db 291 GTCGACGGAAGGCGCTGC 272

RESULT 37
BH764015
LOCUS
DEFINITION
BMBAC321B12SP6 PSU Brugia malayi Genomic Bac Library 3 Brugia
malayi genomic, genomic survey sequence.
ACCESSION
BH764015
VERSION
BH764015.1 GI:19560990
KEYWORDS
GSS.
SOURCE
Brugia malayi
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 597)
Whitton,C., Daub,J., Quail,M., Hall,N., Foster,J., Ware,J.,
Ganatra,M., Slatko,B., Barrell,B. and Blaxter,M.
A genome sequence survey of the filarial nematode Brugia malayi:
repeats, gene discovery, and comparative genomics
Mol. Biochem. Parasitol. 137 (2), 215-227 (2004)
15383292
PUBMED
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology

DEFINITION
sl3DFA07F02FS027 519296 Tall fescue, Festuca arundinacea Schreb,
Field Stress Festuca arundinacea CDNA, mRNA sequence.
ACCESSION
DT685074
VERSION
DT685074.1 GI:74428899
KEYWORDS
EST.
SOURCE
Festuca arundinacea
Festuca arundinacea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Pooideae; Poaeae; Festuca.
1 (bases 1 to 439)
Mian,M.A.R., Wang,Z.Y., Zhang,Y., Zhang,J., Cheng,X., Chen,L.,
Scott,A.D., Harris,A.R., Gonzales,R.A. and May,G.D.
ESTs from field-stressed tall fescue, Festuca arundinacea Schreb,
shoots
Unpublished (2005)
JOURNAL
Contact: May GD
COMMENT
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 224 6650
Fax: 580 224 6692
Email: gdmay@noble.org.
Location/Qualifiers
source
1..439
/organism="Festuca arundinacea"
/mol_type="mRNA"
/db_xref="taxon:4606"
/tissue_type="Field-grown shoots"
/dev_stage="Various ages"
/clone_lib="Tall fescue, Festuca arundinacea Schreb, Field
Stress"
/note="Vector: Lambda Zap; Shoot tissues were collected
from tall fescue, Festuca arundinacea Schreb, cv. Kentucky
31 planted in field during mid-July 2003. Samples were
harvested on July 11, 15, 18, 20, 21 - 2003 with air
temperature at 35.2C, 35.5C, 37.1C, 38.7C, and 37.1C,
respectively. Entire shoots from two tillers of three
plants were collected on each day. Equal amounts of total
RNA from each of the five samples were pooled together for
mRNA isolation and cDNA library construction."

ORIGIN
Query Match 76.4%; Score 16.8; DB 10; Length 439;
Best Local Similarity 90.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGACGGAAGGCGCTTTCG 21
Db 151 TCGAACTGAAAGGCGCTTCG 170

RESULT 37
BH764015
LOCUS
DEFINITION
BMBAC321B12SP6 PSU Brugia malayi Genomic Bac Library 3 Brugia
malayi genomic, genomic survey sequence.
ACCESSION
BH764015
VERSION
BH764015.1 GI:19560990
KEYWORDS
GSS.
SOURCE
Brugia malayi
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 597)
Whitton,C., Daub,J., Quail,M., Hall,N., Foster,J., Ware,J.,
Ganatra,M., Slatko,B., Barrell,B. and Blaxter,M.
A genome sequence survey of the filarial nematode Brugia malayi:
repeats, gene discovery, and comparative genomics
Mol. Biochem. Parasitol. 137 (2), 215-227 (2004)
15383292
PUBMED
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology

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RESULT 40

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CB378019
LOCUS      CB378019      630 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION rQ06a11.Y1 Heterodera glycines J3 Heterodera glycines cDNA 5'
            similar to WP:CE23823 H24K24.4 RNA-binding protein ;, mRNA
            sequence.
ACCESSION  CB378019
VERSION     CB378019.1  GI:29127315
KEYWORDS   Heterodera glycines
SOURCE     Heterodera glycines
ORGANISM   Heterodera glycines
REFERENCE  1 (bases 1 to 630)
AUTHORS    McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
            Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
            Tsegareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
TITLE      Contact: McCarter JP
JOURNAL    The Washington Univ. Nematode EST Project, 1999
COMMENT    Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This library was generated by cloning cDNAs directionally into
            Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI
            are at the 3'-end). The library was excised [now in pBluescript
            SK(+)] and normalized (Bonaldo et al 1996 Genome Research
            6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu),
            Iowa State University, Plant Pathology Department and Jeff
            McDermott (jpmcderm@iastate.edu).
            Seq primer: T3 from Gibco.
FEATURES   source
            1..630
            Location/Qualifiers
            /organism="Heterodera glycines"
            /mol_type="mRNA"
            /db_xref="taxon:51029"
            /sex="mixed"
            /tissue_type="whole organism"
            /dev_stage="3rd stage juvenile"
            /lab_host="DH10B"
            /clone_lib="Heterodera glycines J3"
            /note="Vector: pBluescript SK+ (Stratagene); Site_1: XhoI;
            Site 2: EcoRI; This library was generated by cloning cDNAs
            directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI
            are at the 5'-end and T7/XhoI are at the 3'-end). The
            library was excised [now in pBluescript SK(+)] and
            normalized (Bonaldo et al 1996 Genome Research 6:791-806).
            Library constructed by Thomas Baum (tbaum@iastate.edu),
            Iowa State University, Plant Pathology Department and Jeff
            McDermott (jpmcderm@iastate.edu)."
ORIGIN
Query Match      76.4%; Score 16.8; DB 4; Length 630;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2   TCGAACGGAAGGCGCTTCG 21
        |||||
Db      512 TCGAACGGAAGGCGCTTTGG 531

RESULT 41
DT727398
LOCUS      DT727398      680 bp      mRNA      linear      EST 13-SEP-2005
DEFINITION EST1161248 Aquilegia cDNA library Aquilegia formosa x Aquilegia
            pubescens cDNA clone ColSF66, mRNA sequence.
ACCESSION  DT727398

```

```

DT727398.1  GI:74509752
EST.
KEYWORDS   Aquilegia formosa x Aquilegia pubescens
SOURCE     Aquilegia formosa x Aquilegia pubescens
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
            Ranunculaceae; Aquilegia.
REFERENCE  1 (bases 1 to 680)
AUTHORS    Hodges,S.A., Rensink,W., Buehl,C.R., Borevitz,J., Kramer,E.,
            Nordborg,M. and Tomkins,J.
            Generation of ESTs from Aquilegia
            Unpublished (2005)
            Other ESTs: EST1161249
            Contact: Scott Hodges
            Department of Ecology, Evolution and Marine Biology
            University of California, Santa Barbara
            Santa Barbara, CA 93106, USA
            Tel: 805 893 7813
            Fax: 805 893 4724
            Email: hodges@lifesci.ucsb.edu
            Seq primer: TTTTGTGTTTTTTTTTTTTTTT (where N = A, G & C).
FEATURES   source
            1..680
            Location/Qualifiers
            /organism="Aquilegia formosa x Aquilegia pubescens"
            /mol_type="mRNA"
            /db_xref="taxon:338618"
            /clone="ColSF66"
            /tissue_type="mixed shoot and floral apical meristems,
            flower buds, leaves and roots"
            /lab_host="DH10B T1 (T1 and T5 phage resistance)"
            /clone_lib="Aquilegia cDNA library"
            /note="Vector: pCMV SPORT6.1; Site 1: EcoRI; Site 2: NotI;
            F2, F3, and F4 lines of Aquilegia formosa x A. pubescens
            were grown from seed in greenhouses at UC Santa Barbara.
            From these plants three sets of tissue were collected: 1)
            Small flower buds (<10 mm) and very young inflorescences
            (71 & 29% by weight respectively), 2) Medium (7-20 mm) and
            large (at or near anthesis) flower buds (65 & 35% by
            weight respectively) and 3) Shoot apical meristems. A
            fourth set of tissue was collected from plants of A.
            formosa. These plants were grown from seed in sand and at
            approximately 1 month root tissue and leaf tissue of
            various developmental stages were collected (84 & 16% by
            weight respectively). Total RNA was extracted from each
            set of tissue and pooled in the following proportions:
            1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled
            total RNA, mRNA was extracted and enriched for full-length
            messages and then normalized with proprietary methods by
            Invitrogen."
ORIGIN
Query Match      76.4%; Score 16.8; DB 10; Length 680;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1   GTCGAACGGAAGGCGCTTTC 20
        |||||
Db      163 GTCGAACGGAATGCGCTTCC 182

RESULT 42
DU601889/c
LOCUS      DU601889
DEFINITION OO_Ba0099F04.r OO_Ba Oryza officinalis genomic clone
            OO_Ba0099F04 3', genomic survey sequence.
ACCESSION  DU601889
VERSION     DU601889.1  GI:77564733
KEYWORDS   GSS.
SOURCE     Oryza officinalis
ORGANISM   Oryza officinalis
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
            clade; Ehrhartoideae; Oryzaceae; Oryza.

```

```

REFERENCE
AUTHORS      1 (bases 1 to 777)
              Kim,H., Collura,K., Missotski,M., Byrne,M., Stum,D., Smart,D.,
              Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
              Wing,R.
TITLE        OWPAP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL      Unpublished (2005)
COMMENT      Contact: Rod A. Wing
              Arizona Genomics Institute
              University of Arizona
              Forbes Building Room 303, Tucson, AZ 85721-0036, USA
              Tel: 520 626 9595
              Fax: 520 621 1259
              Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0099 row: F column: 04
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
source      Location/Qualifiers
            1..777
              /organism="Oryza officinalis"
              /mol_type="genomic DNA"
              /db_xref="taxon:4535"
              /clone="OO_Ba0099F04"
              /tissue_type="leaves"
              /lab_host="DH10B"
              /clone_lib="OO_Ba"
              /notes="Vector: pAG1BAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      76.4%; Score 16.8; DB 14; Length 777;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 CGAACGGAAAGGCGCTTCGG 22
      |||||
Db      273 CGAACCGGAAGGCATTTCGG 254

RESULT 43
CF700782/c
LOCUS      CF700782
DEFINITION CF700782TR C.neoformans strain JEC21 mRNA linear EST 16-AUG-2004
            neoformans cDNA clone CCAGU31, mRNA sequence.
ACCESSION  CF700782
VERSION     CF700782.1 GI:41554941
SOURCE      Cryptococcus neoformans var. neoformans (Filobasidiella neoformans
            var. neoformans)
ORGANISM    Cryptococcus neoformans var. neoformans
            Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
            Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
            Filobasidiella.
REFERENCE   1 (bases 1 to 802)
AUTHORS     Loftus,B.
TITLE       End sequencing of clones from a Full length enriched, normalized
            JEC21 cDNA library
JOURNAL     Unpublished (2003)
COMMENT     Other_ESTs: CCAGU31TF
            Contact: Brendan Loftus
            The Institute for Genomic Research (TIGR; www.tigr.org)
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-3543
            Fax: 301-838-0208
            Email: bjoftus@tigr.org
            Seq primer: TR.

FEATURES
source      Location/Qualifiers
            1..802
              /organism="Cryptococcus neoformans var. neoformans"
              /mol_type="mRNA"
              /strain="JEC21"
              /db_xref="taxon:40410"

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```

/clone="CCAGU31"
/clone_lib="C.neoformans strain JEC21"
/note="Vector: pCMVSPORT6; Site_1: NotI_EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"

ORIGIN
Query Match      76.4%; Score 16.8; DB 5; Length 802;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCGAACGGAAAGGCGCTTCG 21
      |||||
Db      350 TCCTAACGGAAGGCGCTTCG 331

RESULT 44
DY361640
LOCUS      DY361640
DEFINITION 3', mRNA sequence.
            824 bp mRNA linear EST 09-FEB-2006
            20_Ed0007M16.r ZO_Ed Zingiber officinale cDNA clone ZO_Ed0007M16
ACCESSION  DY361640
VERSION     DY361640.1 GI:87094856
KEYWORDS    EST.
SOURCE      Zingiber officinale
            Zingiber officinale
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales;
            Zingiberaceae; Zingiber.
REFERENCE   1 (bases 1 to 824)
AUTHORS     Ma,X.O., Koo,H.J., Haller,K.P., Soderlund,C.A. and Gang,D.R.
TITLE       Comparative Analysis of Expressed Sequence Tags from Different
            Organs of Ginger and Turmeric. Insights into Specialized Metabolism
            in Traditional Medicinal Plants
JOURNAL     Unpublished (2006)
COMMENT     Contact: David R. Gang
            Department of Plant Sciences
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 621 7154
            Fax: 520 621 7186
            Email: gang@ag.arizona.edu
            Plate: 0007 row: M column: 16.
            Location/Qualifiers
FEATURES     1..824
            /organism="Zingiber officinale"
            /mol_type="mRNA"
            /cultivar="Yellow Ginger"
            /db_xref="taxon:94328"
            /clone="ZO_Ed0007M16"
            /tissue_type="rhizome"
            /lab_host="TUC 121"
            /clone_lib="ZO_Ed"
            /notes="Vector: pBluescriptIISK-; Site_1: EcoRI; Site_2:
            XhoI; Greenhouse, soil grown"

ORIGIN
Query Match      76.4%; Score 16.8; DB 10; Length 824;
Best Local Similarity 90.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCGCTTTC 20
      |||||
Db      338 GACGAACGGAAAGGCTTTC 357

RESULT 45
CF722314/c
LOCUS      CF722314
DEFINITION CF722314 C.neoformans strain JEC21 Cryptococcus neoformans var.
            neoformans cDNA clone CCAGS66, mRNA sequence.
ACCESSION  CF722314

```

CF722314.1 GI:41576473  
 EST.  
 Cryptococcus neoformans var. neoformans (Filobasidiella neoformans  
 var. neoformans)  
 ORGANISM  
 Cryptococcus neoformans var. neoformans  
 Eukaryota; Fungi; Basidiomycota; Hymenomycetes;  
 Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;  
 Filobasidiella.

REFERENCE  
 1 (bases 1 to 835)

AUTHORS  
 Loftus,B.

TITLE  
 End sequencing of clones from a full length enriched, normalized

JOURNAL  
 JEC21 cDNA library

COMMENT  
 Unpublished (2003)

Other ESTs: CCAGS66TF

Contact: Brendan Loftus

712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: bjloftus@tigr.org

Seq primer: TR.

FEATURES  
 Location/Qualifiers

source  
 1..835  
 /organism="Cryptococcus neoformans var. neoformans"

/mol\_type="mRNA"

/strain="JEC21"

/db\_xref="taxon:40410"

/clone="CCAGS66"

/clone\_lib="C.neoformans strain JEC21"

/note="vector: pCMVSPORT6; Site 1: NotI EcoRV; The full length, normalized library was prepared from a variety of conditions using RNA provided by Joseph Heitman and Jennifer Lodge"

ORIGIN

Query Match 76.4%; Score 16.8; DB 5; Length 835;  
 Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTCG 21

Db 352 TCTAACCGGAAGGCTTTCG 333

RESULT 46  
 CR077081 835 bp DNA linear GSS 05-JUL-2004  
 LOCUS  
 Reverse strand read from insert in 3'HPRT insertion targeting and  
 chromosome engineering clone MHP284c21, genomic survey sequence.

ACCESSION  
 CR077081

VERSION  
 GSS; genome survey sequence; MICER.

KEYWORDS  
 Mus musculus (house mouse)

SOURCE  
 Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 835)

AUTHORS  
 Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,  
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,  
 Rogers,J. and Bradley,A.

Direct Submission

TITLE  
 Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,

JOURNAL  
 CB10 1SA, UK http://www.sanger.ac.uk/MICER

FEATURES  
 Location/Qualifiers

source  
 1..835

/organism="Mus musculus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10090"

/clone="MHP284c21"

/clone\_lib="MHPp"

ORIGIN

Query Match 76.4%; Score 16.8; DB 14; Length 835;  
 Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTCG 21

Db 522 TAGAAGGAAGGCTTTCG 541

RESULT 47

LOCUS  
 DT758502 927 bp mRNA linear EST 13-SEP-2005

DEFINITION  
 EST1192351 Aquilegia cDNA library Aquilegia formosa x Aquilegia  
 pubescens cDNA clone COLY334, mRNA sequence.

ACCESSION  
 DT758502

VERSION  
 DT758502.1 GI:74559683

KEYWORDS  
 EST.

SOURCE  
 Aquilegia formosa x Aquilegia pubescens

ORGANISM  
 Aquilegia formosa x Aquilegia pubescens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;  
 Ranunculaceae; Aquilegia.

REFERENCE  
 1 (bases 1 to 927)

AUTHORS  
 Hodges,S.A., Rensink,W., Buell,C.R., Borevitz,J., Kramer,E.,  
 Nordborg,M. and Tomkins,J.

TITLE  
 Generation of ESTs from Aquilegia

JOURNAL  
 Unpublished (2005)

COMMENT  
 Other ESTs: EST1192352

Contact: Scott Hodges

Department of Ecology, Evolution and Marine Biology

University of California, Santa Barbara

Santa Barbara, CA 93106, USA

Tel: 805 893 7813

Fax: 805 893 4724

Email: hodges@lifesci.ucsb.edu

Seq primer: TTTTITTTTTTTTTTTTTTTT (where N = A, G & C).

FEATURES  
 Location/Qualifiers

source  
 1..927

/organism="Aquilegia formosa x Aquilegia pubescens"

/mol\_type="mRNA"

/db\_xref="taxon:338618"

/clone="COLY334"

/tissue\_type="mixed shoot and floral apical meristems,  
 flower buds, leaves and roots"

/lab\_host="DH10B T1 (T1 and T5 phage resistance)"

/clone\_lib="Aquilegia cDNA library"

/note="vector: pCMV SPORT6.1; Site 1: EcoRI; Site 2: NotI;  
 F2, F3, and F4 lines of Aquilegia formosa X A. pubescens  
 were grown from seed in greenhouses at UC Santa Barbara.  
 From these plants three sets of tissue were collected: 1)  
 Small flower buds (<10 mm) and very young inflorescences  
 (71 & 29% by weight respectively), 2) Medium (7-20 mm) and  
 large (at or near anthesis) flower buds (65 & 35% by  
 weight respectively) and 3) Shoot apical meristems. A  
 fourth set of tissue was collected from plants of A.  
 formosa. These plants were grown from seed in sand and at  
 approximately 1 month root tissue and leaf tissue of  
 various developmental stages were collected (84 & 16% by  
 weight respectively). Total RNA was extracted from each  
 set of tissue and pooled in the following proportions:  
 1.5X from sets 1 & 2, 1X from sets 3 & 4. From the pooled  
 total RNA, mRNA was extracted and enriched for full-length  
 messages and then normalized with proprietary methods by  
 Invitrogen."

ORIGIN

Query Match 76.4%; Score 16.8; DB 10; Length 927;  
 Best Local Similarity 90.0%; Pred. No. 2.2e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCTTTC 20

Db 178 GTCGACGGAAGGCTTTC 197

ORGANISM	/organism="Tribolium castaneum"									
	/mol_type="mRNA"									
	/strain="GA2"									
	/db_xref="taxon:7070"									
	/clone="104E3"									
	/tissue_type="Whole larvae"									
	/dev_stage="larvae"									
	/clone_lib="TL1"									
	/notes=Vector: pCMV-SPORT6; Site_1: NotI; Site_2: MluI; Library constructed by Yoonseong Park"									
Query Match	76.4%;	Score 16.8;	DB 10;	Length 946;						
Best Local Similarity	90.0%;	Pred. No. 2.2e+03;								
Matches	18;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;					
QY	3	CGAACGGAAGGCTTTTCGG	22							
Db	534	CGAAGGGAAGGCTTTGGG	553							
RESULT 50										
CNS06NF5/c										
LOCUS										
DEFINITION	CNS06NF5 958 bp DNA linear GSS 17-JUN-2001									
	T3 end of clone AU00AA011F11 of library AU0AA from strain CBS 3082									
	of Saccharomyces kluyveri, genomic survey sequence.									
ACCESSION	AL406695									
VERSION	AL406695.1 GI:12171027									
KEYWORDS	GSS.									
SOURCE	Saccharomyces kluyveri									
ORGANISM	Saccharomyces kluyveri									
REFERENCE	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;									
AUTHORS	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.									
	1 (bases 1 to 958)									
	Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,									
	Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,									
	de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,									
	Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,									
	Saurin,W., Tekai,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,									
	Wincker,P. and Weissenbach,J.									
TITLE	Genomic exploration of the hemiascomycetous yeasts: 1. A set of									
	yeast species for molecular evolution studies									
JOURNAL	FEBS Lett. 487 (1), 3-12 (2000)									
PUBMED	11152876									
REFERENCE	2 (bases 1 to 958)									
AUTHORS	Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,									
	Gaillardin,C. and Casaregola,S.									
TITLE	Genomic exploration of the hemiascomycetous yeasts: 9.									
JOURNAL	Saccharomyces kluyveri									
PUBMED	FEBS Lett. 487 (1), 56-60 (2000)									
REFERENCE	11152884									
AUTHORS	3 (bases 1 to 958)									
JOURNAL	Genoscope.									
TITLE	Direct Submission									
	Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,									
	2 rue Gaston Creteau, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :									
	segrif@genoscope.cns.fr - Web : www.genoscope.cns.fr)									
COMMENT	This GSS is part of a random genomic sequencing program of thirteen									
	yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces									
	exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,									
	Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces									
	lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia									
	angusta, Debaryomyces Hansenii var. Hansenii, Pichia sorbitophila,									
	Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to									
	5 kb were prepared and both extremities were sequenced. See									
	keywords for description of this sequence and for the sequence of									
	the other extremity of this insert.									
FEATURES	Location/Qualifiers									
source	1..958									
	/organism="Saccharomyces kluyveri"									
	/mol_type="genomic DNA"									
	/strain="CBS 3082"									
	/db_xref="taxon:4934"									



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/misc_feature
/clone="AU00A011F11"
/clone_lib="AU00A"
/note="end : T3"
<1..>54
/inference="non-experimental evidence, no additional
details recorded"
/note="similar to Saccharomyces cerevisiae ORF YDL074c [
weak similarity to spindle pole body protein NUF1 ]"
<798..>956
/inference="non-experimental evidence, no additional
details recorded"
/note="similar to Saccharomyces cerevisiae ORF YLR405w [
similarity to A.brasiliense nifR3 protein ]"

ORIGIN
Query Match 76.4%; Score 16.8; DB 14; Length 959;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTCG 21
|||||
Db 483 TCGAACGGAAGGCTGCCG 464

RESULT 51
CNS04EXR/c
LOCUS
DEFINITION CNS04EXR 1003 bp DNA linear GSS 01-SEP-2000
Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone
105024 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION AL287640
VERSION AL287640.1 GI:8026141
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
PUBMED 10899143
REFERENCE 3 (bases 1 to 1003)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
1. .1003
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="105024"
/note="Genoscope sequence ID : CORG105BH12SP1"

FEATURES
source
1. .1007
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0027F02"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 76.4%; Score 16.8; DB 13; Length 1007;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTC 20
|||||
Db 68 GTCGAACGGAAGGCTTTC 49

RESULT 53
DU772735
LOCUS
DEFINITION APKG3109.b2 HF4000_12-21-03 uncultured marine microorganism
HF4000_12-21-03 genomic clone HF4000_[384]008109, genomic survey
sequence.
ACCESSION DU772735
VERSION DU772735.1 GI:85786920
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF4000_12-21-03
uncultured marine microorganism HF4000_12-21-03

```

```

ORIGIN
Query Match 76.4%; Score 16.8; DB 14; Length 1003;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTC 20
|||||
Db 782 GTCGAACGGAAGGCTTTC 763

RESULT 52
CL295780/c
LOCUS
DEFINITION ZMMBBb0027F02f ZMMBBb (HindIII) Zea mays genomic clone
ZMMBBb0027F02 5', genomic survey sequence.
ACCESSION CL295780
VERSION CL295780.1 GI:42574876
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1007)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PCR (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
130 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 111.
Location/Qualifiers
1. .1007
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBBb0027F02"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match 76.4%; Score 16.8; DB 13; Length 1007;
Best Local Similarity 90.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTC 20
|||||
Db 68 GTCGAACGGAAGGCTTTC 49

RESULT 53
DU772735
LOCUS
DEFINITION APKG3109.b2 HF4000_12-21-03 uncultured marine microorganism
HF4000_12-21-03 genomic clone HF4000_[384]008109, genomic survey
sequence.
ACCESSION DU772735
VERSION DU772735.1 GI:85786920
KEYWORDS GSS.
SOURCE uncultured marine microorganism HF4000_12-21-03
uncultured marine microorganism HF4000_12-21-03

```

unclassified sequences; environmental samples.

#### REFERENCE AUTHORS

1 (bases 1 to 1019)  
DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,  
Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.  
and Karl, D.M.

#### TITLE

Comparative genomics reveals ecological trends in stratified  
microbial communities in the ocean's interior

#### JOURNAL

Science (2006) In press

#### COMMENT

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,  
Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson  
and Edward DeLong

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid  
DNA library prepared from marine picoplankton in the less than 1.6  
um, greater than 0.22 um fraction. Sample Date: 12/21/2003  
Coordinates: 22.45 N, 158 W Depth 4000 m Temperature: 1.46 C  
Salinity: 34.69 Oxygen: 147.8 umol/kg  
Class: fosmid ends.

#### FEATURES

source

1. .1019

/organism="uncultured marine microorganism

HF4000\_12-21-03"

/mol\_type="genomic DNA"

/db\_xref="taxon:361148"

/clone="HF4000\_13841008109"

/cell\_type="marine picoplankton, less than 1.8 um, greater  
than 0.22 um fraction"

/clone\_lib="HF4000\_12-21-03"

/notes="Vector: pCCIFOS; North Pacific Subtropical Gyre  
(Hawaii) picoplankton genomic fosmid DNA library prepared  
from marine picoplankton in the less than 1.6 um, greater  
than 0.22 um fraction. Picoplankton collected at 4000 m  
depth on 10/7/2002. Coordinates: 22.45 N, 158 W. Sample  
Date: 12/21/2003 Coordinates: 22.45 N, 158 W Depth 4000 m  
Temperature: 1.46 C Salinity: 34.69 Oxygen: 147.8 umol/kg"

#### ORIGIN

Query Match 76.4%; Score 16.8; DB 14; Length 1019;

Best Local Similarity 90.0%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGACGGAAAGCCTTTC 20

|||||

Db 303 GTCGACGGAAAGCCATGC 322

#### RESULT 54

DU760208

LOCUS

DEFINITION DU760208 1043 bp DNA linear GSS 27-JAN-2006  
ASNG3054\_b2 HF200\_10-06-02 uncultured marine microorganism  
HF200\_10-06-02 genomic clone HF0200\_090F10, genomic survey

sequence.

DU760208

DU760208.1 GI:85770044

GSS.

uncultured marine microorganism HF200\_10-06-02

uncultured marine microorganism HF200\_10-06-02

unclassified sequences; environmental samples.

1 (bases 1 to 1043)

REFERENCE

AUTHORS

DeLong, E.F., Preston, C.M., Mincer, T., Rich, V., Hallam, S.J.,  
Frigaard, N.U., Martinez, A., Sullivan, M., Edwards, R., Chisholm, S.W.  
and Karl, D.M.

#### TITLE

Comparative genomics reveals ecological trends in stratified  
microbial communities in the ocean's interior

#### JOURNAL

Science (2006) In press

#### COMMENT

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,  
Kerrie Barry, Tijana Glavinadelrio, David Bruce, Paul Richardson  
and Edward DeLong

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: PMRichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid  
DNA library prepared from marine picoplankton in the less than 1.6  
um, greater than 0.22 um fraction. Sample Date: 10/6/2002  
Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C  
Salinity: 35.04 psu Oxygen: 198.8 umol/kg  
Class: fosmid ends.

#### FEATURES

source

1. .1043

/organism="uncultured marine microorganism HF200\_10-06-02"

/mol\_type="genomic DNA"

/db\_xref="taxon:361147"

/clone="HF0200\_090F10"

/cell\_type="marine picoplankton, less than 1.8 um, greater  
than 0.22 um fraction"

/clone\_lib="HF200\_10-06-02"

/notes="Vector: pCCIFOS; North Pacific Subtropical Gyre  
(Hawaii) picoplankton genomic fosmid DNA library prepared  
from marine picoplankton in the less than 1.6 um, greater  
than 0.22 um fraction. Picoplankton collected at 200 m  
depth on 10/6/2002. Coordinates: 22.45 N, 158 W. Sample  
Date: 10/6/2002 Coordinates: 22.45 N, 158 W Depth 200 m  
Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8  
umol/kg"

#### ORIGIN

Query Match 76.4%; Score 16.8; DB 14; Length 1043;

Best Local Similarity 81.8%; Pred. No. 2.2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGACGGAAAGCCTTTCG 22

|||||

Db 83 GNCGCCGGAAGCCTTTTG 104

#### RESULT 55

CO684942

LOCUS

DEFINITION DG11-193n18 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.

CO684942

CO684942.1 GI:50633608

EST.

Canis familiaris (dog)

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

1 (bases 1 to 305)

REFERENCE

AUTHORS

Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,  
Henrich, J., and Loebbert, R.

DOG arrayTAG cDNA clone collection

Unpublished (2004)

COMMENT

Contact: Thomas Schlueter

LION Bioscience AG

Walhoferstrasse 98, D-69123 Heidelberg, Germany

Tel: +49 6221 4038 150

Fax: +49 6221 4038 290

Email: Thomas.Schlueter@lionbioscience.com.

#### FEATURES

source

1. .305

/organism="Canis familiaris"

/mol\_type="mRNA"

/strain="Beagle"

/db\_xref="taxon:9615"

/tissue\_type="kidney"

/dev\_stage="adult"

/lab\_host="DI0B"

/clone\_lib="DG11-kidney"

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ORIGIN
Query Match          74.5%; Score 16.4; DB 8; Length 305;
Best Local Similarity 94.4%; Pred. No. 3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACCGAAAGGCTTTCG 22
    ||| ||||| ||||| |||
Db 135 AACGAAAGGCTTTCG 152

RESULT 56
BF623830
LOCUS
DEFINITION BP863510 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-66-P16 5',
            mRNA sequence.
ACCESSION BP863510
VERSION BP863510.1 GI:59924483
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 412)
AUTHORS Seki,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K.,
        Iida,K., Enju,A., Sakurai,T., Arakawa,T., Carninci,P., Fukuda,S.,
        Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and
        Shinozaki,K.
TITLE Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs
JOURNAL Unpublished (2005)
COMMENT Contact: Motoaki Seki
        Plant Functional Genomics Research Group
        RIKEN Genomic Sciences Center
        3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
        Tel: 81-298-36-4359
        Fax: 81-298-36-9060
        Email: mseki@rtc.riken.go.jp
        An Arabidopsis full-length cDNA library was constructed essentially
        as reported previously (Seki et al., 1998, 2002). This clone is in a
        modified pBluescript vector.
        Please visit our web site (http://pfweb.gsc.riken.jp and
        http://range.gsc.riken.jp) for further details.
FEATURES
            source
                1..412
                    /organism="Arabidopsis thaliana"
                    /mol_type="mRNA"
                    /db_xref="taxon:3702"
                    /clones="RAFL21-66-P16"
                    /lab_host="DH10B"
                    /clone_lib="RAFL21"
                /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
                The sequence was obtained from samples subjected to
                various stress and plant hormones-treated"

ORIGIN
Query Match          74.5%; Score 16.4; DB 3; Length 412;
Best Local Similarity 94.4%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCTTTCG 21
    ||| ||||| ||||| |||
Db 197 GAACGGAAGGCTTTCG 214

RESULT 57
BF623830
LOCUS
DEFINITION BF623830 HVSMEa0007D03f Hordeum vulgare seedling shoot EST library
            HVCdNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone
            HVSMEa0007D03f, mRNA sequence.
ACCESSION BF623830

```

```

VERSION BF623830.2 GI:13082086
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
Clade; Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 492)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
        Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R.,
        Choi,D.W., Fenton,R.D. and Main,D.
TITLE Development of a genetically and physically anchored EST resource
        for barley genomics: Morex cold-stressed seedling shoot cDNA
        library
JOURNAL Unpublished (2001)
COMMENT On Dec 18, 2000 this sequence version replaced gi:11887564.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 241
Seq primer: AATTACCCCTCACTAAGGG
High quality sequence stop: 491.
FEATURES
            source
                1..492
                    /organism="Hordeum vulgare subsp. vulgare"
                    /mol_type="mRNA"
                    /cultivar="Morex"
                    /sub_species="vulgare"
                    /db_xref="taxon:112509"
                    /clones="HVSMEa0007D03f"
                    /tissue_type="Seedling shoot"
                    /lab_host="TJC121"
                    /clone_lib="Hordeum vulgare seedling shoot EST library
                    HVCdNA0001 (Cold stress)"
                /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
                Seeds were surface sterilized then germinated under axenic
                conditions in the dark at room temperature on filter paper
                with water, nystatin and cefotaxime in covered
                crystallization dishes. Five-day old seedlings were
                incubated at 50C for 2 days. Shoots were then harvested,
                total RNA was prepared, poly(A) RNA was purified, One
                primary unamplified cDNA library was made, and 600000 pfu
                were in vivo excised to give pBluescript SK(-) cDNA
                phagemids. These steps were performed in the TJ Close
                laboratory at the University of California, Riverside
                (Choi, Close, Fenton). Phagemids were plated and picked at
                the Clemson University Genomics Institute (CUGI) (Begum,
                Palmer, Frisch, Atkins and Wing). Plasmid DNA
                preparations, DNA sequencing and sequence analysis were
                performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,
                Oates, Rambo, Main). The sequence has been trimmed to
                remove vector sequence and contains a minimum of 100 bases
                of phred value 20 or above. For more details on library
                preparation and sequence analysis see
                http://www.genome.clemson.edu/projects/barley. To order
                this clone see http://www.genome.clemson.edu/orders Also
                see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                Genetically and physically anchored EST resources for
                barley genomics. Barley Genetics Newsletter 31:29-30.
                (http://wheat.pw.usda.gov/ggppages/bgn/31/cover.html)"

ORIGIN
Query Match          74.5%; Score 16.4; DB 7; Length 492;
Best Local Similarity 94.4%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTT 18
    ||| ||||| ||||| |||
Db 472 GTCGAACGGAAGGCTT 489

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RESULT 58  
BF257478

LOCUS  
DEFINITION

ACCESSION  
BF257478

VERSION  
BF257478.2

KEYWORDS  
EST.

SOURCE  
Hordeum vulgare subsp. vulgare

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooleae; Triticeae; Hordeum.

REFERENCE  
AUTHORS  
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.

TITLE  
Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001)

JOURNAL  
COMMENT  
On Nov 16, 2000 this sequence version replaced gi:1186591. Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Total hg bases = 431  
Seq primer: AATTAACTCTACTTAAGGG  
High quality sequence stop: 491.

FEATURES

source

1. .493

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Morex"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HVSMEF0013A10f"

/tissue\_type="Seedling root"

/lab\_host="TJCL121"

/clone\_lib="Hordeum vulgare seedling root EST library HVCDA0007 (Etiolated and unstressed)"

/notes="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)

Query Match

Best Local Similarity

Matches

74.5%;

94.4%;

17;

Score 16.4;

DB 7;

Length 493;

Pred. No. 3.2e+03;

Mismatches 0;

Indels 1;

Gaps 0;

QY

1

GTCGAACGGAAGGCCTT

18

Db

456

GTCGAACGGAAGGCCTT

473

RESULT 59

BF253911

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .544

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Morex"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HVSMEF0002H13f"

/tissue\_type="Seedling root"

/lab\_host="TJCL121"

/clone\_lib="Hordeum vulgare seedling root EST library HVCDA0007 (Etiolated and unstressed)"

/notes="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)

Query Match

Best Local Similarity

Matches

74.5%;

94.4%;

17;

Score 16.4;

DB 7;

Length 493;

Pred. No. 3.2e+03;

Mismatches 0;

Indels 1;

Gaps 0;

QY

1

GTCGAACGGAAGGCCTT

18

Db

456

GTCGAACGGAAGGCCTT

473

RESULT 59

BF253911

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .544

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Morex"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="HVSMEF0002H13f"

/tissue\_type="Seedling root"

/lab\_host="TJCL121"

/clone\_lib="Hordeum vulgare seedling root EST library HVCDA0007 (Etiolated and unstressed)"

/notes="Vector: lambdaZAP; Site\_1: EcoRI; Site\_2: XhoI; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/g99pages/bgn/31/cover.html>)

this clone see <http://www.genome.clemson.edu/orders> Also see close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggp/bgn/31/cover.html>)"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 544;  
Best Local Similarity 94.4%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18  
|||||

Db 141 GTCGAACGGAAGGCCTT 158  
|||||

## RESULT 60

BE571264

DEFINITION BE571264 585 bp mRNA linear EST 15-AUG-2000  
mRNA sequence.

ACCESSION BE571264

VERSION BE571264.1 GI:9814984

KEYWORDS EST

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.

1 (bases 1 to 585)

NH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@remail.nih.gov](mailto:cgapsb@remail.nih.gov)

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LUAM8927 row: a column: 02

High quality sequence start: 4

High quality sequence stop: 583.

## FEATURES

source

1..585

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:3708169"

/sex="female, virgin"

/tissue\_type="infiltrating ductal carcinoma"

/dev\_stage="5 months"

/lab\_host="DH10B"

/clone\_lib="NCI\_CGAP Mam6"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Jeffrey Green, M.D., NIH"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 585;

Best Local Similarity 94.4%; Pred. No. 3.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20

|||||

Db 256 CGAACGGAAGGCCTTTC 273

|||||

## RESULT 61

BE571264

DEFINITION BE571264 585 bp mRNA linear EST 15-AUG-2000

ACCESSION BE571264

VERSION BE571264.1 GI:9814984

KEYWORDS EST

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.

1 (bases 1 to 585)

NH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@remail.nih.gov](mailto:cgapsb@remail.nih.gov)

Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LUAM8927 row: a column: 02

High quality sequence start: 4

High quality sequence stop: 583.

BU398878

LOCUS

DEFINITION

60353950F1 CSEQCHN58 Gallus gallus cDNA clone CHEST492d14 5', mRNA

sequence.

ACCESSION

BU398878

VERSION

BU398878.1 GI:25767934

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 603)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

12445392

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: [Simon.Hubbard@umist.ac.uk](mailto:Simon.Hubbard@umist.ac.uk).

Location/Qualifiers

1..603

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Compton Line 151"

/db\_xref="taxon:9031"

/clone="CHEST492d14"

/sex="Female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSEQCHN58"

/note="Organ: small intestine; Vector: pBluescript II

KS(+); Site 1: EcoRI; Site 2: NotI; This normalized

library was constructed from 1 million independent clones.

cDNA synthesis was initiated using an oligo(dT) primer.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., FNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

## ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 603;

Best Local Similarity 94.4%; Pred. No. 3.3e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTCG 21

|||||

Db 273 GAAAGGAAGGCCTTTCG 290

|||||

## RESULT 62

BU306528

LOCUS

DEFINITION

60373900F1 CSEQCHN56 Gallus gallus cDNA clone CHEST633n2 5', mRNA

sequence.

ACCESSION

BU306528

VERSION

BU306528.1 GI:25756262

KEYWORDS

EST.

SOURCE

Gallus gallus (chicken)

ORGANISM

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
 AUTHORS Boardman,P.E., Sanz-Esquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
 TITLE A Comprehensive Collection of Chicken cDNAs  
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 source  
 1. .625  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Compton Line 151"  
 /db\_xref="taxon:9031"  
 /clone="CHEST633n2"  
 /sex="Female"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQCHN56"  
 /note="Organ: small intestine; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN  
 Query Match 74.5%; Score 16.4; DB 3; Length 625;  
 Best Local Similarity 94.4%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAAGCGCTTTCG 21  
 ||| |||||  
 Db 290 GAAAGGAAGCGCTTTCG 307

RESULT 63  
 BF625550  
 LOCUS  
 DEFINITION BF625550.639 bp mRNA linear EST 17-OCT-2001  
 HVSMEa0011E08f Hordeum vulgare seedling shoot EST library  
 HVCdNA0001 (Cold stress) Hordeum vulgare subsp. vulgare cDNA clone  
 HVSMEa0011E08f, mRNA sequence.

ACCESSION BF625550  
 VERSION BF625550.2 GI:13083410  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE  
 AUTHORS Wing,R., Close,T.J., Kleinhoofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library

REFERENCE  
 AUTHORS Wing,R., Close,T.J., Kleinhoofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library

REFERENCE  
 AUTHORS Wing,R., Close,T.J., Kleinhoofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library

REFERENCE  
 AUTHORS Wing,R., Close,T.J., Kleinhoofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

TITLE Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA library

JOURNAL  
 COMMENT

Unpublished (2001)  
 On Dec 18, 2000 this sequence version replaced gi:11889284.  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hq bases = 490  
 Seq primer: AATTAACCTCTCACTAAAGG  
 High quality sequence stop: 598.

FEATURES  
 source

1. .639  
 Location/Qualifiers  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSMEa0011E08f"  
 /tissue\_type="Seedling shoot"  
 /lab\_host="TJCl21"  
 /clone\_lib="Hordeum vulgare seedling shoot EST library  
 HVCdNA0001 (Cold stress)"  
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 50C for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton) . Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing) . Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TU, Wing R, Kleinhoofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

Query Match 74.5%; Score 16.4; DB 7; Length 639;  
 Best Local Similarity 94.4%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGACGGAAGCGCTT 18  
 |||||  
 Db 474 GTCGACGGAAGCGCTT 491

RESULT 64  
 BU283959  
 LOCUS  
 DEFINITION BU283959.643 bp mRNA linear EST 27-NOV-2002  
 603600041F1 CSEQCHN54 Gallus gallus cDNA clone CHEST573a12 5', mRNA sequence.

ACCESSION BU283959  
 VERSION BU283959.1 GI:25733402  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

```

REFERENCE
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
        Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
        Department of Biomolecular Sciences
        University of Manchester Institute of Science and Technology
        (UMIST)
        PO Box 88, Manchester, M60 1QD, UK
        Tel: 01612008930
        Fax: 01612360409
        Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
    1. 643
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Compton Line 151"
        /db_xref="taxon:9031"
        /clones="CHEST573a12"
        /sex="Female"
        /tissue_type="not cerebrum or cerebellum"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="CSEQCHN54"
        /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
        EcoRI; Site_2: NotI; This normalized library was
        constructed from 1 million independent clones. cDNA
        synthesis was initiated using an oligo(dT) primer, using
        methylated C in the first strand synthesis reaction.
        Following this first strand reaction, double-stranded cDNA
        was blunt-ended, ligated to NotI adapters, digested with
        EcoRI, size-selected, and cloned into the NotI and EcoRI
        compatible sites of a custom modified MCS of the
        pBluescript (KS+) vector. The library was normalized in 2
        rounds using conditions adapted from Soares et al., PNAS
        (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
        (1996): 791, except that a significantly longer
        reannealing hybridization was used."

ORIGIN
Query Match 74.5%; Score 16.4; DB 3; Length 643;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAACGGAAAGCCCTTTCG 21
    ||| ||||| ||||| |||||
Db 10 GAAAGGAAGGCGCTTTCG 27

RESULT 65
BH794488 660 bp DNA linear GSS 02-APR-2002
LOCUS ME MBA0002P13f Manihot esculenta Manihot esculenta genomic clone
DEFINITION ME MBA0002P13f, genomic survey sequence.
ACCESSION BH794488
VERSION BH794488.1 GI:19892621
KEYWORDS GSS.
SOURCE Manihot esculenta (cassava)
ORGANISM Manihot esculenta
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
        rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
        Manihoteae; Manihot.
REFERENCE 1 (bases 1 to 660)
AUTHORS Tomkins,J., Fregene,M., Main,D., Kim,H., Wing,R. and Tohme,J.
TITLE Bacterial artificial chromosome (BAC) library resource for
        positional cloning of pest and disease resistance genes in cassava
        (Manihot esculenta Crantz)
JOURNAL Plant Mol. Biol. 56 (4), 555-561 (2004)
PUBMED 15630619

Phasianinae; Gallus.
1 (bases 1 to 643)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
    1. 643
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="Compton Line 151"
        /db_xref="taxon:9031"
        /clones="CHEST573a12"
        /sex="Female"
        /tissue_type="not cerebrum or cerebellum"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="CSEQCHN54"
        /note="Organ: brain; Vector: pBluescript II KS(+); Site_1:
        EcoRI; Site_2: NotI; This normalized library was
        constructed from 1 million independent clones. cDNA
        synthesis was initiated using an oligo(dT) primer, using
        methylated C in the first strand synthesis reaction.
        Following this first strand reaction, double-stranded cDNA
        was blunt-ended, ligated to NotI adapters, digested with
        EcoRI, size-selected, and cloned into the NotI and EcoRI
        compatible sites of a custom modified MCS of the
        pBluescript (KS+) vector. The library was normalized in 2
        rounds using conditions adapted from Soares et al., PNAS
        (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
        (1996): 791, except that a significantly longer
        reannealing hybridization was used."

ORIGIN
Query Match 74.5%; Score 16.4; DB 11; Length 660;
Best Local Similarity 94.4%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAACGGAAAGCCCTTTCG 21
    ||| ||||| ||||| |||||
Db 225 GAAAGGAAGGCGCTTTCG 242

RESULT 66
BF622265 698 bp mRNA linear EST 17-OCT-2001
LOCUS HVSMEa0002G13f Hordeum vulgare seedling shoot EST library
DEFINITION HVSMEa0002G13f, mRNA sequence.
ACCESSION BF622265
VERSION BF622265.2 GI:13080041
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
        clade; Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 698)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
        Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R.,
        Choi,D.W., Fenton,R.D. and Main,D.
TITLE Development of a genetically and physically anchored EST resource
        for barley genomics: Morex cold-stressed seedling shoot cDNA
        library
JOURNAL Unpublished (2001)
COMMENT On Dec 18, 2000 this sequence version replaced gi:11885999.
Contact: Wing RA
        Clemson University Genomics Institute
        Clemson University
        100 Jordan Hall, Clemson, SC 29634, USA
        Tel: 864 656 7288
        Fax: 864 656 4293
        Email: twing@clemson.edu
        Total hg bases = 356
        Seq primer: AATTAAACCTCACTAAGGG
        High quality sequence stop: 589.

FEATURES
source
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        /mol_type="genomic DNA"
        /strain="MECW72"
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        /clone="ME_MBa0002P13f"
        /tissue_type="Leaf"
        /lab_host="E. coli"
        /clone_lib="Manihot esculenta"
        /note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
        For more details on library preparation and sequence
        analysis see
        http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
        To order clones from this library see
        http://www.genome.clemson.edu/orders "

CONTACT: Tomkins J
        Clemson University Genomics Institute
        Clemson University
        100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
        Tel: 864 656 6419
        Fax: 864 656 4293
        Email: jtmkns@clemson.edu
        Total High Quality bases = 281
        Seq primer: TAATACGACTCACTATAGGG
        Class: BAC ends
        High quality sequence stop: 658.

FEATURES
Location/Qualifiers
    1. 660
        /organism="Manihot esculenta"
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        /strain="MECW72"
        /db_xref="taxon:3983"
        /clone="ME_MBa0002P13f"
        /tissue_type="Leaf"
        /lab_host="E. coli"
        /clone_lib="Manihot esculenta"
        /note="Vector: pCUGIBAC-1; Site_1: HindIII; Site_2: NotI;
        For more details on library preparation and sequence
        analysis see
        http://www.genome.clemson.edu/projects/stc/cassava/ME_MBa
        To order clones from this library see
        http://www.genome.clemson.edu/orders "

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/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
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/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="HVSMEa0002G13f"  
/tissue\_type="Seedling shoot"  
/lab\_host="TJC121"  
/clone\_lib="Hordeum vulgare seedling shoot EST library  
HVCDA0001 (Cold stress)"  
/notes="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
Seeds were surface sterilized then germinated under axenic  
conditions in the dark at room temperature on filter paper  
with water, nystatin and cefotaxime in covered  
crystallization dishes. Five-day old seedlings were  
incubated at 50C for 2 days. Shoots were then harvested,  
total RNA was prepared, poly(A) RNA was purified, one  
primary unamplified cDNA library was made, and 60000 pfu  
were in vivo excised to give pBluescript SK(-) cDNA  
phagemids. These steps were performed in the TJ Close  
laboratory at the University of California, Riverside  
(Choi, Close, Fenton). Phagemids were plated and picked at  
the Clemson University Genomics Institute (CUGI) (Begum,  
Palmer, Frisch, Atkins and Wing). Plasmid DNA  
preparations, DNA sequencing and sequence analysis were  
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,  
Oates, Rambo, Main). The sequence has been trimmed to  
remove vector sequence and contains a minimum of 100 bases  
of phred value 20 or above. For more details on library  
preparation and sequence analysis see  
http://www.genome.clemson.edu/projects/barley. To order  
this clone see http://www.genome.clemson.edu/orders/Also  
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
Genetically and physically anchored EST resources for  
barley genomics. Barley Genetics Newsletter 31:29-30.  
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 698;  
Best Local Similarity 94.4%; Pred. No. 3.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGACCGAAGGCGCTT 18  
|||||  
Db 461 GTCGACCGAAGGCGTT 478  
|||||

RESULT 67  
BU412995  
LOCUS  
DEFINITION  
603154843F1 CSQRBL05 Gallus gallus cDNA clone CHEST167e12 5', mRNA  
sequence.  
ACCESSION  
BU412995  
VERSION  
BU412995.1 GI:25905666  
KEYWORDS  
EST.  
SOURCE  
Gallus gallus (chicken)  
ORGANISM  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 709)  
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,  
Pong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1963-1969 (2002)  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers  
1. .709  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Layer"  
/db\_xref="taxon:9031"  
/clone="CHEST167e12"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQRBL05"  
/notes="Organ: ovary; Vector: pBluescript II KS(+); Site 1:  
EcoRI; Site 2: NotI; Modification of pBluescript II KS(+)  
[Stratagene] vector to accommodate cDNA produced with the  
t-trimmed protocol (Construction of uni-directionally  
cloned cDNA libraries from messenger RNA for improved 3'  
end DNA sequencing by Glenn Fu, et al. U.S. Patent #  
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.  
Ligate in double stranded adaptor containing BsgI and  
BamHI sites [5'ggcgctgagcccgatccgaaaaaaag]  
[5'aattcttttcggatccgggtgcacgc]"

ORIGIN

Query Match 74.5%; Score 16.4; DB 3; Length 709;  
Best Local Similarity 94.4%; Pred. No. 3.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGAAAGGCGCTTCG 21  
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Db 354 GAAAGGAAAGGCGCTTCG 371  
|||||

RESULT 68  
BX855983/c  
LOCUS  
DEFINITION  
BX855983 tcay Oncorhynchus mykiss cDNA clone tcay0040b.g.16 5prim,  
mRNA sequence.  
ACCESSION  
BX855983  
VERSION  
BX855983.2 GI:42752904  
KEYWORDS  
EST.  
SOURCE  
Oncorhynchus mykiss (rainbow trout)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
1 (bases 1 to 740)  
Govoroun,M., Guiguen,Y. and Le Gac,F.  
Construction and primary characterization of normalized cDNA  
libraries in rainbow trout, Oncorhynchus mykiss  
Unpublished (2003)  
On Dec 16, 2003 this sequence version replaced gi:39952993.  
Contact: Guiguen Y  
INRA - SCRIBE  
Campus de beaulieu, RENNES cedex, 35042, France  
Tel: 02.23.48.50.09  
Fax: 02.23.48.50.20  
Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us  
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this  
sequence.  
Plate: 0040 row: g column: 16  
Seq primer: M13R.  
Location/Qualifiers  
1. .740  
/organism="Oncorhynchus mykiss"  
/mol\_type="mRNA"  
/db\_xref="taxon:8022"  
/clone="tcay0040b.g.16"  
/tissue\_type="adipose tissue, blood, brain,  
differentiating gonads, gills, interrenal, intestine,  
kidney, liver, muscle, ovary, pituitary, testis"  
/dev\_stage="from embryos to adults"



/lab host="DH10B"  
 /clone lib="tcay"  
 /note=Vector: pT73D-PacI; Rainbow trout multi-tissues -  
 normalized + 1 subtraction (tcay) : Clone distribution :  
 AGENAE Resource centre. Francois PIUMI,  
 Francois.PIUMI@jouy.inra.fr, INRA, CEA radiobiologie et  
 Etude du genome (LREG), Domaine de Vilvert, 78352,  
 Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33  
 (0) 1.34.65.22.73"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 4; Length 740;  
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCCTT 18  
 |||||  
 Db 549 GTCGAACGGAAGGCCTT 532

RESULT 69  
 BF982698 747 bp mRNA linear EST 23-JAN-2001  
 LOCUS 602305084F1 NIH\_MGC\_88 Homo sapiens cDNA clone IMAGE:4396461 5',  
 DEFINITION mRNA sequence.

ACCESSION BF982698  
 VERSION BF982698.1 GI:12385510  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 747)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

AUTHORS Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov

JOURNAL Tissue Procurement: ATCC  
 COMMENT CDNA Library Preparation: Life Technologies, Inc.  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LHAM10095 row: g column: 22  
 High quality sequence stop: 659.

## FEATURES

source  
 1..747  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4396461"  
 /tissue\_type="duodenal adenocarcinoma, cell line"  
 /lab host="DH10B (phage-resistant)"  
 /clone lib="NIH\_MGC 88"  
 /note="Organ: small intestine; Vector: pCMV-SPORT6;  
 Site1: NotI; Site2: SalI; Cloned unidirectionally;  
 oligo-dr primed. Average insert size 1.767 kb. Library  
 enriched for full-length clones and constructed by Life  
 Technologies. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 74.5%; Score 16.4; DB 2; Length 747;  
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GTCGAACGGAAGGCCTT 18  
 |||||  
 Db 664 GTCGAACGGAAGGCCTT 681

RESULT 70  
 BE195630  
 LOCUS  
 DEFINITION

799 bp mRNA linear EST 22-OCT-2001  
 HVSMEH0089P24f Hordeum vulgare 5-45 DAP spike EST library  
 HVCDA0009 (5 to 45 DAP) Hordeum vulgare subsp. vulgare cDNA clone  
 HVSMEH0089P24f, mRNA sequence.

ACCESSION BE195630

VERSION BE195630.3 GI:16321335

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP  
 clade; Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 799)

AUTHORS Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D.,  
 Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W.,  
 Fenton, R.D., Close, S.J., Oates, R., and Main, D.

TITLE Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex 5-45 DAP spike cDNA library

JOURNAL Unpublished (2001)

COMMENT On Jun 26, 2000 this sequence version replaced gi:11188307.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: [rwing@clemson.edu](mailto:rwing@clemson.edu)

Total hq bases = 293

Seq primer: AATTACCCCTCACTAAAGG

High quality sequence stop: 769.

## FEATURES

source  
 1..799  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSMEH0089P24f"  
 /tissue\_type="5-45 DAP Spike"  
 /lab\_host="SOLR"  
 /clone lib="Hordeum vulgare 5-45 DAP spike EST library  
 HVCDA0009 (5 to 45 DAP)"  
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Plants were grown in the greenhouse at the University of  
 California, Riverside (Fenton, SJ Close, TJ Close). Whole  
 spikes with awns trimmed were collected at 5, 10, 15, 20,  
 30 and 45 DAP (Fenton). Total RNA was prepared from each  
 pool, equal quantities of all six RNA pools were combined,  
 poly(A) RNA was purified from the mixture, one primary  
 unamplified cDNA library was made, and 1 million pfu were  
 in vivo excised to give pluescript SK(-) cDNA phagemids  
 (Choi) in the TJ Close lab at the University of California,  
 Riverside. Phagemids were plated and picked at the Clemson  
 University Genomics Institute (CUGI) (Begum, Palmer,  
 Frisch, Atkins and Wing). Plasmid DNA preparations, DNA  
 sequencing and sequence analysis were performed at CUGI  
 (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).  
 The sequence has been trimmed to remove vector sequence  
 and contains a minimum of 100 bases of phred value 20 or  
 above. For more details on library preparation and  
 sequence analysis see  
<http://www.genome.clemson.edu/projects/barley>. To order  
 this clone see <http://www.genome.clemson.edu/orders> Also  
 see Close TJ, Wing R, Kleinohs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 7; Length 799;  
 Best Local Similarity 94.4%; Pred. No. 3.4e+03;

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Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
    |||||
Db 471 GTCGAACGGAAGGCCTT 488

RESULT 71
LOCUS BU409605 847 bp mRNA linear EST 29-NOV-2002
DEFINITION 60315733F1 CSEORBL03 Gallus gallus cdna clone CHEST174b10 5', mRNA
sequence.
ACCESSION BU409605
VERSION BU409605.1 GI:25902276
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 847)
AUTHORS Boardman,P.E., Sanz-Esquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(JMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .847
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST174b10"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEORBL03"
/notes="vector: pBluescript II KS(+); Site_1: EcoRI;
Site_2: NotI; Modification of pBluescript II KS(+)
[Stratagene] vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'ggcgcgtgcagcccgatccgaaaaaag]
[5'aattcttttttggatccgggtgcacgc]"

ORIGIN
Query Match 74.5%; Score 16.4; DB 3; Length 847;
Best Local Similarity 94.4%; Pred. No. 3.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTCG 21
    |||
Db 278 GAAAGGAAGGCCTTTCG 295

RESULT 72
CNS029222/c
LOCUS CNS029222 883 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
245N04 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION CNS029222
VERSION CNS029222.1 GI:245N04
KEYWORDS EST.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
REFERENCE 1 (bases 1 to 883)
AUTHORS Pizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
PUBMED 10899143
COMMENT Roest Crolius H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Pizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
10899143
3 (bases 1 to 883)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. .883
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="245N04"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG245DG02SP1
end : PUC-Ori"

ORIGIN
Query Match 74.5%; Score 16.4; DB 14; Length 883;
Best Local Similarity 94.4%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    |||||
Db 368 TTGACGGAAGGCCTTT 351

RESULT 73
CNS83238/c
LOCUS CNS83238 944 bp mRNA linear EST 20-JUL-2004
DEFINITION ILLUMIGEN_MQ_44583 Katze MMLV Macaca mulatta cDNA clone
IBIUM:16736 5' similar to Bases 1 to 944 highly similar to human
ITI13 (Hs.76716), mRNA sequence.
ACCESSION CNS83238
VERSION CNS83238.1 GI:50415893
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
REFERENCE 1 (bases 1 to 944)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 944)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proli,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and

```

```

sequence.
AL186707
AL186707.1 GI:7824811
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
Roest Crolius H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Pizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
10835645
2
Roest Crolius H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Pizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
10899143
3 (bases 1 to 883)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
1. .883
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="245N04"
/clone_lib="G"
/notes="Genoscope sequence ID : COAG245DG02SP1
end : PUC-Ori"

ORIGIN
Query Match 74.5%; Score 16.4; DB 14; Length 883;
Best Local Similarity 94.4%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    |||||
Db 368 TTGACGGAAGGCCTTT 351

RESULT 73
CNS83238/c
LOCUS CNS83238 944 bp mRNA linear EST 20-JUL-2004
DEFINITION ILLUMIGEN_MQ_44583 Katze MMLV Macaca mulatta cDNA clone
IBIUM:16736 5' similar to Bases 1 to 944 highly similar to human
ITI13 (Hs.76716), mRNA sequence.
ACCESSION CNS83238
VERSION CNS83238.1 GI:50415893
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
REFERENCE 1 (bases 1 to 944)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 944)
Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agy,M.B.,
Proli,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and

```

**TITLE**  
**JOURNAL**  
**PUBLISHED**  
**COMMENT**

Idonato,S.P.  
 Analysis of the Macaca mulatta transcriptome and the sequence divergence between Macaca and human  
 Genome Biol. 6 (7), R60 (2005)  
 15998449  
 Contact: C. Magness  
 Illumigen Biosciences Inc.  
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
 Tel: 2063780400  
 Fax: 2063780408  
 Email: cmagness@illumigen.com  
 Sequenced on 2004.06.18. 633 Q20 bases. Library Preparation: Prof. Michael Katze Lab at University of Washington DNA Sequencing: Illumigen Biosciences Inc. For further information, see <http://www.macaque.org>  
 PCR Primers  
 FORWARD: CCCTCACTAAGGGAACAAAA  
 BACKWARD: CACTATAGGCGGATTTGGTA  
 Insert Length: 944 Std Error: 0.00  
 Plate: CL000392 row: H column: 04  
 Seq primer: CCCTCACTAAGGGAACAAAA  
 POLYA=No.

**FEATURES**  
 source

1. .944  
 /location="Qualifiers  
 /organism="Macaca mulatta"  
 /mol\_type="mRNA"  
 /strain="Indian"  
 /db\_xref="taxon:9544"  
 /clone="IBIUM:16736"  
 /sex="female"  
 /dev\_stage="adult"  
 /lab\_host="Electromax DH10B"  
 /clone\_lib="Katze MMLV"  
 /note="Organ: liver; Vector: pDONR 222; Site 1: BarG I; Site 2: BarG I; Created from CloneMiner cDNA Library Construction kit (catalog #8249-029)"

**ORIGIN**

Query Match 74.5%; Score 16.4; DB 8; Length 944;  
 Best Local Similarity 94.4%; Pred. No. 3.5e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTTCGG 22  
 |||||  
 Db 837 AACGGAAGGCTTTCGG 820

**RESULT 74**  
 CC213477/c  
**LOCUS**  
 DEFINITION CC213477.1 CH261 Gallus gallus genomic clone CH261-65024,  
 genomic survey sequence.  
**ACCESSION** CC213477  
**VERSION** CC213477.1 GI:30532145  
**KEYWORDS** GSS.  
**SOURCE** Gallus gallus (chicken)  
**ORGANISM** Gallus gallus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 1124)  
 Warren,W., Graves,T., Higginsbotham,J., Wylie,K., Carter,J., McPherson,J.,  
 Kremitzki,C., Higginsbotham,J., Mardis,E. and Wilson,R.  
 Gallus gallus BAC End Reads  
 Unpublished (2003)  
 Contact: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)  
 Insert Length: 182000 Std Error: 0.00  
 Seq primer: Sp6 ATTAGTGACACTATAG  
 Class: BAC ends  
 High quality sequence start: 103

**FEATURES**  
 source

1. .1124  
 /organism="Gallus gallus"  
 /mol\_type="genomic DNA"  
 /strain="Red Jungle Fowl"  
 /db\_xref="taxon:9031"  
 /clone="CH261-65024"  
 /sex="female"  
 /cell\_line="UCD001, inbred 256"  
 /clone\_lib="CH261"  
 /note="Vector: pIARAC2.1; Site 1: EcoRI; Site 2: EcoRI;  
 CH261 Female Chicken library - For library and clone  
 ordering information: <http://www.chori.org/bacpac>"

**ORIGIN**

Query Match 74.5%; Score 16.4; DB 12; Length 1124;  
 Best Local Similarity 94.4%; Pred. No. 3.6e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18  
 |||||  
 Db 34 GTCGAACGGAAGGCCTT 17

**RESULT 75**  
 DR139870/c  
**LOCUS**  
 DEFINITION DR139870.1 1173 bp mRNA linear EST 16-JUN-2005  
 49349140 Drosophila pseudoobscura embryonic cDNA library Drosophila  
 pseudoobscura cDNA clone A7 3', mRNA sequence.  
**ACCESSION** DR139870  
**VERSION** DR139870.1 GI:67884960  
**KEYWORDS** EST.  
**SOURCE** Drosophila pseudoobscura  
**ORGANISM** Drosophila pseudoobscura  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 1173)  
 Richards,S., Liu,Y., Bettencourt,B.R., Hradecky,P., Letovsky,S.,  
 Nielsen,R., Thornton,K., Hubisz,M.J., Chen,R., Meisel,R.P.,  
 Couronne,O., Hua,S., Smith,M.A., Zhang,P., Liu,J., Bussemaker,H.J.,  
 van Batenburg,M.F., Howells,S.L., Scherer,S.E., Sodergren,E.,  
 Matthews,B.B., Crosby,M.A., Schroeder,A.J., Ortiz-Barrientos,D.,  
 Rives,C.M., Metzker,M.L., Muzny,D.M., Scott,G., Steffen,D.,  
 Wheeler,D.A., Worley,K.C., Havlak,P., Durbin,K.J., Egan,A.,  
 Gill,R., Hume,J., Morgan,M.B., Miner,G., Hamilton,C., Huang,Y.,  
 Waldron,L., Verdusco,D., Clerc-Blankenburg,K.P., Dubchak,I.,  
 Noor,M.A., Anderson,W., White,K.P., Clark,A.G., Schaeffer,S.W.,  
 Galbart,W., Weinstock,G.M. and Gibbs,R.A.  
 Comparative genome sequencing of Drosophila pseudoobscura:  
 chromosomal, gene, and cis-element evolution  
 Genome Res. 15 (1), 1-18 (2005)  
 15632085  
 Contact: Stephen Richards  
 Human Genome Sequencing Center  
 Baylor College of Medicine  
 One Baylor Plaza, Houston, TX 77030, USA  
 Tel: 713-798-6667  
 Email: [stephen@bcm.tmc.edu](mailto:stephen@bcm.tmc.edu)  
 NCBI Trace Archive: 226722030  
 Insert Length: 1750 Std Error: 0.25.  
 Location/Qualifiers

**FEATURES**  
 source

1. .1173  
 /organism="Drosophila pseudoobscura"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7237"  
 /clone="A7"  
 /dev\_stage="0-18h embryos"  
 /clone\_lib="Drosophila pseudoobscura embryonic cDNA  
 library"  
 /note="Vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo  
 dt priming from poly A+ RNA, directionally cloned"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 9; Length 1173;  
 Best Local Similarity 89.5%; Pred. No. 3.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19  
 ||||| ||||| |||||  
 Db 54 GTCGACGGAAGACCTTT 36

## RESULT 76

BZ548902/c 1330 bp DNA linear GSS 17-DEC-2002  
 LOCUS pacsi-60\_1548.s1 pacsi-60 Pseudomonas aeruginosa genomic clone  
 DEFINITION pacsi-60\_1548, genomic survey sequence.

ACCESSION BZ548902

VERSION BZ548902.1 GI:27152483

KEYWORDS GSS.

SOURCE Pseudomonas aeruginosa

## ORGANISM

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 Pseudomonadaceae; Pseudomonas.

## REFERENCE

1 (bases 1 to 1330)  
 Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,  
 Burns, J.L., Kaul, R. and Olsen, M.V.

## AUTHORS

Whole-Genome-Sequence variation among multiple isolates of

## TITLE

## JOURNAL

## COMMENT

Pseudomonas aeruginosa library  
 J. Bacteriol. (2002) in press  
 Contact: Chris K. Raymond  
 Genome Center  
 University of Washington  
 Box 352145, Seattle, WA 98105-2145, USA  
 Tel: 20622216954  
 Fax: 2066857244  
 Email: craymond@u.washington.edu  
 Class: shotgun.

## FEATURES

source

1..1330  
 /organism="Pseudomonas aeruginosa"  
 /mol\_type="genomic DNA"  
 /strain="1-60"  
 /db\_xref="taxon:287"  
 /clone="pacsi-60\_1548"  
 /clone\_lib="pacsi-60"  
 /note="Clinical isolate 1-60 Whole genomic shotgun  
 library."

## ORIGIN

Query Match 74.5%; Score 16.4; DB 11; Length 1330;  
 Best Local Similarity 94.4%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACGGAAGGCCTTTCGG 22  
 ||||| ||||| |||||  
 Db 1240 AAGGGAAGGCCTTTCGG 1223

## RESULT 77

DT975169 1370 bp mRNA linear EST 22-SEP-2005  
 LOCUS CLJ157-C04.y1d-s SHGC-CLJ Gasterosteus aculeatus cDNA clone  
 DEFINITION CLJ157-C04 5', mRNA sequence.

ACCESSION DT975169

VERSION DT975169.1 GI:76098976

KEYWORDS EST.

## SOURCE

Gasterosteus aculeatus (three spined stickleback)

## ORGANISM

Gasterosteus aculeatus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
 Gasterosteidae; Gasterosteus.  
 1 (bases 1 to 1370)

## REFERENCE

## AUTHORS

TITLE JOURNAL  
 COMMENT

Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,  
 Schmutz, J. and Myers, R.M.  
 Expressed sequence tags from *Gasterosteus aculeatus*  
 Unpublished (2003)  
 Contact: Grimwood, Jane  
 Stanford Human Genome Center  
 Stanford University School of Medicine  
 975 S California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 320 5917  
 Fax: 650 320 5801  
 Email: jane@shgc.stanford.edu  
 Plate: 157  
 High quality sequence stop: 822.

## FEATURES

source

1..1370  
 /organism="Gasterosteus aculeatus"  
 /mol\_type="mRNA"  
 /strain="Bittorfjordur marine sticklebacks, Iceland"  
 /db\_xref="taxon:69293"  
 /clone="CLJ157-C04"  
 /sex="mixed male and female"  
 /tissue\_type="whole larva"  
 /dev\_stage="21 day old larvae collected at Swarup Stage 30  
 (J. Embryol. Exp. Morphol 6: 373-383.1958)"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="SHGC-CLJ"  
 /note="Vector: Express 1; Total and poly A+ RNA was  
 isolated from the indicated stickleback tissue, and a cDNA  
 library was constructed in the Express 1 plasmid vector by  
 Open Biosystems. First strand cDNA synthesis was primed  
 with an 54 bp linker primer containing an oligodT sequence  
 preceded by a synthetic NotI site (first strand primer:  
 5'-GACTAGTTCTAGATCGAGCGGCCGCTT25-3'). Following  
 second strand synthesis, cDNAs were made blunt at the end  
 corresponding to the original 5 prime end of mRNA, and  
 cloned directionally into the NotI and EcoRV sites of  
 Express 1. Note that the EcoRV site is typically destroyed  
 in the blunt end cloning, leaving a junction of the form  
 'xxxATC' (where is ATC is the second half of the EcoRV  
 site, and xxx is derived from the cDNA sequence). A map of  
 the Express 1 vector is available at:  
 http://www.openbiosystems.com/cdna.library.construction.fa  
 g.php#8 The primary library was transformed and amplified  
 in DH10B (T1 phage resistant) bacteria. Clones available  
 from Open Biosystems:  
 http://www.openbiosystems.com/stickleback"

## ORIGIN

Query Match 74.5%; Score 16.4; DB 10; Length 1370;  
 Best Local Similarity 94.4%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCCTTT 19  
 ||||| ||||| |||||  
 Db 982 TCTACGGAAGGCCTTT 999

## RESULT 78

DN730360 1462 bp mRNA linear EST 31-MAR-2005  
 LOCUS CNB52-E02.x1d-t SHGC-CNB Gasterosteus aculeatus cDNA clone  
 DEFINITION CNB52-E02 3', mRNA sequence.

ACCESSION DN730360

VERSION DN730360.1 GI:62106596

KEYWORDS EST.

## SOURCE

Gasterosteus aculeatus (three spined stickleback)

## ORGANISM

Gasterosteus aculeatus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;  
 Gasterosteidae; Gasterosteus.  
 1 (bases 1 to 1462)

## REFERENCE

1 (bases 1 to 1462)  
 Kingsley, D.M., Peichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,



```

/clone_lib="QCJ"

ORIGIN
Query Match      73.6%; Score 16.2; DB 5; Length 267;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2   TCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db      186 TCGAACGGAAGGCTTTCGG 206

RESULT 81
CF044432      288 bp      mRNA      linear      EST 17-JUL-2003
LOCUS      QCJ2907.yg QCJ Zea mays cDNA clone QCJ2907, mRNA sequence.
DEFINITION
ACCESSION      CF044432
VERSION      CF044432.1 GI:32939613
KEYWORDS      EST.
SOURCE
ORGANISM      Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 288)
Genoplante.
Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
JOURNAL
COMMENT      Contact: Genoplante
Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com)
and http://genoplante-info.infobiogen.fr.

FEATURES
source
1..288
/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="QCJ2907"
/tissue_type="cell lignification part of the 6th leaf"
/clone_lib="QCJ"

ORIGIN
Query Match      73.6%; Score 16.2; DB 5; Length 289;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2   TCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db      207 TCGAACGGAAGGCTTTCGG 227

RESULT 82
BW531407      294 bp      mRNA      linear      EST 12-SEP-2005
LOCUS      BW531407 Yutaka Satou unpublished cDNA library (cslv) Ciona
DEFINITION      savigny cDNA clone cslv017020 5', mRNA sequence.
ACCESSION      BW531407
VERSION      BW531407.1 GI:51693105
KEYWORDS      EST.
SOURCE      Ciona savignyi
ORGANISM      Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 294)
Vinson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,E.K.,
Strange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
Nusbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
Assembly of polymorphic genomes: Algorithms and application to

/clone_lib="QCJ"

Ciona savignyi
Genome Res. 15 (8), 1127-1135 (2005)
16077012
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-Ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@cscience.kyoto-u.ac.jp.
Location/Qualifiers
1..294
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cslv017020"
/dev_stage="larva"
/clone_lib="Yutaka Satou unpublished cDNA library (cslv)"

FEATURES
source
1..294
/organism="Ciona savignyi"
/mol_type="mRNA"
/db_xref="taxon:51511"
/clone="cslv017020"
/dev_stage="larva"
/clone_lib="Yutaka Satou unpublished cDNA library (cslv)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 4; Length 294;
Best Local Similarity 85.7%; Pred. No. 3.7e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2   TCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db      271 TCGCCGGGATGCGCTTTCGG 291

RESULT 83
BQ980749      298 bp      mRNA      linear      EST 03-OCT-2005
LOCUS      QGE11022.yg.abl QG-EFGHJ lettuce serriola Lactuca serriola cDNA
DEFINITION      clone QGE11022, mRNA sequence.
ACCESSION      BQ980749
VERSION      BQ980749.1 GI:22398272
KEYWORDS      EST.
SOURCE      Lactuca serriola
ORGANISM      Lactuca serriola
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 298)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
singleton, see http://cgdb.ucdavis.edu/ for details.
Plate: QGE11 row: 0 column: 22.
Location/Qualifiers
1..298
/organism="Lactuca serriola"
/mol_type="mRNA"
/db_xref="taxon:75943"
/clone="QGE11022"
/lab_host="E.coli"
/clone_lib="QG-EFGHJ lettuce serriola"
/notes="vector: pBRCDNASFIAB: The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
```



REFERENCE AUTHORS	1 (bases 1 to 346) McCulloch,A., Wilson,T., Molenaar,A., Grigor,M., Davis,S., Glenn,M., Havukkala,I., Watson,J., Crawford,A., Wheeler,T., Hagemann,L., Lee,R., Hein,W., Johnstone,P., Maqbool,N., McMahon,C., McCracken,J., Stelwagen,K., Farr,V., Singh,K., Whitley,J., Nicholas,K., Savin,K., Mather,A., McPartlan,H., Whitley,J., Wells,M., Bowman,P., Goddard,M., Langford,C., McEwan,J. and Atkinson,P.
TITLE	AgResearch, Genesis and Primary Industry Victoria Bovine EST Project
JOURNAL COMMENT	Unpublished (2006) Contact: Maqbool N AgResearch Ltd. Invermay Agricultural Centre, Puddle Alley, Private Bag 50034, Mosgiel, New Zealand Email: nauman.maqbool@agresearch.co.nz.
FEATURES source	Location/Qualifiers 1. .346 /organism="Bos taurus" /mol_type="mRNA" /db_xref="taxon:9913" /tissue_type="Posterior brain" /clone_lib="BPBA" /notes="Vector: pBK-CMV; Bovine posterior brain stem cDNA library derived from tissue harvested from an unknown breed calf by Allan Crawford on 28/09/99"
ORIGIN	Query Match 73.6%; Score 16.2; DB 10; Length 346; Best Local Similarity 85.7%; Pred. No. 3.8e+03; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 2 TCGAACGGAAGGCCTTCGG 22       Db 96 TCAAAAGGAAGGCATTTCGG 116 
RESULT 87	
CZ003780/c	
LOCUS	CZ003780 370 bp DNA linear GSS 04-JAN-2005
DEFINITION	OA_BBa0052008.r OA_BBa Oryza alta genomic clone OA_BBa0052008 3', genomic survey sequence.
ACCESSION	CZ003780
VERSION	CZ003780.1 GI:57034984
KEYWORDS	GSS.
SOURCE	Oryza alta
ORGANISM	Oryza alta Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE AUTHORS	1 (bases 1 to 370) SanMiguel,P., Westerman,R., Kim,H., Yu,Y., Wissotski,M., Yost,D., Scum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A. OMAP (Oryza Map Alignment Project) - Purdue University Unpublished (2004) Contact: Scott A. Jackson Jackson Laboratory Purdue University 915 W. State St., West Lafayette, IN 47907, USA Tel: 7654963621 Fax: 7654967255 Email: sjackson@purdue.edu
TITLE	Basecalling by phred version 0.020425.c. This sequence was derived from the raw sequence read by clipping with Lucy version 1.19e.
JOURNAL COMMENT	Bases 180-549 of the raw sequence (length 978) were retained after clipping. Plate: 0052 row: 0 column: 08 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.
FEATURES source	Location/Qualifiers 1. .370 /organism="Oryza alta"
REFERENCE AUTHORS	1 (bases 1 to 379) Email: cgabbs-r@mail.nih.gov Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html
TITLE	Trace considered overall poor quality Insert Length: 705 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 1.
FEATURES source	Location/Qualifiers 1. .379 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:1188756" /sex="Male" /dev_stage="45 years old" /lab_host="DH10B" /clone_lib="NCI CGAP Pr2" /notes="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with oligo(dT)17 on 50 ng of DNase-treated, total cellular RNA obtained from 5,000-10,000 microdissected preneoplastic cells histologically-determined to be prostatic intraepithelial neoplasia 2 (PIN2) cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was
ORIGIN	Query Match 73.6%; Score 16.2; DB 13; Length 370; Best Local Similarity 85.7%; Pred. No. 3.8e+03; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Qy 2 TCGAACGGAAGGCCTTCGG 22       Db 47 TCGAACGGAAGGCCTCCCG 27 
RESULT 88	
AA652906	
LOCUS	AA652906 379 bp mRNA linear EST 25-NOV-1997
DEFINITION	ns68a07.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1188756 similar to gb:U01124 40S RIBOSOMAL PROTEIN S13 (HUMAN);, mRNA sequence.
ACCESSION	AA652906
VERSION	AA652906.1 GI:2584558
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE AUTHORS	1 (bases 1 to 379) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov
JOURNAL COMMENT	Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html



```

ORIGIN
Query Match      73.6%; Score 16.2; DB 1; Length 379;
Best Local Similarity 85.7%; Pred. No. 3.8e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 352 TCGAAAGGAAGGCGCTTTCGG 372

RESULT 89
CK291892
LOCUS
DEFINITION
EST754606 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMC541 3'
end, mRNA sequence.
CK291892
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 390)
AUTHORS
Buell, C.R., Hart, A., Zismann, V., Katamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE
Generation of EST sequences from Nicotiana benthamiana
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST754605
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

FEATURES
Location/Qualifiers
source
1..390
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMC541"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomatos 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      73.6%; Score 16.2; DB 5; Length 390;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 241 TCGAAAGGGAAGGCGCTTTCGG 261

RESULT 90

```

```

AW400594
LOCUS
DEFINITION
LamdiSest091est L.digitata sporophyte Lambda ZapII Laminaria
digitata cDNA, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Laminaria digitata
Laminaria digitata
Eukaryota; stramenopiles; Phaeophyceae; Laminariales;
Laminariaceae; Laminaria.
1 (bases 1 to 399)
REFERENCE
AUTHORS
Crepineau, F., Roscoe, T., Kaas, R., Kloareg, B. and Boyen, C.
TITLE
Characterisation of complementary DNAs from the expressed sequence
tag analysis of life cycle stages of Laminaria digitata
(Phaeophyceae)
JOURNAL
Plant Mol. Biol. 43 (4), 503-513 (2000)
PUBMED
11052202
COMMENT
Contact: Boyen C
Centre d'Etudes Oceanologique et de Biologie Marine
CNRS-LPR9042, Universite P. & M. Curie
BP74, F-29682 Roscoff cedex, France
Tel: 33 2 98 29 23 32
Fax: 33 2 98 29 23 24
Email: est@sb-roscoff.fr.
FEATURES
Location/Qualifiers
source
1..399
/organism="Laminaria digitata"
/mol_type="mRNA"
/db_xref="taxon:80365"
/dev_stage="sporophyte"
/lab_host="SOLR"
/clone_lib="L.digitata sporophyte Lambda ZapII"
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:
XhoI; The Laminaria sporophyte library, constructed by T
Roscoe and F Crepineau, was oligo-(dT) primed and
directionally cloned into a Uni-ZAPTM XR vector
(Stratagene, la Jolla, CA, USA) using total mRNA from
sporophytes harvested at 1'ile de Sieck (F)."

ORIGIN
Query Match      73.6%; Score 16.2; DB 7; Length 399;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 199 TCGAACGTAAGACCTGTCGG 219

RESULT 91
CG857155/c
LOCUS
DEFINITION
ZMMBBC0465N21r ZMMBBC (EcoRI) Zea mays genomic clone ZMMBBC0265N21
3', genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 431)
REFERENCE
AUTHORS
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
TITLE
Sequencing of the maize genome at PGR (2003c)
JOURNAL
Unpublished (2003)
COMMENT
Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA

```

```

Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 105.
Location/Qualifiers
  1. .431
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /cultivar="B73"
  /db_xref="taxon:4577"
  /clone="ZMMBc0265N21"
  /lab_host="E. coli DH10B"
  /clone_lib="ZMMBc (EcoRI)"
  /notes="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      73.6%; Score 16.2; DB 12; Length 431;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GTCAACGGAAGGCGCTTCG 21
      ||||| || ||||| |||||
DB   78  GTCGAGCGTCAAGGCGCTTCG 58

RESULT 92
BW530083
LOCUS
DEFINITION      490 bp mRNA linear EST 23-AUG-2005
savigny Ciona savignyi cDNA clone cs1v013h24 5', mRNA sequence.
ACCESSION      BW530083
VERSION
KEYWORDS
SOURCE
ORGANISM        Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE
  1 (bases 1 to 490)
  Vanson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,E.K.,
  Strange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
  Nussbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
  Assembly of polymorphic genomes: Algorithms and application to
  Ciona savignyi
  Genome Res. 15 (8), 1127-1135 (2005)
16077012
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
  source
  1. .490
  /organism="Ciona savignyi"
  /mol_type="mRNA"
  /db_xref="taxon:51511"
  /clone="cs1v013h24"
  /dev_stage="larva"
  /clone_lib="Yutaka Satou unpublished cDNA library (cs1v)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 4; Length 490;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TCGAACGGAAGGCGCTTCG 22
      ||||| ||||| ||||| |||||
DB   257  TCGCCGGAATGCGCTTCG 277

Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 105.
Location/Qualifiers
  1. .431
  /organism="Zea mays"
  /mol_type="genomic DNA"
  /cultivar="B73"
  /db_xref="taxon:4577"
  /clone="ZMMBc0265N21"
  /lab_host="E. coli DH10B"
  /clone_lib="ZMMBc (EcoRI)"
  /notes="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN
Query Match      73.6%; Score 16.2; DB 12; Length 431;
Best Local Similarity 85.7%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  1  GTCAACGGAAGGCGCTTCG 21
      ||||| || ||||| |||||
DB   78  GTCGAGCGTCAAGGCGCTTCG 58

RESULT 92
BW530083
LOCUS
DEFINITION      490 bp mRNA linear EST 23-AUG-2005
savigny Ciona savignyi cDNA library (cs1v) Ciona
ACCESSION      BW530083
VERSION
KEYWORDS
SOURCE
ORGANISM        Ciona savignyi
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE
  1 (bases 1 to 490)
  Vanson,J.P., Jaffe,D.B., O'Neill,K., Karlsson,E.K.,
  Strange-Thomann,N., Anderson,S., Mesirov,J.P., Satoh,N., Satou,Y.,
  Nussbaum,C., Birren,B., Galagan,J.E. and Lander,E.S.
  Assembly of polymorphic genomes: Algorithms and application to
  Ciona savignyi
  Genome Res. 15 (8), 1127-1135 (2005)
16077012
Contact: Yutaka Satou
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4095
Fax: 81-75-705-1113
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

FEATURES
  source
  1. .490
  /organism="Ciona savignyi"
  /mol_type="mRNA"
  /db_xref="taxon:51511"
  /clone="cs1v013h24"
  /dev_stage="larva"
  /clone_lib="Yutaka Satou unpublished cDNA library (cs1v)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 4; Length 490;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TCGAACGGAAGGCGCTTCG 22
      ||||| ||||| ||||| |||||
DB   257  TCGCCGGAATGCGCTTCG 277

RESULT 93
AA640643
LOCUS
DEFINITION      492 bp mRNA linear EST 27-OCT-1997
nr22c11.r1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1168724
similar to SW:SSRE_HUMAN P43308 TRANSLOCON-ASSOCIATED PROTEIN, BETA
SUBUNIT PRECURSOR ;, mRNA sequence.
ACCESSION      AA640643
VERSION
KEYWORDS
SOURCE
ORGANISM        Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 492)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/brp/image/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 314.
Location/Qualifiers
  1. .492
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:1168724"
  /sex="Male"
  /dev_stage="45 years old"
  /lab_host="DH10B"
  /clone_lib="NCI_CGAP_Pr2"
  /notes="Vector: pAMP10; Site_1: NotI; Site_2: EcoRI; 1st
  strand cDNA was primed with oligo(dT)17 on 50 ng of
  DNase-treated, total cellular RNA obtained from
  5,000-10,000 microdissected preneoplastic cells
  histologically determined to be prostatic intraepithelial
  neoplasia 2 (PIN2) cells. Double-stranded cDNA was
  ligated to EcoRI adaptors, 5 cycles of PCR applied to the
  cDNA with an adaptor-specific primer, and the resulting
  PCR product subcloned into pAMP10 by the UDG-cloning
  method (Life Technologies). Average insert size is 600
  bp. NOTE: Not directionally cloned. This library was
  constructed by David Krizman."

ORIGIN
Query Match      73.6%; Score 16.2; DB 1; Length 492;
Best Local Similarity 85.7%; Pred. No. 4e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY  2  TCGAACGGAAGGCGCTTCG 22
      ||||| ||||| ||||| |||||
DB   1  TCGACCGGAAGGCGCTTCG 21

RESULT 94
DU596062
LOCUS
DEFINITION      498 bp DNA linear GSS 12-OCT-2005
OO_Ba0091105.r OO_Ba Oryza officinalis genomic clone
OO_Ba0091105 3', genomic survey sequence.
ACCESSION      DU596062
VERSION
KEYWORDS
SOURCE
ORGANISM        Oryza officinalis

```

Query Match 73.6%; Score 16.2;

Best Local Similarity 85.7%; Pred. No. 4e+03; Mismatches 3; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 2 TCGAACGGAAGGCTTTTCG 22  
|||||  
Db 83 TCGAACGGAATGCTGCGG 103  
|||||

RESULT 97  
LOCUS CX608591/c  
DEFINITION ANR1\_39\_B09\_g1\_A002 mRNA linear EST 14-JAN-2005  
ANR1\_39\_B09\_A002 5', mRNA sequence.  
ACCESSION CX608591  
VERSION CX608591.1 GI:57807311  
KEYWORDS EST.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
REFERENCE 1 (Bases 1 to 537)  
Cordonnier-Pratt,M.-M., Suzuki,Y., Sugano,S., Klein,R., Lim,S.,  
Liang,C., Sun,F. and Pratt,L.H.  
A Sorghum EST database: anaerobic roots  
Unpublished (2005)  
Other\_ESTs: ANR1\_39\_B09.bi\_A002  
Contact: Cordonnier-Pratt MM  
Laboratory for Genomics and Bioinformatics  
The University of Georgia, Department of Plant Biology  
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
Tel: 706 542 1860  
Fax: 706 583 0210  
Email: mmpratt@uga.edu  
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
the Human Genome Center, University of Tokyo Institute of Medical  
Science; plant material and RNA prepared at Texas A & M University;  
sequencing done in the Laboratory for Genomics and Bioinformatics,  
University of Georgia. Sequence ends have been trimmed to exclude  
vector and regions below Phred quality 16. Three-prime sequences  
are presented as their reverse complement and have been trimmed to  
exclude polyA.  
Seq primer: Sug5 (CTTCTGCTCTAAAGCTCGC).

FEATURES  
source  
Location/Qualifiers  
1..537  
/organism="Sorghum bicolor"  
/mol\_type="mRNA"  
/cultivar="BTx623"  
/db\_xref="taxon:4558"  
/clone="ANR1\_39\_B09\_A002"  
/lab\_host="Anaerobic roots"  
/clone\_lib="Anaerobic roots"  
/note="Organ: Root; Vector: pME18S-FL3; Site 1: XhoI;  
Site 2: XhoI; The library was prepared from polyA+ RNA  
isolated from seedlings of sorghum BTx623 grown in  
hydroponic culture. At 8 days of age, medium was purged  
with nitrogen gas for 3 hr prior to stopping aeration.  
Roots were harvested after 3, 27, and 72 hr. Material from  
all time points was combined prior to RNA isolation.  
Double-stranded cDNA was cloned unidirectionally into  
different DraIII sites of the pME18S-FL3 vector (5-prime  
DraIII site is CACTGTGTG, 3-prime DraIII site is  
CACCATGTG). XhoI excises the cDNA insert."

ORIGIN  
Query Match 73.6%; Score 16.2; DB 9; Length 537;  
Best Local Similarity 85.7%; Pred. No. 4.1e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 TCGAACGGAAGGCTTTTCG 22  
|||||  
Db 21 TCGAACTGAAGGCTTTTGGG 1  
|||||

RESULT 98  
LOCUS CB826166/c  
DEFINITION

ACCESSION CB826166.1 GI:29963900  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

The Washington Univ. Nematode EST Project, 1999  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
This library was generated by cloning cDNAs directionally into  
Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI  
are at the 3'-end). The library was excised [now in pBluescript  
SK(+)] and normalized (Bonaldo et al 1996 Genome Research  
6:791-806). Library constructed by Thomas Baum (tbaum@iastate.edu),  
Iowa State University, Plant Pathology Department and Jeff  
McDermott (jpmcderm@iastate.edu).  
Seq primer: -40RP from Gibco  
High quality sequence stop: 466.

FEATURES  
source  
Location/Qualifiers  
1..548  
/organism="Heterodera glycines"  
/mol\_type="mRNA"  
/db\_xref="taxon:51029"  
/sex="female"  
/tissue\_type="whole organism"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Heterodera glycines virgin female"  
/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;  
Site 2: EcoRI; This library was generated by cloning cDNAs  
directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI  
are at the 5'-end and T7/XhoI are at the 3'-end). The  
library was excised [now in pBluescript SK(+)] and  
normalized (Bonaldo et al 1996 Genome Research 6:791-806).  
Library constructed by Thomas Baum (tbaum@iastate.edu),  
Iowa State University, Plant Pathology Department and Jeff  
McDermott (jpmcderm@iastate.edu)."

ORIGIN  
Query Match 73.6%; Score 16.2; DB 4; Length 548;  
Best Local Similarity 85.7%; Pred. No. 4.1e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GTCGAACGGAAGGCTTTTCG 21  
|||||  
Db 94 GCCAAACGGAAATGCTTTTCG 74  
|||||

RESULT 99  
LOCUS AV822903  
DEFINITION

AV822903 565 bp mRNA linear EST 01-APR-2002

```

DEFINITION AV822903 RAFL5 Arabidopsis thaliana cDNA clone RAFL05-13-A02 5',
mRNA sequence.
ACCESSION AV822903
VERSION AV822903.1 GI:19864955
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 565)
AUTHORS Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@r.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
further details.

FEATURES             source
     source
     1..565
         /organism="Arabidopsis thaliana"
         /mol_type="mRNA"
         /db_xref="taxon:3702"
         /clone="RAFL05-13-A02"
         /dev_stage="rosette plants"
         /lab_host="SOLR"
         /clone_lib="RAFL5"
         /note="Site 1: SstI; Site 2: XhoI; subjected to
dehydration-treated(1,2,5,10,24 hr)"

ORIGIN
Query Match      73.6%; Score 16.2; DB 7; Length 565;
Best Local Similarity 81.8%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 446 GTCGAAAGGAAGGACTTTCG 467

RESULT 100
CW966724/C
LOCUS CW966724 569 bp DNA linear GSS 21-DEC-2004
DEFINITION A1AA-aab55f11.g1 Ancylostoma caninum whole genome shotgun library
(A1AAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.
ACCESSION CW966724
VERSION CW966724.1 GI:56767451
KEYWORDS GSS.
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Ancylostoma caninum
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidae; Ancylostomatidae; Ancylostominae; Ancylostoma.
REFERENCE 1 (bases 1 to 569)
AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Ritter,E., Tsagareishvili,R.,
Ronko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D.,
Waterston,R.H., Clifton,S.W. and Wilson,R.
TITLE Genome Survey sequences from the parasitic nematode Ancylostoma
caninum
JOURNAL Unpublished (2004)
COMMENT Contact: Mitreva M
Washington University in St. Louis
Washington University School of Medicine

```

```

FEATURES             source
     source
     1..569
         /organism="Ancylostoma caninum"
         /mol_type="genomic DNA"
         /strain="Baltimore"
         /db_xref="taxon:29170"
         /dev_stage="Adult"
         /lab_host="GS10"
         /clone_lib="Ancylostoma caninum whole genome shotgun
library (A1AAGSS 001)"
         /note="Vector: POTW13; Site 1: BstXI; Site 2: BstXI;
Ancylostoma caninum genomic DNA was randomly sheared,
end-repaired and size fractionated to enrich for 2-4 kb
fragments. Genomic DNA was provided by John Hawdon
(mtmjnh@gwumc.edu) at George Washington University.
Sequencing by Washington University Genome Sequencing
Center, St. Louis, MO."

ORIGIN
Query Match      73.6%; Score 16.2; DB 13; Length 569;
Best Local Similarity 85.7%; Pred. No. 4.1e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22
    ||||| ||||| ||||| ||||| |||||
Db 510 TCGAACTGAAATGCTTTAGG 490

```

Search completed: May 19, 2006, 07:06:01  
Job time : 1491.35 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 18, 2006, 23:59:38 ; Search time 67.3253 Seconds

(without alignments)  
611.425 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacggaaggcttcgg 22

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database :

Issued Patents\_NA.\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq.\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq.\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq.\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq.\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq.\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq.\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq.\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq.\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq.\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	3	US-09-738-274-23
2	21	95.5	24	3	US-09-738-274-22
3	21	95.5	25	3	US-09-738-274-21
4	19	86.4	19	3	US-09-738-274-24
5	18.8	85.5	1584	3	US-09-949-230A-1
6	17.4	79.1	25	2	US-08-485-602-61
7	17.4	79.1	25	2	US-08-757-180-60
8	17.4	79.1	25	2	US-08-745-638-61
9	17.4	79.1	32	3	US-09-738-972-7
10	17.4	79.1	32	3	US-09-738-972-14
11	17.2	78.2	1437	3	US-10-085-871C-1
12	17.2	78.2	1471	3	US-10-085-871C-2
13	17.2	78.2	1488	5	US-10-756-683B-1
14	17	77.3	1475	3	US-08-641-291A-92
15	16.4	74.5	23	2	US-08-485-602-56
16	16.4	74.5	23	2	US-08-757-180-55
17	16.4	74.5	23	2	US-08-745-638-56
18	16	72.7	23	3	US-09-738-274-27
19	16	72.7	26	3	US-09-738-274-28
20	16	72.7	1460	3	US-09-463-618A-1
21	16	72.7	1460	3	US-10-062-777-1
22	15.8	71.8	32	3	US-09-738-274-14
23	15.8	71.8	375	3	US-09-489-039A-1391

Sequence 7, Appli	15.8	71.8	573	2	US-08-008-216-7	Sequence 7, Appli
Sequence 7, Appli	15.8	71.8	573	2	US-08-459-569-7	Sequence 7, Appli
Sequence 7, Appli	15.8	71.8	573	2	US-08-458-831-7	Sequence 7, Appli
Sequence 6, Appli	15.8	71.8	1074	2	US-08-008-216-6	Sequence 6, Appli
Sequence 6, Appli	15.8	71.8	1074	2	US-08-459-569-6	Sequence 6, Appli
Sequence 6, Appli	15.8	71.8	1074	2	US-08-458-831-6	Sequence 6, Appli
Sequence 1, Appli	15.8	71.8	1464	2	US-08-938-858-1	Sequence 1, Appli
Sequence 7, Appli	15.8	71.8	1464	3	US-09-726-774-7	Sequence 7, Appli
Sequence 19, Appli	15.8	71.8	21126	2	US-08-008-216-19	Sequence 19, Appli
Sequence 19, Appli	15.8	71.8	21126	2	US-08-459-569-19	Sequence 19, Appli
Sequence 134, Appli	15.8	71.8	21126	2	US-08-458-831-19	Sequence 134, Appli
Sequence 134, Appli	15.8	71.8	36241	3	US-08-311-731A-134	Sequence 134, Appli
Sequence 134, Appli	15.8	71.8	36241	3	US-08-311-731A-123	Sequence 134, Appli
Sequence 2, Appli	15.8	71.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
Sequence 2, Appli	15.8	71.8	4411529	3	US-09-103-840A-1	Sequence 2, Appli
Sequence 27, Appli	15.6	70.9	439	3	US-09-585-173B-27	Sequence 27, Appli
Sequence 175493	15.6	70.9	601	3	US-09-949-016-175492	Sequence 175493
Sequence 3119, Ap	15.6	70.9	601	3	US-09-949-016-175493	Sequence 3119, Ap
Sequence 190, App	15.6	70.9	1662	3	US-09-489-039A-3119	Sequence 190, App
Sequence 3095, Ap	15.6	70.9	2444	3	US-09-640-211A-190	Sequence 3095, Ap
Sequence 39, Appli	15.6	70.9	3111	3	US-09-489-039A-3095	Sequence 39, Appli
Sequence 16723, A	15.6	70.9	3257	3	US-09-585-173B-39	Sequence 16723, A
Sequence 53, Appli	15.6	70.9	157822	3	US-09-949-016-16723	Sequence 53, Appli
Sequence 52, Appli	15.4	70.0	27	2	US-08-485-602-53	Sequence 52, Appli
Sequence 8, Appli	15.4	70.0	27	2	US-08-757-180-52	Sequence 8, Appli
Sequence 15, Appli	15.4	70.0	28	3	US-09-738-972-8	Sequence 15, Appli
Sequence 60, Appli	15.4	70.0	28	3	US-09-738-972-15	Sequence 60, Appli
Sequence 1958, Ap	15.4	70.0	455	3	US-09-640-211A-60	Sequence 1958, Ap
Sequence 474, Ap	15.4	70.0	455	3	US-09-640-211A-1958	Sequence 474, Ap
Sequence 21756, A	15.4	70.0	466	3	US-09-270-767-6474	Sequence 21756, A
Sequence 4420, Ap	15.4	70.0	466	3	US-09-270-767-21756	Sequence 4420, Ap
Sequence 1218, Ap	15.4	70.0	861	3	US-09-902-540-4420	Sequence 1218, Ap
Sequence 1639, Ap	15.4	70.0	23677	3	US-09-902-540-1218	Sequence 1639, Ap
Sequence 135682, App	15.2	69.1	409	3	US-09-533-559-1639	Sequence 135682, App
Sequence 21, Appli	15.2	69.1	601	3	US-09-949-016-125682	Sequence 21, Appli
Sequence 21, Appli	15.2	69.1	601	3	US-09-221-017B-580	Sequence 21, Appli
Sequence 2261, Ap	15.2	69.1	622	3	US-09-657-289A-21	Sequence 2261, Ap
Sequence 15307, A	15.2	69.1	1392	3	US-09-257-584-1	Sequence 15307, A
Sequence 16038, A	15.2	69.1	1542	3	US-09-134-000C-2261	Sequence 16038, A
Sequence 209, App	15.2	69.1	13282	3	US-09-949-016-15307	Sequence 209, App
Sequence 689, App	15.2	69.1	166698	3	US-09-949-016-16038	Sequence 689, App
Sequence 221, App	15.2	69.1	611587	4	US-09-531-120-209	Sequence 221, App
Sequence 221, App	15.2	69.1	1429	3	US-09-023-655-689	Sequence 221, App
Sequence 221, App	14.8	67.3	87	2	US-08-433-126A-221	Sequence 221, App
Sequence 221, App	14.8	67.3	87	2	US-08-433-126A-221	Sequence 221, App
Sequence 221, App	14.8	67.3	87	3	US-08-976-413A-221	Sequence 221, App
Sequence 408, App	14.8	67.3	87	7	PCT-US96-06059-221	Sequence 408, App
Sequence 2742, Ap	14.8	67.3	107	3	US-09-016-434-408	Sequence 2742, Ap
Sequence 5578, Ap	14.8	67.3	362	3	US-09-513-999C-2742	Sequence 5578, Ap
Sequence 5650, Ap	14.8	67.3	532	3	US-09-270-767-29724	Sequence 5650, Ap
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c 108	14.6	66.4	417	3	US-09-252-991A-3429	Sequence 3429, Ap	181	14.4	65.5	37068	3	US-09-949-016-12543	Sequence 12543, A
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ALIGNMENTS

; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-23

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Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GTCGAACGGAAGGCTTTCG 22

RESULT 2
US-09-738-274-22
; Sequence 22, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: primer
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US-09-738-274-22

Query Match 95.5%; Score 21; DB 3; Length 24;
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RESULT 3
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; Sequence 21, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
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; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
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US-09-738-274-21

Query Match 95.5%; Score 21; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.19;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
US-09-738-274-24  
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; Patent No. 6664081  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-24

Query Match 86.4%; Score 19; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 GAACGGAAGCCCTTCG 19

RESULT 5  
US-09-949-230A-1  
; Sequence 1, Application US/09949230A  
; Patent No. 6551591  
; GENERAL INFORMATION:  
; APPLICANT: Essential Therapeutics, Inc.  
; TITLE OF INVENTION: New Antibiotics for Microbispora  
; FILE REFERENCE: 262/095

; CURRENT APPLICATION NUMBER: US/09/949,230A  
; CURRENT FILING DATE: 2001-09-07  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1584  
; TYPE: DNA  
; ORGANISM: Microbispora corallina  
; FEATURE:  
; NAME/KEY: n  
; LOCATION: (1350)..(1584)  
; OTHER INFORMATION: Unsure  
; NAME/KEY: misc feature  
; LOCATION: (1350)..(1584)  
; OTHER INFORMATION: Unsure  
US-09-949-230A-1

Query Match 85.5%; Score 18.8; DB 3; Length 1584;  
Best Local Similarity 90.9%; Pred. No. 5.7;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 128 GTCGAGCGGAAGCCCTTCG 149

RESULT 6  
US-08-485-602-61  
; Sequence 61, Application US/08485602  
; Patent No. 5712095  
; GENERAL INFORMATION:  
; APPLICANT: Britschgi, Theresa B.  
; APPLICANT: Cangelosi, Gerard A.  
; TITLE OF INVENTION: Rapid and Sensitive Detection of  
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide  
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,602  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/261,068  
; FILING DATE: 16-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 11652-79-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: rRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium habana  
US-08-485-602-61

Query Match 79.1%; Score 17.4; DB 2; Length 25;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22  
||||| :|||  
Db 1 CGAACGGAAGNCCUUCGG 20

## RESULT 7

US-08-757-180-60  
; Sequence 60, Application US/08757180  
; Patent No. 5726021  
; GENERAL INFORMATION:  
; APPLICANT: Britschgi, Theresa B  
; APPLICANT: Cangelosi, Gerard A  
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT  
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM  
; NUMBER OF SEQUENCES: 98  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10020  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,180  
; FILING DATE: 27-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/261,068  
; FILING DATE: 16-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hsi, Petrina S  
; REGISTRATION NUMBER: 38,496  
; REFERENCE/DOCKET NUMBER: BD3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-596-9000  
; TELEFAX: 212-596-9090  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: rRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium simiae  
US-08-757-180-60

Query Match 79.1%; Score 17.4; DB 2; Length 25;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22  
||||| :|||  
Db 1 CGAACGGAAGNCCUUCGG 20

## RESULT 8

US-08-745-638-61  
; Sequence 61, Application US/08745638  
; Patent No. 5770373  
; GENERAL INFORMATION:  
; APPLICANT: Britschgi, Theresa B.  
; APPLICANT: Cangelosi, Gerard A.

; TITLE OF INVENTION: Rapid and Sensitive Detection of  
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide  
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors  
; NUMBER OF SEQUENCES: 89  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Street Tower  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105-1492

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/745,638  
; FILING DATE: 08-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,602  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/261,068  
; FILING DATE: 16-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 11652-79-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: rRNA  
; ORIGINAL SOURCE:  
; ORGANISM: Mycobacterium habana  
US-08-745-638-61

Query Match 79.1%; Score 17.4; DB 2; Length 25;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 16; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTCGG 22  
||||| :|||  
Db 1 CGAACGGAAGNCCUUCGG 20

## RESULT 9

US-09-738-972-7  
; Sequence 7, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES  
; FILE REFERENCE: GP119-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: primer  
US-09-738-972-7

Query Match 79.1%; Score 17.4; DB 3; Length 32;  
Best Local Similarity 94.7%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19  
Db 5 GTCGAACGGAAGGCCTCT 23

## RESULT 10

US-09-738-972-14/C  
; Sequence 14, Application US/09738972  
; Patent No. 6747141  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: LANKFORD, Roger L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM  
; FILE REFERENCE: GPl19-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,972  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/171,202  
; PRIOR FILING DATE: 1999-12-15  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-738-972-14

Query Match 79.1%; Score 17.4; DB 3; Length 32;  
Best Local Similarity 94.7%; Pred. No. 14;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19  
Db 28 GTCGAACGGAAGGCCTCT 10

## RESULT 11

US-10-085-871C-1  
; Sequence 1, Application US/10085871C  
; Patent No. 6716615  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Schung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/085,871C  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1437  
; TYPE: DNA  
; ORGANISM: Saccharothrix 44442  
US-10-085-871C-1

Query Match 78.2%; Score 17.2; DB 3; Length 1437;  
Best Local Similarity 86.4%; Pred. No. 38;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

## RESULT 12

US-10-085-871C-2  
; Sequence 2, Application US/10085871C  
; Patent No. 6716615  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Fang-Yu  
; APPLICANT: Lee, Ming-Liang  
; APPLICANT: Anderson, Hong C.  
; APPLICANT: Chiu, Schung-Ching  
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
; FILE REFERENCE: 004135.P005  
; CURRENT APPLICATION NUMBER: US/10/085,871C  
; CURRENT FILING DATE: 2002-02-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 1471  
; TYPE: DNA  
; ORGANISM: Saccharothrix 45494  
US-10-085-871C-2

Query Match 78.2%; Score 17.2; DB 3; Length 1471;  
Best Local Similarity 86.4%; Pred. No. 38;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

## RESULT 13

US-10-756-683B-1  
; Sequence 1, Application US/10756683B  
; Patent No. 7022875  
; GENERAL INFORMATION:  
; APPLICANT: Hwang, Byung Kook  
; APPLICANT: Lee, Jung Yeop  
; TITLE OF INVENTION: THIOTUTACIN AND ANTIFUNGAL AND ANTIOOMYCETE COMPOSITION FOR  
; TITLE OF INVENTION: CONTROLLING PLANT DISEASES USING THE SAME  
; FILE REFERENCE: 4228-102  
; CURRENT APPLICATION NUMBER: US/10/756,683B  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: KR 10-2003-0015628  
; PRIOR FILING DATE: 2003-03-13  
; PRIOR APPLICATION NUMBER: KR 10-2003-0015629  
; PRIOR FILING DATE: 2003-03-13  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1488  
; TYPE: DNA  
; ORGANISM: Lechevalieria aerocolonigenes  
US-10-756-683B-1

Query Match 78.2%; Score 17.2; DB 5; Length 1488;  
Best Local Similarity 86.4%; Pred. No. 38;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
Db 46 GTCGAGCGGTAAGGCCCTTCGG 67

## RESULT 14

US-08-641-291A-92  
; Sequence 92, Application US/08641291A  
; Patent No. 6037122

```
;
; GENERAL INFORMATION:
; APPLICANT: MABILAT Claude
; TITLE OF INVENTION: NUCLEOTIDE FRAGMENT OF THE 16S RIBOSOMAL RNA OF CORYNEBACTERI
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release # 1.0, version # 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/641,291A
; FILING DATE: 30-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 38273
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1475 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: rRNA
; US-08-641-291A-92

Query Match 77.3%; Score 17; DB 3; Length 1475;
Best Local Similarity 88.2%; Pred. No. 48;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCT 17
   |||||
Db 28 GUCGAACGGAAGGCCU 44

RESULT 15
US-08-485-602-56
; Sequence 56, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; US-08-485-602-56

Query Match 74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTCGG 22
   |||||
Db 1 GAACGGAAGNCCUCCG 19

RESULT 16
US-08-757-180-55
; Sequence 55, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B
; APPLICANT: Cangelosi, Gerard A
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
```

```
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
US-08-757-180-55

Query Match          74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22
Db 1 GAACGGAAGNCCCUCCG 19

RESULT 17
US-08-745-638-56
; Sequence 56, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: tRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
US-08-745-638-56

Query Match          74.5%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 44;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22
Db 1 GAACGGAAGNCCCUCCG 19

, RESULT 18
```

```
US-09-738-274-27
; Sequence 27, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-27

Query Match          72.7%; Score 16; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 4 GTCGAACGGAAGGCC 19

RESULT 19
US-09-738-274-28
; Sequence 28, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-28

Query Match          72.7%; Score 16; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 1 GTCGAACGGAAGGCC 16
```

```
RESULT 20
US-09-463-618A-1
; Sequence 1, Application US/09463618A
; Patent No. 6368835
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/09/463,618A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-09-463-618A-1

Query Match          72.7%; Score 16; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 42 GTCGAACGGAAGGCC 57

RESULT 21
US-10-062-777-1
; Sequence 1, Application US/10062777
; Patent No. 6589774
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142WO
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          72.7%; Score 16; DB 3; Length 1460;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 42 GTCGAACGGAAGGCC 57

RESULT 22
US-09-738-274-14
; Sequence 14, Application US/09738274
; Patent No. 6664081
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
```

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; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GPl07-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-14

Query Match          71.8%; Score 15.8; DB 3; Length 32;
Best Local Similarity 89.5%; Pred. No. 95;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTT 19
Db 5 GTCGAACGGAAGGCTCT 23

RESULT 23
US-09-489-039A-1391
; Sequence 1391, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709, 2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1391
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1391

Query Match          71.8%; Score 15.8; DB 3; Length 375;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCCTTTTCG 21
Db 332 CGAACGGAAGGCCCTTTTCG 350

RESULT 24
US-08-008-216-7
; Sequence 7, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: R1 T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
```

```
;
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: through 5643 of Seq. ID No. 5366887 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-008-216-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAAGGCCTTT 19
|||||
Db 507 GTCGACGCGACAGGCCTTT 525

RESULT 25
US-08-459-569-7
; Sequence 7, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: through 5643 of Seq. ID No. 5543501 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-459-569-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGCGAAAGGCCTTT 19
|||||
Db 507 GTCGACGCGACAGGCCTTT 525

RESULT 26
US-08-458-831-7
; Sequence 7, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 573 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (1..573)
; OTHER INFORMATION: /label= ORF7
; OTHER INFORMATION: /note= "Sequence ORF7 corresponds to bases 5071
; Patent No. 5824866
; OTHER INFORMATION: through 5643 of Seq. ID No. 5824866 19. It is read 5' to
; OTHER INFORMATION: 3' from the complementary strand."
; US-08-458-831-7

Query Match 71.8%; Score 15.8; DB 2; Length 573;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 19
Db 507 GTCGAACGACAGGCGCTTT 525

RESULT 27
US-08-008-216-6
; Sequence 6, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048

; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; OTHER INFORMATION: through 6216 of Seq. ID No. 5366887 19."
; US-08-008-216-6

Query Match 71.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 19
Db 435 GTCGAACGACAGGCGCTTT 453

RESULT 28
US-08-459-569-6
; Sequence 6, Application US/08459569
; Patent No. 5543501
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,569
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
```

```
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; Patent No. 5543501
; OTHER INFORMATION: through 6216 of Seq. ID No. 5543501 19."
US-08-459-569-6

Query Match 71.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
Db 435 GTCGACGACGAAGGCCTTT 453

RESULT 29
US-08-458-831-6
; Sequence 6, Application US/08458831
; Patent No. 5824866
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tedfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,831
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,216
; FILING DATE: 25-JAN-1993
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: Strain A4
; IMMEDIATE SOURCE:
; LIBRARY: Convolvulus arvensis plant cells
; CLONE: Clone 7
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..1074
; OTHER INFORMATION: /label= ORF6
; OTHER INFORMATION: /note= "Sequence ORF6 corresponds to bases 5143
; Patent No. 5824866
; OTHER INFORMATION: through 6216 of Seq. ID No. 5824866 19."
US-08-458-831-6

Query Match 71.8%; Score 15.8; DB 2; Length 1074;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCCTTT 19
Db 435 GTCGACGACGAAGGCCTTT 453

RESULT 30
US-08-938-858-1
; Sequence 1, Application US/08938858
; Patent No. 5985569
; GENERAL INFORMATION:
; APPLICANT: Foxall, Paul A.
; APPLICANT: Kumar, Harish
; TITLE OF INVENTION: Primers for Amplification of a Genus
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Becton Dickinson and Company
; STREET: 1 Becton Drive
; CITY: Franklin Lakes
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07417-6800
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,858
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fugit, Donna R.
; REGISTRATION NUMBER: 32,135
; REFERENCE/DOCKET NUMBER: P-3490/5510-12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-847-7166
; TELEFAX: 201-848-9228
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1464 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
US-08-938-858-1

Query Match 71.8%; Score 15.8; DB 2; Length 1464;
Best Local Similarity 89.5%; Pred. No. 2e+02;
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCCTTT 19
      |||||
Db 24 GTCGAACGGAAGGTCTCT 42
      |||||

RESULT 31
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. 6677153
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; FILE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match 71.8%; Score 15.8; DB 3; Length 1464;
Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GTCGAACGGAAGGCCTTT 19
      |||||
Db 24 GTCGAACGGAAGGTCTCT 42
      |||||

RESULT 32
US-08-008-216-19
; Sequence 19, Application US/08008216
; Patent No. 5366887
; GENERAL INFORMATION:
; APPLICANT: Slightom, Jerry L.
; APPLICANT: Tepfer, David A.
; TITLE OF INVENTION: Ri T-DNA Promoters
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY, CARY, AMES & FRYE
; STREET: 401 B Street, Suite 1700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-4297
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/008,216
; FILING DATE: 25-JAN-1993
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/725,368
; FILING DATE: 22-APR-1985
; ATTORNEY/AGENT INFORMATION:
; NAME: Barnhorst, Marnie W.
; REGISTRATION NUMBER: 36,740
; REFERENCE/DOCKET NUMBER: P1020US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 699-2700
; TELEFAX: (619) 236-1048
; INFORMATION FOR SEQ ID NO: 19:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21126 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Agrobacterium rhizogenes
; STRAIN: STRAIN A4
; IMMEDIATE SOURCE:
; LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS
; CLONE: CLONE 7
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (937..2262)
; OTHER INFORMATION: /label= ORF1SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (2649..3458)
; OTHER INFORMATION: /label= ORF2SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3726..4799
; OTHER INFORMATION: /label= ORF3SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4041..4400)
; OTHER INFORMATION: /label= ORF4SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (4607..4918)
; OTHER INFORMATION: /label= ORF5SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 5143..6216
; OTHER INFORMATION: /label= ORF6SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (5071..5643)
; OTHER INFORMATION: /label= ORF7SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 6609..8888
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (6576..6830)
; OTHER INFORMATION: /label= ORF9SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 9748..10044
; OTHER INFORMATION: /label= ORF10SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (10509..11282)
; OTHER INFORMATION: /label= ORF11SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 12466..13002
; OTHER INFORMATION: /label= ORF12SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 13723..14319
; OTHER INFORMATION: /label= ORF13SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 15659..16210
; OTHER INFORMATION: /label= ORF14SUBSEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: complement (16517..17545)
; OTHER INFORMATION: /label= ORF15SUBSEQUENCE
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FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (17737..18189)  
OTHER INFORMATION: /label= ORF16SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (18177..18743)  
OTHER INFORMATION: /label= ORF17SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (19031..19390)  
OTHER INFORMATION: /label= ORF18SUBSEQUENC  
US-08-008-216-19  
Query Match 71.8%; Score 15.8; DB 2; Length 21126;  
Best Local Similarity 89.5%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CTCGAACGGAAGGCGCTTT 19  
Db 5577 CTCGAACGACGAAGGCGCTTT 5595  
RESULT 33  
US-08-459-569-19  
Sequence 19, Application US/08459569  
Patent No. 5543501  
GENERAL INFORMATION:  
APPLICANT: Slightom, Jerry L.  
APPLICANT: Tepfer, David A.  
TITLE OF INVENTION: Ri T-DNA Promoters  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GRAY, CARY, AMES & FRYE  
STREET: 401 B Street, Suite 1700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-4297  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,569  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/008,216  
FILING DATE: 25-JAN-1993  
APPLICATION NUMBER: US 06/725,368  
FILING DATE: 22-APR-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Barnhorst, Marnie W.  
REGISTRATION NUMBER: 36,740  
REFERENCE/DOCKET NUMBER: P1020US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 699-2700  
TELEFAX: (619) 236-1048  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21126 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORGANISM: Agrobacterium rhizogenes  
STRAIN: STRAIN A4  
IMMEDIATE SOURCE:  
LIBRARY: CONVULVULUS ARVENSIS PLANT CELLS

CLONE 7  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (937..2262)  
OTHER INFORMATION: /label= ORF1SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (2649..3458)  
OTHER INFORMATION: /label= ORF2SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 3726..4799  
OTHER INFORMATION: /label= ORF3SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (4041..4400)  
OTHER INFORMATION: /label= ORF4SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (4607..4918)  
OTHER INFORMATION: /label= ORF5SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 5143..6216  
OTHER INFORMATION: /label= ORF6SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (5071..5643)  
OTHER INFORMATION: /label= ORF7SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 6609..8888  
OTHER INFORMATION: /label= ORF8SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (6576..6830)  
OTHER INFORMATION: /label= ORF9SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 9748..10044  
OTHER INFORMATION: /label= ORF10SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (10509..11282)  
OTHER INFORMATION: /label= ORF11SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 12466..13002  
OTHER INFORMATION: /label= ORF12SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 13723..14319  
OTHER INFORMATION: /label= ORF13SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 15659..16210  
OTHER INFORMATION: /label= ORF14SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (16517..17545)  
OTHER INFORMATION: /label= ORF15SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (17737..18189)  
OTHER INFORMATION: /label= ORF16SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (18177..18743)  
OTHER INFORMATION: /label= ORF17SUBSEQUENC  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: complement (19031..19390)  
OTHER INFORMATION: /label= ORF18SUBSEQUENC

US-08-459-569-19

Query Match 71.8%; Score 15.8; DB 2; Length 21126;  
Best Local Similarity 89.5%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19  
|||||  
Db 5577 GTCGAACGACAAAGGCCTTT 5595

RESULT 34

US-08-458-831-19  
; Sequence 19, Application US/08458831  
; Patent No. 5824866  
; GENERAL INFORMATION:  
; APPLICANT: Slightcom, Jerry L.  
; APPLICANT: Tepfer, David A.  
; TITLE OF INVENTION: R1 T-DNA Promoters  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRAY, CARY, AMES & FRYE  
; STREET: 401 B Street, Suite 1700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-4297  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,831  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/008,216  
; FILING DATE: 25-JAN-1993  
; APPLICATION NUMBER: US 06/725,368  
; FILING DATE: 22-APR-1985  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barnhorst, Marnie W.  
; REGISTRATION NUMBER: 36,740  
; REFERENCE/DOCKET NUMBER: P1020U51  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 699-2700  
; TELEFAX: (619) 236-1048  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 21126 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ORGANISM: Agrobacterium rhizogenes  
; STRAIN: STRAIN A4  
; IMMEDIATE SOURCE:  
; LIBRARY: CONVOLVULUS ARVENSIS PLANT CELLS  
; CLONE: CLONE 7  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (937..2262)  
; OTHER INFORMATION: /label= ORF1SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (2649..3458)  
; OTHER INFORMATION: /label= ORF2SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 3726..4799

; OTHER INFORMATION: /label= ORF3SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (4041..4400)  
; OTHER INFORMATION: /label= ORF4SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (4607..4918)  
; OTHER INFORMATION: /label= ORF5SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 5143..8216  
; OTHER INFORMATION: /label= ORF6SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (5071..5643)  
; OTHER INFORMATION: /label= ORF7SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 6609..8888  
; OTHER INFORMATION: /label= ORF8SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (6576..6830)  
; OTHER INFORMATION: /label= ORF9SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 9748..10044  
; OTHER INFORMATION: /label= ORF10SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (10509..11282)  
; OTHER INFORMATION: /label= ORF11SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 12466..13002  
; OTHER INFORMATION: /label= ORF12SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 15659..16210  
; OTHER INFORMATION: /label= ORF14SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 13723..14319  
; OTHER INFORMATION: /label= ORF13SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (16517..17545)  
; OTHER INFORMATION: /label= ORF15SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (17737..18189)  
; OTHER INFORMATION: /label= ORF16SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (18177..18743)  
; OTHER INFORMATION: /label= ORF17SUBSEQUENCE  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: complement (19031..19390)  
; OTHER INFORMATION: /label= ORF18SUBSEQUENCE  
US-08-458-831-19

Query Match 71.8%; Score 15.8; DB 2; Length 21126;  
Best Local Similarity 89.5%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTT 19  
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Db 5577 GTCGAACGACAAAGGCCTTT 5595

RESULT 35

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US-08-311-731A-134/c
; Sequence 134, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36241 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae
;
US-08-311-731A-134

Query Match 71.8%; Score 15.8; DB 3; Length 36241;
Best Local Similarity 89.5%; Pred.No.3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGACGGAAAGCCCTTT 19
Db 3937 GTCGACGGAAAGGCTCT 3919

RESULT 36
US-08-311-731A-123/c
; Sequence 123, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210

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RESULT 38
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007, 00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      71.8%; Score 15.8; DB 3; Length 4411529;
Best Local Similarity 89.5%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 19
Db 1471907 GTCGAACGGAAGGCTCT 1471925

RESULT 39
US-09-585-173B-27/c
; Sequence 27, Application US/09585173B
; Patent No. 6570063
; GENERAL INFORMATION:
; APPLICANT: Butler, Karlene
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Gutteridge, Steven
; APPLICANT: Maxwell, Carl
; TITLE OF INVENTION: Magnesium Chelataase
; FILE REFERENCE: BB1370 US NA
; CURRENT APPLICATION NUMBER: US/09/585,173B
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 27
; LENGTH: 439
; TYPE: DNA
; ORGANISM: Zea mays
US-09-585-173B-27

Query Match      70.9%; Score 15.6; DB 3; Length 439;
Best Local Similarity 81.8%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 22
Db 182 GTCGAACGGAAGGACTTCGG 161

RESULT 40
US-09-949-016-175492
; Sequence 175492, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175492
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175492

Query Match      70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 22
Db 209 GTAGAAGGTACAGGCGCTTCGG 230

RESULT 41
US-09-949-016-175493
; Sequence 175493, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175493
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-175493

Query Match      70.9%; Score 15.6; DB 3; Length 601;
Best Local Similarity 81.8%; Pred. No. 2.1e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCGCTTT 22
Db 43 GTAGAAGGTACAGGCGCTTCGG 64

RESULT 42
US-09-489-039A-3119/c
; Sequence 3119, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342

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; SEQ ID NO 3119
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3119

Query Match          70.9%; Score 15.6; DB 3; Length 1662;
Best Local Similarity 81.8%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
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Db 1527 GTCGAAGCGAAAGCCCTCTCGG 1506

RESULT 43
US-09-640-211A-190/c
; Sequence 190, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 190
; LENGTH: 2444
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-190

Query Match          70.9%; Score 15.6; DB 3; Length 2444;
Best Local Similarity 81.8%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 1935 GTCGAACGGAAGGCTTTTCGG 1914

RESULT 44
US-09-489-039A-3095
; Sequence 3095, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3095
; LENGTH: 3111
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3095

Query Match          70.9%; Score 15.6; DB 3; Length 3111;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 970 GTCGAAGCGAAAGCCCTCTCGG 991

RESULT 45
US-09-585-173B-39/c
; Sequence 39, Application US/09585173B
; Patent No. 6570063
; GENERAL INFORMATION:
; APPLICANT: Butler, Karlene
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Gutteridge, Steven
; APPLICANT: Maxwell, Carl
; TITLE OF INVENTION: Magnesium Chelataase
; FILE REFERENCE: BB1370 US NA
; CURRENT APPLICATION NUMBER: US/09/585,173B
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 3257
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-585-173B-39

Query Match          70.9%; Score 15.6; DB 3; Length 3257;
Best Local Similarity 81.8%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 2498 GTCGAACGCAAAAGACTTTCGG 2477

RESULT 46
US-09-949-016-16723
; Sequence 16723, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16723
; LENGTH: 157822
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16723

Query Match          70.9%; Score 15.6; DB 3; Length 157822;
Best Local Similarity 81.8%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCGG 22
||||| ||||| ||||| ||||| |||||
Db 145332 GTAGAAGGTACAGGCTTTTCGG 145353

RESULT 47
US-08-485-602-53
; Sequence 53, Application US/08485602
; Patent No. 5712095
; GENERAL INFORMATION:
```



```

; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,602
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
; US-08-485-602-53

Query Match 70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCTTT 19
Db 1 CGAACGGAAGGCTTT 17

RESULT 49
US-08-757-180-52
; Sequence 52, Application US/08757180
; Patent No. 5726021
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: RAPID LYSIS METHODS FOR RELEASING INTACT
; TITLE OF INVENTION: RIBOSOMAL RNA PRECURSORS FROM MYCOBACTERIUM
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,180
; FILING DATE: 27-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hsi, Petrina S.
; REGISTRATION NUMBER: 38,496
; REFERENCE/DOCKET NUMBER: BD3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
; US-08-757-180-52

Query Match 70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCTTT 19
Db 1 CGAACGGAAGGCTTT 17

RESULT 49
US-08-745-638-53
; Sequence 53, Application US/08745638
; Patent No. 5770373
; GENERAL INFORMATION:
; APPLICANT: Britschgi, Theresa B.
; APPLICANT: Cangelosi, Gerard A.
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Antibiotic-Resistant Mycobacteria Using Oligonucleotide
; TITLE OF INVENTION: Probes Specific for Ribosomal RNA Precursors
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/745,638
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,602
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/261,068
; FILING DATE: 16-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 11652-79-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600

```

```
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: rRNA
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium avium
US-08-745-638-53

Query Match          70.0%; Score 15.4; DB 2; Length 27;
Best Local Similarity 82.4%; Pred. No. 1.5e+02;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTT 19
Db 1 CGAACGGAAGGCCUCU 17

RESULT 50
US-09-738-972-8
; Sequence 8, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-8

Query Match          70.0%; Score 15.4; DB 3; Length 28;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTT 19
Db 1 CGAACGGAAGGCCCTCT 17

RESULT 51
US-09-738-972-15/C
; Sequence 15, Application US/09738972
; Patent No. 6747141
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 28

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-738-972-15

Query Match          70.0%; Score 15.4; DB 3; Length 28;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTT 19
Db 1 CGAACGGAAGGCCCTCT 17

RESULT 52
US-09-640-211A-60
; Sequence 60, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-60

Query Match          70.0%; Score 15.4; DB 3; Length 455;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTC 20
Db 27 GACCGGAAGGCCTTTC 43

RESULT 53
US-09-640-211A-1958
; Sequence 1958, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-640-211A-1958

Query Match          70.0%; Score 15.4; DB 3; Length 455;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GAACGGAAGGCGCTTTC 20
Db 27 GACCGGAAAGGCGCTTTC 43

RESULT 54
US-09-270-767-6474/c
; Sequence 6474, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6474
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-6474

Query Match 70.0%; Score 15.4; DB 3; Length 466;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACGGAAGGCGCTTCG 21
Db 448 AACGTAAGGCGCTTCG 432

RESULT 55
US-09-270-767-21756/c
; Sequence 21756, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21756
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-21756

Query Match 70.0%; Score 15.4; DB 3; Length 466;
Best Local Similarity 94.1%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AACGGAAGGCGCTTCG 21
Db 448 AACGTAAGGCGCTTCG 432

RESULT 56
US-09-540-4420
; Sequence 4420, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4420
; LENGTH: 861
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4420

Query Match 70.0%; Score 15.4; DB 3; Length 861;
Best Local Similarity 94.1%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCGCTTTC 20
Db 3 GAACGGAAGGCGCTTTC 19

RESULT 57
US-09-902-540-1218/c
; Sequence 1218, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1218
; LENGTH: 23677
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1218

Query Match 70.0%; Score 15.4; DB 3; Length 23677;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCGCTTTC 20
Db 23339 GAACGGAAGGCGCTTTC 23323

RESULT 58
US-09-533-559-1639/c
; Sequence 1639, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1639
```

```
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(409)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1639

Query Match          69.1%; Score 15.2; DB 3; Length 409;
Best Local Similarity 77.3%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GTCGACGGAAGGCCTTTCCG 22
Db      336  GNCGAAGGAAAGTCCTTTCCG 315

RESULT 59
US-09-949-016-125682/c
; Sequence 125682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125682.
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-125682

Query Match          69.1%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  CGAACGGAAGGCCTTTCCG 22
Db      382  CGATCAGAAAGCCTTTCCAG 363

RESULT 60
US-09-221-017B-580
; Sequence 580, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Monroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 580:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 603 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...603
US-09-221-017B-580

Query Match          69.1%; Score 15.2; DB 3; Length 603;
Best Local Similarity 85.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      3  CGAACGGAAGGCCTTTCCG 22
Db      447  CGAACGGAAGTCCTTTCCG 466

RESULT 61
US-09-657-289A-21/c
; Sequence 21, Application US/09657289A
; Patent No. 6737245
; GENERAL INFORMATION:
; APPLICANT: Francis, Kevin P.
; APPLICANT: Contag, Pamela R.
; APPLICANT: Joh, Danny J.
; TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
; FILE REFERENCE: 9400-0006
; CURRENT APPLICATION NUMBER: US/09/657,289A
; CURRENT FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: base_polymorphism
; LOCATION: 7
; OTHER INFORMATION: /note = "n' represents an a or g or t or c polymorphism at this
; NAME/KEY: base_polymorphism
; LOCATION: 33
```

```

RESULT 63
US-09-134-000C-2261
; Sequence 2261, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynnn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2261
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Enterococcus faecalis

```

Query Match 69.1%; Score 15.2; DB 3; Length 166698;  
Best Local Similarity 85.0%; Pred. No. 9.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTTC 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 116338 GTCGAACGCAAGTCCTTTC 116319

## RESULT 66

US-09-531-120-209  
; Sequence 209, Application US/09531120  
; Patent No. 6972197  
; GENERAL INFORMATION:  
; APPLICANT: PREUSS, DAPHNE  
; APPLICANT: COPENHAVER, GREGORY  
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS  
; FILE REFERENCE: ARCD:309US  
; CURRENT APPLICATION NUMBER: US/09/531.120  
; CURRENT FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/125,219  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 212  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 209  
; LENGTH: 611587  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-531-120-209

Query Match 69.1%; Score 15.2; DB 4; Length 611587;  
Best Local Similarity 85.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGCCCTTTCG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 452361 TCGACAGGAAGTCCTTCG 452280

## RESULT 67

US-09-023-655-689  
; Sequence 689, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023.655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 689:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1429 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: TLYMNOT02  
; CLONE: 450088  
US-09-023-655-689

Query Match 68.2%; Score 15; DB 3; Length 1429;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GGAAAGCCCTTCGG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 264 GGAAAGCCCTTCGG 278

## RESULT 68

US-08-433-126A-221/c  
; Sequence 221, Application US/08433126A  
; Patent No. 5688935  
; GENERAL INFORMATION:  
; APPLICANT: STEPHENS, ANDREW  
; APPLICANT: SCHNEIDER, DAN  
; APPLICANT: GOLD, LARRY  
; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE  
; TITLE OF INVENTION: TARGET  
; NUMBER OF SEQUENCES: 241  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 E. Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
; COMPUTER: IBM pc compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/433.126A  
; FILING DATE: 03 MAY 1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/714,131  
; FILING DATE: 10-JUNE-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/536,428  
; FILING DATE: 11-JUNE-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/964,624  
; FILING DATE: 21-OCTOBER-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barry J. Swanson  
; REGISTRATION NUMBER: 33,215  
; REFERENCE/DOCKET NUMBER: NEX31.2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 793-3333  
; TELEFAX: (303) 793-3433  
; INFORMATION FOR SEQ ID NO: 221:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 87 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

; TOPOLOGY: linear  
 ; FEATURE:  
 ; OTHER INFORMATION: All C's are 2'-F cytosine  
 ; FEATURE:  
 ; OTHER INFORMATION: All U's are 2'-F uracil  
 US-08-433-126A-221

Query Match 67.3%; Score 14.8; DB 2; Length 87;  
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AACGGAAGGCTTCGG 22  
 DB 50 ATCGTAAGGCTTCGG 33

RESULT 69  
 US-08-433-124A-221/c  
 ; Sequence 221, Application US/08433124A  
 ; Patent No. 5750342  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STEPHENS, ANDREW  
 ; APPLICANT: SCHNEIDER, DAN  
 ; APPLICANT: GOLD, LARRY  
 ; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE  
 ; TITLE OF INVENTION: TARGET  
 ; NUMBER OF SEQUENCES: 241  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
 ; COMPUTER: IBM pc compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 6.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/433,124A  
 ; FILING DATE: 03 MAY 1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/714,131  
 ; FILING DATE: 10-JUNE-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/536,428  
 ; FILING DATE: 11-JUNE-1990  
 ; APPLICATION NUMBER: 07/964,624  
 ; FILING DATE: 21-OCTOBER-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barry J. Swanson  
 ; REGISTRATION NUMBER: 33,215  
 ; REFERENCE/DOCKET NUMBER: NEX31.2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 793-3333  
 ; TELEFAX: (303) 793-3433  
 ; INFORMATION FOR SEQ ID NO: 221:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 87 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; OTHER INFORMATION: All C's are 2'-F cytosine  
 ; FEATURE:  
 ; OTHER INFORMATION: All U's are 2'-F uracil  
 US-08-433-124A-221

Query Match 67.3%; Score 14.8; DB 2; Length 87;  
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 AACGGAAGGCTTCGG 22  
 DB 50 ATCGTAAGGCTTCGG 33

RESULT 70  
 US-08-976-413A-221/c  
 ; Sequence 221, Application US/08976413A  
 ; Patent No. 6127119  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STEPHENS, ANDREW  
 ; APPLICANT: GOLD, LARRY  
 ; APPLICANT: SPECK, ULRICH  
 ; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE TARGET  
 ; NUMBER OF SEQUENCES: 440  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
 ; COMPUTER: IBM pc compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 8.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/976,413A  
 ; FILING DATE: 21-NOVEMBER-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/433,124  
 ; FILING DATE: 03-MAY-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/714,131  
 ; FILING DATE: 10-JUNE-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/536,428  
 ; FILING DATE: 11-JUNE-1990  
 ; APPLICATION NUMBER: 07/964,624  
 ; FILING DATE: 21-OCTOBER-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barry J. Swanson  
 ; REGISTRATION NUMBER: 33,215  
 ; REFERENCE/DOCKET NUMBER: NEX31/CIP  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 793-3333  
 ; TELEFAX: (303) 793-3433  
 ; INFORMATION FOR SEQ ID NO: 221:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 87 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE: INFORMATION: All C's are 2'-F cytosine  
 ; FEATURE:  
 ; OTHER INFORMATION: All U's are 2'-F uracil  
 US-08-976-413A-221

Query Match 67.3%; Score 14.8; DB 3; Length 87;  
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AACGGAAGGCTTCGG 22  
 DB 50 ATCGTAAGGCTTCGG 33

## RESULT 71

PCT-US96-06059-221/c  
 ; Sequence 221, Application PC/TUS9606059  
 ; GENERAL INFORMATION:  
 ; APPLICANT: STEPHENS, ANDREW  
 ; APPLICANT: SCHNEIDER, DAN  
 ; APPLICANT: GOLD, LARRY  
 ; TITLE OF INVENTION: NUCLEIC ACID LIGANDS OF TISSUE  
 ; TITLE OF INVENTION: TARGET  
 ; NUMBER OF SEQUENCES: 241  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Swanson & Bratschun, L.L.C.  
 ; STREET: 8400 E. Prentice Avenue, Suite 200  
 ; CITY: Englewood  
 ; STATE: Colorado  
 ; COUNTRY: USA  
 ; ZIP: 80111

COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MG  
 ; COMPUTER: IBM pc compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 6.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US96/06059  
 ; FILING DATE:  
 ; CLASSIFICATION:

PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/433,124  
 ; FILING DATE: 03-MAY-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/433,126  
 ; FILING DATE: 03-MAY-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/714,131  
 ; FILING DATE: 10-JUNE-1991  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/536,428  
 ; FILING DATE: 11-JUNE-1990  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/964,624  
 ; FILING DATE: 21-OCTOBER-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barry J. Swanson  
 ; REGISTRATION NUMBER: 33,215  
 ; REFERENCE/DOCKET NUMBER: NEX31.2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (303) 793-3333  
 ; TELEFAX: (303) 793-3433  
 ; INFORMATION FOR SEQ ID NO: 221:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 87 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; OTHER INFORMATION: All C's are 2'-F cytosine  
 ; FEATURE:  
 ; OTHER INFORMATION: All U's are 2'-F uracil  
 PCT-US96-06059-221

Query Match 67.3%; Score 14.8; DB 7; Length 87;  
 Best Local Similarity 88.9%; Pred. No. 3.8e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTCGG 22  
 |||||  
 Db 50 ATCGGTAGGCTTCGG 33

## RESULT 72

US-09-016-434-408  
 ; Sequence 408, Application US/09016434  
 ; Patent No. 6500938

## ; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young  
 ; APPLICANT: Jeffrey J. Seilhamer  
 ; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
 ; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
 ; NUMBER OF SEQUENCES: 1490  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 ; STREET: 3174 PORTER DRIVE  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/016,434  
 ; FILING DATE: HERewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Zeller, Karen J.  
 ; REGISTRATION NUMBER: 37,071  
 ; REFERENCE/DOCKET NUMBER: PA-0002 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (650) 855-0555  
 ; TELEFAX: (650) 845-4166  
 ; INFORMATION FOR SEQ ID NO: 408:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 107 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: BRSTNOT07  
 ; CLONE: 2122627  
 US-09-016-434-408

Query Match 67.3%; Score 14.8; DB 3; Length 107;  
 Best Local Similarity 88.9%; Pred. No. 4e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAAGGCTTTC 20  
 |||||  
 Db 71 CGAACGGCAAGCCTTTC 88

## RESULT 73

US-09-513-999C-2742  
 ; Sequence 2742, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6783961  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2742  
 ; LENGTH: 362  
 ; TYPE: DNA



```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 146..361
US-09-513-999C-2742

Query Match      67.3%; Score 14.8; DB 3; Length 362;
Best Local Similarity 88.9%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCCTTTC 20
    ||||| ||||| |||||
Db 108 CGAACGGAAGGCCTTTC 125

RESULT 74
US-09-270-767-29724/c
; Sequence 29724, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29724
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29724

Query Match      67.3%; Score 14.8; DB 3; Length 532;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCCTTT 19
    ||||| ||||| |||||
Db 248 TCGAACGGAAGGCCTTT 231

RESULT 75
US-09-252-991A-5578
; Sequence 5578, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5578
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5578

Query Match      67.3%; Score 14.8; DB 3; Length 543;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTTCG 21
    ||||| ||||| |||||
Db 145 GAACGGATAGGCTGTGC 162

RESULT 76
US-09-252-991A-5650/c
; Sequence 5650, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5650
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5650

Query Match      67.3%; Score 14.8; DB 3; Length 600;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTTCG 21
    ||||| ||||| |||||
Db 468 GAACGGATAGGCTGTGC 451

RESULT 77
US-09-949-016-82725
; Sequence 82725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82725
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82725

Query Match      67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
    ||||| ||||| |||||
Db 438 GTCGAACGGAAGGCATT 455

RESULT 78
US-09-949-016-82726
; Sequence 82726, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match      67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTT 18
    ||||| ||||| |||||
Db 438 GTCGAACGGAAGGCATT 455
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82726
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82726

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 205 GTCAACGGAAGGCATT 222

RESULT 79
US-09-949-016-82727
; Sequence 82727, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82727
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-82727

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 46 GTCAACGGAAGGCATT 63

RESULT 80
US-09-949-016-148702/c
; Sequence 148702, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
```

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148702
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-148702

Query Match          67.3%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTTCG 21
   ||| ||||| ||||| |||
Db 249 GAACAGAAAGCCTTTTG 232

RESULT 81
US-09-533-559-7113
; Sequence 7113, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7113
; LENGTH: 637
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-7113

Query Match          67.3%; Score 14.8; DB 3; Length 637;
Best Local Similarity 88.9%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
   ||| ||||| ||||| |||
Db 32 GTCGAACGGAAGGCATT 49

RESULT 82
US-09-248-796A-4578/c
; Sequence 4578, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4578
```

```
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4578

Query Match          67.3%; Score 14.8; DB 3; Length 645;
Best Local Similarity 88.9%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20
    ||||| ||||| |||||
Db 602 CGAACGGAAGGCATTC 585

RESULT 83
US-09-328-352-3521/c
; Sequence 3521, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 3521
; LENGTH: 795
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3521

Query Match          67.3%; Score 14.8; DB 3; Length 795;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    ||||| ||||| |||||
Db 453 TCGAACGTACAGGCCTT 436

RESULT 84
US-09-270-767-13705/c
; Sequence 13705, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13705
; LENGTH: 1160
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13705

Query Match          67.3%; Score 14.8; DB 3; Length 1160;
Best Local Similarity 88.9%; Pred. No. 6.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19
    ||||| ||||| |||||
Db 876 TCGAACAGAAAGGCCTTT 859

RESULT 85
US-09-949-016-2374
; Sequence 2374, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2374

Query Match          67.3%; Score 14.8; DB 3; Length 1945;
Best Local Similarity 88.9%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20
    ||||| ||||| |||||
Db 247 CGAACGGCACGCCTTTC 264

RESULT 86
US-09-270-767-163
; Sequence 163, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 4029
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-163

Query Match          67.3%; Score 14.8; DB 3; Length 4029;
Best Local Similarity 88.9%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
    ||||| ||||| |||||
Db 1401 GGCGAACGGAAGGCCAT 1418

RESULT 87
US-09-270-767-15445
; Sequence 15445, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15445
; LENGTH: 4029
; TYPE: DNA
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; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: n means any nucleotide  
US-09-270-767-15445

Query Match 67.3%; Score 14.8; DB 3; Length 4029;  
Best Local Similarity 88.9%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGACGGAAGGCTT 18  
| | | | | | | | | | | | | | | | | |  
Db 1401 GCGACGGAAGGCGCAT 1418

RESULT 88  
US-09-949-016-14116  
; Sequence 14116, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14116  
; LENGTH: 11050  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14116

Query Match 67.3%; Score 14.8; DB 3; Length 11050;  
Best Local Similarity 88.9%; Pred. No. 9.6e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTC 20  
| | | | | | | | | | | | | | | | | |  
Db 5117 CGAACGGAAGGCTTTC 5134

RESULT 89  
US-09-949-016-15957/c  
; Sequence 15957, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15957  
; LENGTH: 35916  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-15957

Query Match 67.3%; Score 14.8; DB 3; Length 35916;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTC 20  
| | | | | | | | | | | | | | | | | |  
Db 4145 CGACGGAAGGCTTTC 4128

RESULT 90  
US-09-949-016-17095/c  
; Sequence 17095, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17095  
; LENGTH: 36855  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17095

Query Match 67.3%; Score 14.8; DB 3; Length 36855;  
Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTC 19  
| | | | | | | | | | | | | | | | | |  
Db 8257 TCGAACGGAAGGCTTTC 8240

RESULT 91  
US-09-949-016-15116/c  
; Sequence 15116, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15116  
; LENGTH: 83462  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1) -- (83462)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15116

Query Match 67.3%; Score 14.8; DB 3; Length 83462;

```
Best Local Similarity 88.9%; Pred. No. 1.4e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCGCTTTC 20
    ||||| ||||| |||||
Db 2869 CGACAGACAGGCGCTTTC 2852

RESULT 92
US-09-949-016-13629
; Sequence 13629, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13629
; LENGTH: 93894
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(93894)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13629

Query Match 67.3%; Score 14.8; DB 3; Length 93894;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTC 21
    ||||| ||||| |||||
Db 26767 GAACGGAAGGCGCTTTC 26784

RESULT 93
US-09-949-016-15921/c
; Sequence 15921, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15921
; LENGTH: 124480
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15921

Query Match 67.3%; Score 14.8; DB 3; Length 124480;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Qy 4 GAACGGAAGGCGCTTTC 21
    ||||| ||||| |||||
Db 118710 GAACGGAAGGCGCTTTC 118693

RESULT 94
US-09-949-016-13845/c
; Sequence 13845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13845
; LENGTH: 152132
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13845

Query Match 67.3%; Score 14.8; DB 3; Length 152132;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
    ||||| ||||| |||||
Db 13321 TCGAACGGAAGGCGCTTT 13304

RESULT 95
US-09-949-016-12371/c
; Sequence 12371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12371
; LENGTH: 152145
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12371

Query Match 67.3%; Score 14.8; DB 3; Length 152145;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTT 19
    ||||| ||||| |||||
Db 13321 TCGAACGGAAGGCGCTTT 13304
```

```
RESULT 96
US-09-949-016-12086/c
; Sequence 12086, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12086
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152582)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12086

Query Match      67.3%; Score 14.8; DB 3; Length 152582;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 97
US-09-949-016-17390/c
; Sequence 17390, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17390
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152583)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17390

Query Match      67.3%; Score 14.8; DB 3; Length 152583;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 98
US-09-949-016-17391/c
; Sequence 17391, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17391
; LENGTH: 152583
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152583)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17391

Query Match      67.3%; Score 14.8; DB 3; Length 152583;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCCTT 19
Db      60573 TCGAATGGAAGGCCCTT 60556

RESULT 99
US-09-820-007-3
; Sequence 3, Application US/09820007
; Patent No. 6830900
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match      67.3%; Score 14.8; DB 3; Length 213456;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCCTT 18
Db      60573 TCGAATGGAAGGCCCTT 60556
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Job time : 86.3253 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:46:33 ; Search time 882.518 Seconds  
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306.314 Million cell updates/sec

Title: US-10-665-708-23

Perfect score: 22

Sequence: 1 gtcgaacgaaagccttcgg 22

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications NA Main:\*

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- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10J\_PUBCOMB.seq.\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10K\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	100.0	22	3	US-09-738-274-23
2	22	100.0	22	10	US-10-665-708-23
3	21	95.5	24	3	US-09-738-274-22
4	21	95.5	24	10	US-10-665-708-22
5	21	95.5	25	3	US-09-738-274-21
6	21	95.5	25	10	US-10-665-708-21
7	20.4	92.7	454	7	US-10-438-774-15
8	20.4	92.7	1449	10	US-10-697-802A-6
9	20.4	92.7	1455	10	US-10-697-802A-13
10	20.4	92.7	1482	10	US-10-697-802A-5
11	19	86.4	19	3	US-09-738-274-24
12	19	86.4	19	10	US-10-665-708-24
13	18.8	85.5	1403	10	US-10-522-454-1
14	18.8	85.5	1443	13	US-11-045-628-1
15	18.8	85.5	1443	13	US-11-045-628-1
16	18.8	85.5	1461	10	US-10-697-802A-7
17	18.8	85.5	1480	16	US-11-228-416-5

18	18.8	85.5	1480	16	US-11-228-416-6	Sequence 6, Appli
19	18.8	85.5	1480	16	US-11-228-416-8	Sequence 8, Appli
20	18.8	85.5	1480	16	US-11-228-416-9	Sequence 9, Appli
21	18.8	85.5	1481	16	US-11-228-416-3	Sequence 3, Appli
22	18.8	85.5	1482	16	US-11-228-416-4	Sequence 4, Appli
23	18.8	85.5	1483	16	US-11-228-416-7	Sequence 7, Appli
24	17.8	80.9	1439	7	US-10-230-026-6	Sequence 6, Appli
25	17.8	80.9	1439	9	US-10-486-307-6	Sequence 6, Appli
26	17.4	79.1	25	8	US-10-220-212A-31	Sequence 31, Appli
27	17.4	79.1	25	8	US-10-220-212A-33	Sequence 33, Appli
28	17.4	79.1	32	3	US-09-738-972-7	Sequence 7, Appli
29	17.4	79.1	32	3	US-09-738-972-14	Sequence 14, Appli
30	17.4	79.1	32	9	US-10-862-026-7	Sequence 7, Appli
31	17.4	79.1	32	9	US-10-862-026-14	Sequence 14, Appli
32	17.4	79.1	560	10	US-10-478-633A-23	Sequence 23, Appli
33	17.4	79.1	1421	10	US-10-697-802A-12	Sequence 12, Appli
34	17.4	79.1	1454	10	US-10-697-802A-2	Sequence 2, Appli
35	17.4	79.1	1465	7	US-10-029-397A-32	Sequence 32, Appli
36	17.2	78.2	513	4	US-09-925-065A-544396	Sequence 544396,
37	17.2	78.2	513	4	US-09-925-065A-544397	Sequence 544397,
38	17.2	78.2	513	5	US-09-925-065A-544396	Sequence 544396,
39	17.2	78.2	513	5	US-09-925-065A-544397	Sequence 544397,
40	17.2	78.2	620	8	US-10-437-963-34505	Sequence 34505, A
41	17.2	78.2	638	6	US-10-027-632-292604	Sequence 292604,
42	17.2	78.2	638	6	US-10-027-632-292605	Sequence 292605,
43	17.2	78.2	638	7	US-10-027-632-292604	Sequence 292604,
44	17.2	78.2	638	7	US-10-027-632-292605	Sequence 292605,
45	17.2	78.2	1437	7	US-10-085-871C-1	Sequence 1, Appli
46	17.2	78.2	1437	10	US-10-727-643-1	Sequence 1, Appli
47	17.2	78.2	1471	7	US-10-085-871C-2	Sequence 2, Appli
48	17.2	78.2	1471	10	US-10-727-643-2	Sequence 2, Appli
49	17.2	78.2	1488	9	US-10-756-683-1	Sequence 1, Appli
50	17.2	78.2	1514	9	US-10-875-161-2	Sequence 2, Appli
51	17	77.3	30	11	US-10-831-286A-1517	Sequence 1517, Ap
52	16.4	74.5	30	11	US-10-831-286A-8212	Sequence 8212, Ap
53	16.2	73.6	367	7	US-10-062-674-613	Sequence 613, App
54	16.2	73.6	622	8	US-10-767-701-31297	Sequence 31297, A
55	16.2	73.6	635	9	US-10-425-115-59269	Sequence 59269, A
56	16	72.7	20	11	US-10-831-286A-12801	Sequence 12801, A
57	16	72.7	20	11	US-10-831-286A-23905	Sequence 23905, A
58	16	72.7	23	3	US-09-738-274-27	Sequence 27, Appli
59	16	72.7	23	10	US-10-665-708-27	Sequence 27, Appli
60	16	72.7	26	3	US-09-738-274-28	Sequence 28, Appli
61	16	72.7	26	10	US-10-665-708-28	Sequence 28, Appli
62	16	72.7	80	9	US-10-830-943-11	Sequence 11, Appli
63	16	72.7	560	10	US-10-478-633A-24	Sequence 24, Appli
64	16	72.7	935	10	US-10-779-543-8365	Sequence 8365, Ap
65	16	72.7	1321	10	US-10-697-802A-11	Sequence 11, Appli
66	16	72.7	1415	10	US-10-697-802A-14	Sequence 14, Appli
67	16	72.7	1460	6	US-10-062-777-1	Sequence 1, Appli
68	16	72.7	1460	7	US-10-419-095-1	Sequence 1, Appli
69	16	72.7	1462	10	US-10-697-802A-16	Sequence 16, Appli
70	16	72.7	1484	10	US-10-697-802A-15	Sequence 15, Appli
71	16	72.7	1527	10	US-10-697-802A-8	Sequence 8, Appli
72	15.8	71.8	32	3	US-09-738-274-14	Sequence 14, Appli
73	15.8	71.8	32	10	US-10-665-708-14	Sequence 14, Appli
74	15.8	71.8	170	6	US-10-062-727-254	Sequence 254, App
75	15.8	71.8	305	6	US-10-062-727-376	Sequence 376, App
76	15.8	71.8	381	10	US-10-450-763-13678	Sequence 13678, A
77	15.8	71.8	468	7	US-10-438-774-17	Sequence 17, Appli
78	15.8	71.8	576	10	US-10-450-763-3105	Sequence 3105, Ap
79	15.8	71.8	625	12	US-10-301-480-442948	Sequence 442948,
80	15.8	71.8	625	12	US-10-301-480-1056357	Sequence 1056357,
81	15.8	71.8	634	4	US-09-925-065A-373045	Sequence 373045,
82	15.8	71.8	634	5	US-09-925-065A-373045	Sequence 373045,
83	15.8	71.8	1416	10	US-10-697-802A-17	Sequence 17, Appli
84	15.8	71.8	1421	10	US-10-697-802A-3	Sequence 3, Appli
85	15.8	71.8	1463	10	US-10-697-802A-10	Sequence 10, Appli
86	15.8	71.8	1464	3	US-09-726-774-7	Sequence 7, Appli
87	15.8	71.8	1464	8	US-10-719-633-7	Sequence 7, Appli
88	15.8	71.8	1524	8	US-10-220-212A-34	Sequence 34, Appli
89	15.8	71.8	1536	7	US-10-029-397A-33	Sequence 33, Appli
90	15.8	71.8	1536	7	US-10-029-397A-34	Sequence 34, Appli

c 91	15.8	71.8	2896	10	US-10-488-528-3	Sequence 3, Appli	c 164	15.2	69.1	499	3	US-09-918-995-261	Sequence 261, App
c 92	15.8	71.8	2919	7	US-10-369-493-35634	Sequence 35634, A	165	15.2	69.1	558	16	US-11-096-568A-27724	Sequence 27724, A
c 93	15.8	71.8	2954	10	US-10-488-528-1	Sequence 1, Appli	166	15.2	69.1	561	3	US-09-925-299-10	Sequence 10, Appl
c 94	15.8	71.8	6883	3	US-09-764-877-3363	Sequence 3363, Ap	167	15.2	69.1	561	3	US-09-925-299-10	Sequence 10, Appl
c 95	15.8	71.8	6883	3	US-10-242-515-3363	Sequence 3363, Ap	168	15.2	69.1	603	6	US-10-194-163-580	Sequence 580, App
c 96	15.8	71.8	21126	8	US-10-465-008-10	Sequence 10, Appl	c 169	15.2	69.1	641	4	US-09-925-065A-750529	Sequence 750529,
c 97	15.6	70.9	297	7	US-10-012-697-422	Sequence 422, App	c 170	15.2	69.1	641	5	US-09-925-065A-750529	Sequence 750529,
c 98	15.6	70.9	297	10	US-10-779-543-22422	Sequence 22422, A	171	15.2	69.1	658	4	US-09-925-065A-220788	Sequence 220788,
c 99	15.6	70.9	439	7	US-10-410-681-27	Sequence 27, Appl	172	15.2	69.1	658	5	US-09-925-065A-220788	Sequence 220788,
c 100	15.6	70.9	471	11	US-10-932-182A-77805	Sequence 77805, A	173	15.2	69.1	671	6	US-10-027-632-32863	Sequence 32863, A
c 101	15.6	70.9	524	3	US-09-770-152-949	Sequence 949, App	174	15.2	69.1	671	7	US-10-027-632-32863	Sequence 32863, A
c 102	15.6	70.9	530	8	US-10-767-701-30317	Sequence 30317, A	175	15.2	69.1	693	6	US-10-027-632-102406	Sequence 102406,
c 103	15.6	70.9	600	4	US-09-925-065A-906221	Sequence 906221, A	176	15.2	69.1	693	6	US-10-027-632-102407	Sequence 102407,
c 104	15.6	70.9	600	5	US-09-925-065A-906221	Sequence 906221, A	177	15.2	69.1	693	7	US-10-027-632-102406	Sequence 102406,
c 105	15.6	70.9	600	10	US-10-972-079-86404	Sequence 86404, A	178	15.2	69.1	693	7	US-10-027-632-102407	Sequence 102407,
c 106	15.6	70.9	624	10	US-10-487-804-136	Sequence 804, App	c 179	15.2	69.1	766	4	US-09-925-065A-85410	Sequence 85410, A
c 107	15.6	70.9	654	4	US-09-925-065A-481777	Sequence 481777, A	c 180	15.2	69.1	766	5	US-09-925-065A-85410	Sequence 85410, A
c 108	15.6	70.9	654	5	US-09-925-065A-481777	Sequence 481777, A	c 181	15.2	69.1	766	5	US-09-925-065A-85410	Sequence 85410, A
c 109	15.6	70.9	659	8	US-10-424-599-80785	Sequence 80785, A	c 182	15.2	69.1	766	12	US-10-301-480-186650	Sequence 186650,
c 110	15.6	70.9	786	16	US-11-096-568A-32833	Sequence 32833, A	c 183	15.2	69.1	766	12	US-10-301-480-800059	Sequence 800059,
c 111	15.6	70.9	960	6	US-10-087-132-1004	Sequence 10833, A	c 184	15.2	69.1	861	3	US-10-467-657-2959	Sequence 2959, Ap
c 112	15.6	70.9	999	7	US-10-156-761-5559	Sequence 5559, Ap	c 185	15.2	69.1	978	3	US-09-876-143-1060	Sequence 1060, Ap
c 113	15.6	70.9	1062	8	US-10-424-599-55432	Sequence 55432, A	c 186	15.2	69.1	1341	8	US-10-767-701-10349	Sequence 10349, A
c 114	15.6	70.9	1101	7	US-10-369-493-40702	Sequence 40702, A	c 187	15.2	69.1	1420	8	US-10-050-704-89	Sequence 89, Appl
c 115	15.6	70.9	1111	8	US-10-425-114-7767	Sequence 7767, Ap	c 188	15.2	69.1	1420	8	US-10-798-512-89	Sequence 89, Appl
c 116	15.6	70.9	1197	7	US-10-156-761-1373	Sequence 1373, Ap	c 189	15.2	69.1	1632	16	US-11-079-463-4538	Sequence 4538, Ap
c 117	15.6	70.9	1675	7	US-10-369-493-32574	Sequence 32574, A	c 190	15.2	69.1	1736	4	US-09-925-065A-79104	Sequence 79104, A
c 118	15.6	70.9	1718	8	US-10-425-114-72	Sequence 72, Appl	c 191	15.2	69.1	1736	4	US-09-925-065A-79105	Sequence 79105, A
c 119	15.6	70.9	1729	8	US-10-424-599-80784	Sequence 80784, A	c 192	15.2	69.1	1736	4	US-09-925-065A-79106	Sequence 79106, A
c 120	15.6	70.9	2389	8	US-10-437-963-60191	Sequence 60191, A	c 193	15.2	69.1	1736	5	US-09-925-065A-79105	Sequence 79105, A
c 121	15.6	70.9	2397	11	US-10-932-182A-254	Sequence 254, App	c 194	15.2	69.1	1736	5	US-09-925-065A-79106	Sequence 79106, A
c 122	15.6	70.9	2427	8	US-10-425-114-30952	Sequence 30952, A	c 195	15.2	69.1	1736	12	US-10-301-480-180343	Sequence 180343,
c 123	15.6	70.9	2444	9	US-10-856-499-190	Sequence 190, App	c 196	15.2	69.1	1736	12	US-10-301-480-180344	Sequence 180344,
c 124	15.6	70.9	2982	3	US-09-938-842A-2525	Sequence 2525, Ap	c 197	15.2	69.1	1736	12	US-10-301-480-180345	Sequence 180345,
c 125	15.6	70.9	2982	3	US-09-938-842A-2525	Sequence 2525, Ap	c 198	15.2	69.1	1736	12	US-10-301-480-793752	Sequence 793752,
c 126	15.6	70.9	3096	9	US-10-425-115-40860	Sequence 40860, A	c 199	15.2	69.1	1736	12	US-10-301-480-793753	Sequence 793753,
c 127	15.6	70.9	3257	7	US-10-410-681-39	Sequence 39, Appl	c 200	15.2	69.1	1736	12	US-10-301-480-793754	Sequence 793754,
c 128	15.6	70.9	3913	9	US-10-425-115-85383	Sequence 8383, A	c 201	15.2	69.1	2635	6	US-10-128-714-1270	Sequence 1270, Ap
c 129	15.6	70.9	12368	10	US-10-893-671-83	Sequence 83, Appl	c 202	15.2	69.1	2937	3	US-10-282-122A-11160	Sequence 11160, A
c 130	15.6	70.9	43800	6	US-10-087-192-1003	Sequence 1003, Ap	c 203	15.2	69.1	2964	6	US-10-128-714-6270	Sequence 6270, Ap
c 131	15.6	70.9	268685	7	US-10-265-071-22	Sequence 22, Appl	c 204	15.2	69.1	3485	3	US-09-070-927A-283	Sequence 283, App
c 132	15.6	70.9	268685	7	US-10-025-966A-22	Sequence 22, Appl	c 205	15.2	69.1	4635	6	US-10-128-714-270	Sequence 270, App
c 133	15.6	70.9	268685	10	US-10-933-025-22	Sequence 22, Appl	c 206	15.2	69.1	4964	6	US-10-128-714-5270	Sequence 5270, Ap
c 134	15.6	70.9	268685	16	US-11-219-360-22	Sequence 22, Appl	c 207	15.2	69.1	5694	8	US-10-437-963-9515	Sequence 9515, Ap
c 135	15.6	70.9	387780	10	US-10-395-561-13259	Sequence 13259, A	c 208	15.2	69.1	5913	8	US-10-437-963-66272	Sequence 66272, A
c 136	15.6	70.9	495269	8	US-10-398-221-8	Sequence 8, Appli	c 209	15.2	69.1	42104	6	US-10-087-192-1138	Sequence 1138, Ap
c 137	15.6	70.9	3011208	8	US-10-398-221-2058	Sequence 2058, Ap	c 210	15.2	69.1	89328	3	US-09-873-367C-332	Sequence 332, App
c 138	15.6	70.9	9025608	7	US-10-156-761-1	Sequence 15, Appli	c 211	15.2	69.1	611587	15	US-11-117-187-209	Sequence 209, App
c 139	15.4	70.0	25	9	US-10-719-900-43767	Sequence 43767, A	c 212	15.2	69.1	1163020	8	US-10-398-221-10	Sequence 10, Appl
c 140	15.4	70.0	28	3	US-09-738-972-8	Sequence 8, Appli	c 213	15.2	69.1	1694969	12	US-10-506-454-1590	Sequence 1690, Ap
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c 142	15.4	70.0	28	9	US-10-862-026-8	Sequence 8, Appli	c 215	15.2	69.1	259903	10	US-10-756-149-3550	Sequence 3550, Ap
c 143	15.4	70.0	28	9	US-10-862-026-15	Sequence 15, Appl	c 216	15.2	69.1	260549	9	US-10-741-600-17723	Sequence 17723, A
c 144	15.4	70.0	30	11	US-10-831-286A-4582	Sequence 4582, Ap	c 217	15.2	69.1	611587	15	US-11-117-187-209	Sequence 209, App
c 145	15.4	70.0	455	9	US-10-856-499-60	Sequence 60, Appl	c 218	15.2	69.1	1163020	8	US-10-398-221-10	Sequence 10, Appl
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c 147	15.4	70.0	1164	7	US-10-369-493-32250	Sequence 32250, A	c 220	15.2	69.1	284428	16	US-11-045-004-1	Sequence 1, Appli
c 148	15.4	70.0	1187	10	US-10-750-185-42960	Sequence 42960, A	c 221	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 149	15.4	70.0	1187	10	US-10-750-623-42960	Sequence 42960, A	c 222	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 150	15.4	70.0	2642	13	US-11-097-143-31768	Sequence 31768, A	c 223	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 151	15.4	70.0	2642	13	US-10-750-185-34543	Sequence 34543, A	c 224	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 152	15.4	70.0	2665	10	US-10-750-623-34543	Sequence 34543, A	c 225	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 153	15.4	70.0	3581	13	US-11-097-143-31795	Sequence 31795, A	c 226	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
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c 155	15.4	70.0	7162	13	US-11-097-143-3736	Sequence 3736, Ap	c 228	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 156	15.2	69.1	25	13	US-11-036-317-106689	Sequence 106689, A	c 229	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
c 157	15.2	69.1	201	9	US-10-741-600-48545	Sequence 48545, A	c 230	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
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c 159	15.2	69.1	365	8	US-10-717-897-63	Sequence 63, Appl	c 232	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
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c 161	15.2	69.1	414	10	US-10-779-543-10690	Sequence 10690, A	c 234	15.2	69.1	3011208	8	US-10-398-221-2058	Sequence 2058, Ap
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c 241	14.8	67.3	201	10	US-10-995-561-80905	Sequence 80905, A
c 242	14.8	67.3	260	8	US-10-424-599-30752	Sequence 30752, A
c 243	14.8	67.3	275	8	US-10-437-963-91974	Sequence 91974, A
c 244	14.8	67.3	298	8	US-10-424-599-83605	Sequence 83605, A
c 245	14.8	67.3	321	3	US-09-294-093B-5542	Sequence 5542, Ap
c 246	14.8	67.3	321	3	US-09-764-891-1073	Sequence 1073, Ap
c 247	14.8	67.3	341	3	US-09-764-869-1510	Sequence 1510, Ap
c 248	14.8	67.3	341	3	US-09-764-869-1511	Sequence 1511, Ap
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c 250	14.8	67.3	341	6	US-10-091-504-1511	Sequence 1511, Ap
c 251	14.8	67.3	341	7	US-10-227-577-1510	Sequence 1510, Ap
c 252	14.8	67.3	341	7	US-10-227-577-1511	Sequence 1511, Ap
c 253	14.8	67.3	352	3	US-09-764-869-1514	Sequence 1514, App
c 254	14.8	67.3	352	6	US-10-091-504-1514	Sequence 1514, App
c 255	14.8	67.3	352	7	US-10-227-577-1514	Sequence 1514, App
c 256	14.8	67.3	352	8	US-10-424-599-79317	Sequence 79317, A
c 257	14.8	67.3	364	8	US-10-424-599-9437	Sequence 9437, Ap
c 258	14.8	67.3	369	8	US-10-437-963-65283	Sequence 65283, A
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c 263	14.8	67.3	529	4	US-09-925-065A-187308	Sequence 187308, A
c 264	14.8	67.3	529	5	US-09-925-065A-187308	Sequence 187308, A
c 265	14.8	67.3	529	12	US-10-301-480-277352	Sequence 277352, A
c 266	14.8	67.3	541	4	US-09-925-065A-632445	Sequence 632445, A
c 267	14.8	67.3	541	5	US-09-925-065A-632445	Sequence 632445, A
c 268	14.8	67.3	545	4	US-09-925-065A-632445	Sequence 632445, A
c 269	14.8	67.3	545	5	US-09-925-065A-768288	Sequence 768288, A
c 270	14.8	67.3	545	5	US-09-925-065A-768288	Sequence 768288, A
c 271	14.8	67.3	559	9	US-10-363-345A-15387	Sequence 15387, A
c 272	14.8	67.3	559	9	US-10-363-345A-15388	Sequence 15388, A
c 273	14.8	67.3	559	10	US-10-363-483A-15387	Sequence 15387, A
c 274	14.8	67.3	559	10	US-10-363-483A-15388	Sequence 15388, A
c 275	14.8	67.3	561	4	US-09-925-065A-171262	Sequence 171262, A
c 276	14.8	67.3	561	4	US-09-925-065A-171263	Sequence 171263, A
c 277	14.8	67.3	561	4	US-09-925-065A-171264	Sequence 171264, A
c 278	14.8	67.3	561	4	US-09-925-065A-171265	Sequence 171265, A
c 279	14.8	67.3	561	5	US-09-925-065A-171262	Sequence 171262, A
c 280	14.8	67.3	561	5	US-09-925-065A-171263	Sequence 171263, A
c 281	14.8	67.3	561	5	US-09-925-065A-171264	Sequence 171264, A
c 282	14.8	67.3	561	5	US-09-925-065A-171265	Sequence 171265, A
c 283	14.8	67.3	572	12	US-10-301-480-263018	Sequence 263018, A
c 284	14.8	67.3	572	12	US-10-301-480-263019	Sequence 263019, A
c 285	14.8	67.3	572	12	US-10-301-480-263020	Sequence 263020, A
c 286	14.8	67.3	572	12	US-10-301-480-263021	Sequence 263021, A
c 287	14.8	67.3	572	12	US-10-301-480-876427	Sequence 876427, A
c 288	14.8	67.3	572	12	US-10-301-480-876428	Sequence 876428, A
c 289	14.8	67.3	572	12	US-10-301-480-876429	Sequence 876429, A
c 290	14.8	67.3	572	12	US-10-301-480-876430	Sequence 876430, A
c 291	14.8	67.3	580	9	US-10-425-115-182434	Sequence 182434, A
c 292	14.8	67.3	591	3	US-09-864-761-16483	Sequence 16483, A
c 293	14.8	67.3	597	5	US-09-925-065A-848570	Sequence 848570, A
c 294	14.8	67.3	597	5	US-09-925-065A-848570	Sequence 848570, A
c 295	14.8	67.3	617	12	US-10-301-480-48861	Sequence 48861, A
c 296	14.8	67.3	617	12	US-10-301-480-48862	Sequence 48862, A
c 297	14.8	67.3	617	12	US-10-301-480-662270	Sequence 662270, A
c 298	14.8	67.3	617	12	US-10-301-480-662271	Sequence 662271, A
c 299	14.8	67.3	633	4	US-09-925-065A-692790	Sequence 692790, A
c 300	14.8	67.3	633	5	US-09-925-065A-692790	Sequence 692790, A

ALIGNMENTS

GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-23

Query Match 100.0%; Score 22; DB 3; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22  
|||||

Db 1 GTCGAACGGAAGGCTTTTCGG 22  
|||||

RESULT 2

US-10-665-708-23  
; Sequence 23, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZIAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 23  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-23

Query Match 100.0%; Score 22; DB 10; Length 22;  
Best Local Similarity 100.0%; Pred. No. 0.68;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCTTTTCGG 22  
|||||

Db 1 GTCGAACGGAAGGCTTTTCGG 22  
|||||

RESULT 3

RESULT 1  
US-09-738-274-23  
; Sequence 23, Application US/09738274  
; Publication No. US20030165824A1

US-09-738-274-22  
; Sequence 22, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-22

Query Match 95.5%; Score 21; DB 3; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21  
|||||  
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 4  
US-10-665-708-22  
; Sequence 22, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-22

Query Match 95.5%; Score 21; DB 10; Length 24;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21  
|||||  
Db 4 GTCGAACGGAAGGCTTTTCG 24

RESULT 5  
US-09-738-274-21  
; Sequence 21, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-21

Query Match 95.5%; Score 21; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21  
|||||  
Db 5 GTCGAACGGAAGGCTTTTCG 25

RESULT 6  
US-10-665-708-21  
; Sequence 21, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-21

Query Match 95.5%; Score 21; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 21  
|||||  
DB 5 GTCGAACGGAAGGCGCTTTCG 25

## RESULT 7

US-10-438-774-15  
; Sequence 15, Application US/10438774  
; Publication No. US20040010504A1  
; GENERAL INFORMATION:  
; APPLICANT: Hinrichs, Steven  
; APPLICANT: Ali, Hesham  
; APPLICANT: Kuyper, Dan  
; TITLE OF INVENTION: Custom Sequence Databases and Methods of  
; FILE REFERENCE: UNMC-63174-US  
; CURRENT APPLICATION NUMBER: US/10/438,774  
; CURRENT FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: 60/381,015  
; PRIOR FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-438-774-15

Query Match 92.7%; Score 20.4; DB 7; Length 454;  
Best Local Similarity 95.5%; Pred. No. 4.6;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22  
|||||  
DB 1 GTCGAACGGAAGGCGCTTTCG 22

## RESULT 8

US-10-697-802A-6  
; Sequence 6, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 6  
; LENGTH: 1449  
; TYPE: DNA  
; ORGANISM: Mycobacterium fortuitum  
US-10-697-802A-6

Query Match 92.7%; Score 20.4; DB 10; Length 1449;  
Best Local Similarity 95.5%; Pred. No. 4.7;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22  
|||||  
DB 24 GTCGAACGGAAGGCGCTTTCG 45

## RESULT 9

US-10-697-802A-13  
; Sequence 13, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG

; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 13  
; LENGTH: 1455  
; TYPE: DNA  
; ORGANISM: Mycobacterium mucogenicum  
US-10-697-802A-13

Query Match 92.7%; Score 20.4; DB 10; Length 1455;  
Best Local Similarity 95.5%; Pred. No. 4.7;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22  
|||||  
DB 34 GTCGAACGGAAGGCGCTTTCG 55

## RESULT 10

US-10-697-802A-5  
; Sequence 5, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 5  
; LENGTH: 1482  
; TYPE: DNA  
; ORGANISM: Mycobacterium farcinogenes  
US-10-697-802A-5

Query Match 92.7%; Score 20.4; DB 10; Length 1482;  
Best Local Similarity 95.5%; Pred. No. 4.7;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GTCGAACGGAAGGCGCTTTCG 22  
|||||  
DB 32 GTCGAACGGAAGGCGCTTTCG 53

## RESULT 11

US-09-738-274-24  
; Sequence 24, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer

```
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      86.4%; Score 19; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCGCTTTTCGG 19

RESULT 12
US-10-665-708-24
; Sequence 24, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GPI07-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-10-665-708-24

Query Match      86.4%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| |||||
Db 1 GAACGGAAGGCGCTTTTCGG 19

RESULT 13
US-10-522-454-1
; Sequence 1, Application US/10522454
; Publication No. US20050244938A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Russell T.
; APPLICANT: Hamann, Mark T.
; APPLICANT: Peraud, Olivier
; APPLICANT: Kasanah, Noer
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES
; FILE REFERENCE: 4115-180
; CURRENT APPLICATION NUMBER: US/10/522,454
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: PCT/USO3/24238
; PRIOR FILING DATE: 2003-08-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Actinomycetes sp.
US-10-522-454-1

; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

Query Match      85.5%; Score 18.8; DB 10; Length 1403;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| |||||
Db 29 GTCGAGCGGAAGGCGCTTCGG 50

RESULT 14
US-11-035-296-1
; Sequence 1, Application US/11035296
; Publication No. US20050203005A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-195
; CURRENT APPLICATION NUMBER: US/11/035,296
; CURRENT FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-035-296-1

Query Match      85.5%; Score 18.8; DB 13; Length 1443;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTTCGG 22
    ||||| ||||| ||||| |||||
Db 34 GTCGAGCGGAAGGCGCTTCGG 55

RESULT 15
US-11-045-628-1
; Sequence 1, Application US/11045628
; Publication No. US20050233952A1
; GENERAL INFORMATION:
; APPLICANT: VICURON PHARMACEUTICALS INC.
; APPLICANT: LAZZARINI, Ameriga
; APPLICANT: GASTALDO, Luciano
; APPLICANT: CANDIANI, Gianpaolo
; APPLICANT: CICILIATO, Ismaela
; APPLICANT: LOSI, Daniele
; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12
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; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

Query Match      85.5%; Score 18.8; DB 13; Length 1443;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db  34  GTCGAGCGGAAGGCTTTCGG 55

RESULT 16
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Mycobacterium goodnae
US-10-697-802A-7

Query Match      85.5%; Score 18.8; DB 10; Length 1461;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db  24  GTCGAACGTAAGGCTTTCGG 45

RESULT 17
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH898 16S ribosomal RNA gene, partial sequence
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

Query Match      85.5%; Score 18.8; DB 16; Length 1480;
Best Local Similarity 90.9%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1  GTCGAACGGAAGGCTTTCGG 22
      ||||| ||||| ||||| ||||| |||||
Db  54  GTCGAGCGGAAGGCTTTCGG 75

RESULT 18
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
```

; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-6

Query Match 85.5%; Score 18.8; DB 16; Length 1480;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22  
||||| ||||||| |||||||  
Db 54 GTCGAGCGGAAAGCCCTTCGG 75

## RESULT 19

US-11-228-416-8  
; Sequence 8, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8

LENGTH: 1480  
TYPE: DNA  
ORGANISM: Salinospora sp. CNH725 16S ribosomal RNA gene, partial sequence

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (198)..(198)  
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (351)..(351)  
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (442)..(442)  
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (443)..(443)  
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1423)..(1423)  
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA

US-11-228-416-8  
Query Match 85.5%; Score 18.8; DB 16; Length 1480;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22  
||||| ||||||| |||||||  
Db 54 GTCGAGCGGAAAGCCCTTCGG 75

## RESULT 20

US-11-228-416-9  
; Sequence 9, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William

; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9

LENGTH: 1480  
TYPE: DNA  
ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (198)..(198)  
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (351)..(351)  
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (442)..(442)  
OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (443)..(443)  
OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1423)..(1423)  
OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA

US-11-228-416-9  
Query Match 85.5%; Score 18.8; DB 16; Length 1480;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTCGG 22  
||||| ||||||| |||||||  
Db 54 GTCGAGCGGAAAGCCCTTCGG 75

## RESULT 21

US-11-228-416-3  
; Sequence 3, Application US/11228416  
; Publication No. US20060008852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT APPLICATION NUMBER: US/11/228,416  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3

LENGTH: 1481  
TYPE: DNA  
ORGANISM: Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (198)..(198)



OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (352)..(352)  
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (443)..(443)  
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (444)..(444)  
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1424)..(1424)  
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-3

Query Match 85.5%; Score 18.8; DB 16; Length 1481;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTCGACGGAAGGCCCTTCGG 22  
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 22  
US-11-228-416-4  
; Sequence 4, Application US/11228416  
; Publication No. US2006000852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1482  
; TYPE: DNA  
; ORGANISM: Salinospora sp. CNH646 16S ribosomal RNA gene, partial sequence  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (198)..(198)  
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (351)..(351)  
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (442)..(442)  
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (443)..(443)  
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1425)..(1425)  
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-4

Query Match 85.5%; Score 18.8; DB 16; Length 1482;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTCGACGGAAGGCCCTTCGG 22  
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 23  
US-11-228-416-7  
; Sequence 7, Application US/11228416  
; Publication No. US2006000852A1  
; GENERAL INFORMATION:  
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO  
; APPLICANT: FENICAL, William  
; APPLICANT: JENSEN, Paul R.  
; APPLICANT: MINCER, Tracy J.  
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO  
; FILE REFERENCE: UCSD1630-1  
; CURRENT FILING DATE: 2005-09-15  
; PRIOR APPLICATION NUMBER: US/09/991,518B  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: US 60/249,356  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 1483  
; TYPE: DNA  
; ORGANISM: Salinospora sp. CNH536 16S ribosomal RNA gene, partial sequence  
; FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (198)..(198)  
OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (351)..(351)  
OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (443)..(443)  
OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (444)..(444)  
OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1426)..(1426)  
OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA  
US-11-228-416-7

Query Match 85.5%; Score 18.8; DB 16; Length 1483;  
Best Local Similarity 90.9%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GTCGACGGAAGGCCCTTCGG 22  
Db 54 GTCGAGCGGAAGGCCCTTCGG 75

RESULT 24  
US-10-230-026-6  
; Sequence 6, Application US/10230026  
; Publication No. US20030124695A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAEL G. BRAMUCCI  
; APPLICANT: PATRICIA C. BRZOSTOWICZ  
; APPLICANT: KRISTY N. KOSTICHKA  
; APPLICANT: VASANTHA NAGARAJAN  
; APPLICANT: PIERRE E. ROUVIERE

```
; APPLICANT: STUART M. THOMAS
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: C11789 US NA
; CURRENT APPLICATION NUMBER: US/10/230,026
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-230-026-6
Query Match      80.9%; Score 17.8; DB 7; Length 1439;
Best Local Similarity 90.5%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAGGCGCTTTTCGG 22
Db  36  TCGAGCGGTAAGGCGCTTTTCGG 56

RESULT 25
US-10-486-307-6
; Sequence 6, Application US/10486307
; Publication No. US20040267001A1
; GENERAL INFORMATION:
; APPLICANT: E. I. duPont de Nemours, Inc.
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES
; FILE REFERENCE: C11789 PCT
; CURRENT APPLICATION NUMBER: US/10/486,307
; CURRENT FILING DATE: 2004-02-05
; PRIOR APPLICATION NUMBER: 60/315,546
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 1439
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis AN12
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1417)..(1417)
; OTHER INFORMATION: N = G or A or T or C
US-10-486-307-6
Query Match      80.9%; Score 17.8; DB 9; Length 1439;
Best Local Similarity 90.5%; Pred. No. 97;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  TCGAACGGAAGGCGCTTTTCGG 22
Db  36  TCGAGCGGTAAGGCGCTTTTCGG 56

RESULT 26
US-10-220-212A-31
; Sequence 31, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
```

```
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
US-10-220-212A-31
Query Match      79.1%; Score 17.4; DB 8; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4  GAACGGAAGGCGCTTTTCGG 22
Db  1  GAACGGAAGGCGCTTTTCGG 19

RESULT 27
US-10-220-212A-33
; Sequence 33, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mycobacterium-specific oligonucleotide
US-10-220-212A-33
Query Match      79.1%; Score 17.4; DB 8; Length 25;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4  GAACGGAAGGCGCTTTTCGG 22
Db  1  GAACGGAAGGCGCTTTTCGG 19

RESULT 28
US-09-738-972-7
; Sequence 7, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-09-738-972-7

Query Match          79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 5 GTCGAACGGAAGGCCTCT 23
    |||||

RESULT 29
US-09-738-972-14/c
; Sequence 14, Application US/09738972
; Patent No. US20020012918A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,972
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-09-738-972-14

Query Match          79.1%; Score 17.4; DB 3; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10
    |||||

RESULT 30
US-10-862-026-7
; Sequence 7, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: primer
US-10-862-026-7

Query Match          79.1%; Score 17.4; DB 9; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 5 GTCGAACGGAAGGCCTCT 23
    |||||

RESULT 31
US-10-862-026-14/c
; Sequence 14, Application US/10862026
; Publication No. US20040224348A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: LANKFORD, Roger L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION OF MYCOBACTERIUM
; TITLE OF INVENTION: AVIUM COMPLEX SPECIES
; FILE REFERENCE: GP119-02.UT
; CURRENT APPLICATION NUMBER: US/10/862,026
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/171,202
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: probe
US-10-862-026-14

Query Match          79.1%; Score 17.4; DB 9; Length 32;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
    |||||
Db 28 GTCGAACGGAAGGCCTCT 10
    |||||

RESULT 32
US-10-478-633A-23
; Sequence 23, Application US/10478633A
; Publication No. US20050059000A1
; GENERAL INFORMATION:
; APPLICANT: TAKARA BIO INC.
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent fo
; FILE REFERENCE: 663232
; CURRENT APPLICATION NUMBER: US/10/478,633A
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: JP 2001-177737
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: JP 2001-249689
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 173
; SEQ ID NO 23
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Mycobacterium avium
US-10-478-633A-23

Query Match          79.1%; Score 17.4; DB 10; Length 560;
Best Local Similarity 94.7%; Pred. No. 1.5e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```



```

1  APPLICANT: wang, David G.
2  TITLE OF INVENTION: Identification and Mapping of Single
3  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
4  FILE REFERENCE: 108827.135
5  CURRENT APPLICATION NUMBER: US/09/925,065A
6  CURRENT FILING DATE: 2001-08-08
7  PRIOR APPLICATION NUMBER: US 60/243,096
8  PRIOR FILING DATE: 2000-10-24

```

```

RESULT 41
US-10-027-632-292604
; Sequence 292604, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and
; TITLE OF INVENTION: Polymorphisms in t

```

Qy 1 GTCGAACGGAAGGCCTTTCGG 22

; SEQ TD NO 292605

; LENGTH: 638  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-292605

Query Match	78.2%	Score 17.2;	DB 7;	Length 638;
Best Local Similarity	86.4%	Pred. No. 1.9e+02;		
Matches 19; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

**Qy**

1 GTCGAACGAAAGCCTTTCGG 22  
||| ||| ||| ||| ||| ||| ||| |||  
**Db**

225 GTGGAAGGGAAGGCCATTTCGG 248

RESULT 45  
US-10-085-871C-1  
; Sequence 1, Application US/10085871C  
; Publication No. US20030199047A1

; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Fang-Yu  
 ; APPLICANT: Lee, Ming-Liang  
 ; APPLICANT: Anderson, Hong C.

; APPLICANT: Chiu, Chung-Ching  
 ; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin U  
 ; TITLE OF INVENTION: Strains and Isolation Process of (HMG)-COA Reductase  
 ; FILE REFERENCE: 004135.P005  
 ; CURRENT AND PAST CLASSIFICATION: C12N1/00, C12P1/00, C12P1/02, C12P1/04, C12P1/06, C12P1/08, C12P1/10, C12P1/12, C12P1/14, C12P1/16, C12P1/18, C12P1/20, C12P1/22, C12P1/24, C12P1/26, C12P1/28, C12P1/30, C12P1/32, C12P1/34, C12P1/36, C12P1/38, C12P1/40, C12P1/42, C12P1/44, C12P1/46, C12P1/48, C12P1/50, C12P1/52, C12P1/54, C12P1/56, C12P1/58, C12P1/60, C12P1/62, C12P1/64, C12P1/66, C12P1/68, C12P1/70, C12P1/72, C12P1/74, C12P1/76, C12P1/78, C12P1/80, C12P1/82, C12P1/84, C12P1/86, C12P1/88, C12P1/90, C12P1/92, C12P1/94, C12P1/96, C12P1/98, C12P1/100, C12P1/102, C12P1/104, C12P1/106, C12P1/108, C12P1/110, C12P1/112, C12P1/114, C12P1/116, C12P1/118, C12P1/120, C12P1/122, C12P1/124, C12P1/126, C12P1/128, C12P1/130, C12P1/132, C12P1/134, C12P1/136, C12P1/138, C12P1/140, C12P1/142, C12P1/144, C12P1/146, C12P1/148, C12P1/150, C12P1/152, C12P1/154, C12P1/156, C12P1/158, C12P1/160, C12P1/162, C12P1/164, C12P1/166, C12P1/168, C12P1/170, C12P1/172, C12P1/174, C12P1/176, C12P1/178, C12P1/180, C12P1/182, C12P1/184, C12P1/186, C12P1/188, C12P1/190, C12P1/192, C12P1/194, C12P1/196, C12P1/198, C12P1/200, C12P1/202, C12P1/204, C12P1/206, C12P1/208, C12P1/210, C12P1/212, C12P1/214, C12P1/216, C12P1/218, C12P1/220, C12P1/222, C12P1/224, C12P1/226, C12P1/228, C12P1/230, C12P1/232, C12P1/234, C12P1/236, C12P1/238, C12P1/240, C12P1/242, C12P1/244, C12P1/246, C12P1/248, C12P1/250, C12P1/252, C12P1/254, C12P1/256, C12P1/258, C12P1/260, C12P1/262, C12P1/264, C12P1/266, C12P1/268, C12P1/270, C12P1/272, C12P1/274, C12P1/276, C12P1/278, C12P1/280, C12P1/282, C12P1/284, C12P1/286, C12P1/288, C12P1/290, C12P1/292, C12P1/294, C12P1/296, C12P1/298, C12P1/300, C12P1/302, C12P1/304, C12P1/306, C12P1/308, C12P1/310, C12P1/312, C12P1/314, C12P1/316, C12P1/318, C12P1/320, C12P1/322, C12P1/324, C12P1/326, C12P1/328, C12P1/330, C12P1/332, C12P1/334, C12P1/336, C12P1/338, C12P1/340, C12P1/342, C12P1/344, C12P1/346, C12P1/348, C12P1/350, C12P1/352, C12P1/354, C12P1/356, C12P1/358, C12P1/360, C12P1/362, C12P1/364, C12P1/366, C12P1/368, C12P1/370, C12P1/372, C12P1/374, C12P1/376, C12P1/378, C12P1/380, C12P1/382, C12P1/384, C12P1/386, C12P1/388, C12P1/390, C12P1/392, C12P1/394, C12P1/396, C12P1/398, C12P1/400, C12P1/402, C12P1/404, C12P1/406, C12P1/408, C12P1/410, C12P1/412, C12P1/414, C12P1/416, C12P1/418, C12P1/420, C12P1/422, C12P1/424, C12P1/426, C12P1/428, C12P1/430, C12P1/432, C12P1/434, C12P1/436, C12P1/438, C12P1/440, C12P1/442, C12P1/444, C12P1/446, C12P1/448, C12P1/450, C12P1/452, C12P1/454, C12P1/456, C12P1/458, C12P1/460, C12P1/462, C12P1/464, C12P1/466, C12P1/468, C12P1/470, C12P1/472, C12P1/474, C12P1/476, C12P1/478, C12P1/480, C12P1/482, C12P1/484, C12P1/486, C12P1/488, C12P1/490, C12P1/492, C12P1/494, C12P1/496, C12P1/498, C12P1/500, C12P1/502, C12P1/504, C12P1/506, C12P1/508, C12P1/510, C12P1/512, C12P1/514, C12P1/516, C12P1/518, C12P1/520, C12P1/522, C12P1/524, C12P1/526, C12P1/528, C12P1/530, C12P1/532, C12P1/534, C12P1/536, C12P1/538, C12P1/540, C12P1/542, C12P1/544, C12P1/546, C12P1/548, C12P1/550, C12P1/552, C12P1/554, C12P1/556, C12P1/558, C12P1/560, C12P1/562, C12P1/564, C12P1/566, C12P1/568, C12P1/570, C12P1/572, C12P1/574, C12P1/576, C12P1/578, C12P1/580, C12P1/582, C12P1/584, C12P1/586, C12P1/588, C12P1/590, C12P1/592, C12P1/594, C12P1/596, C12P1/598, C12P1/600, C12P1/602, C12P1/604, C12P1/606, C12P1/608, C12P1/610, C12P1/612, C12P1/614, C12P1/616, C12P1/618, C12P1/620, C12P1/622, C12P1/624, C12P1/626, C12P1/628, C12P1/630, C12P1/632, C12P1/634, C12P1/636, C12P1/638, C12P1/640, C12P1/642, C12P1/644, C12P1/646, C12P1/648, C12P1/650, C12P1/652, C12P1/654, C12P1/656, C12P1/658, C12P1/660, C12P1/662, C12P1/664, C12P1/666, C12P1/668, C12P1/670, C12P1/672, C12P1/674, C12P1/676, C12P1/678, C12P1/680, C12P1/682, C12P1/684, C12P1/686, C12P1/688, C12P1/690, C12P1/692, C12P1/694, C12P1/696, C12P1/698, C12P1/700, C12P1/702, C12P1/704, C12P1/706, C12P1/708, C12P1/710, C12P1/712, C12P1/714, C12P1/716, C12P1/718, C12P1/720, C12P1/722, C12P1/724, C12P1/726, C12P1/728, C12P1/730, C12P1/732, C12P1/734, C12P1/736, C12P1/738, C12P1/740, C12P1/742, C12P1/744, C12P1/746, C12P1/748, C12P1/750, C12P1/752, C12P1/754, C12P1/756, C12P1/758, C12P1/760, C12P1/762, C12P1/764, C12P1/766, C12P1/768, C12P1/770, C12P1/772, C12P1/774, C12P1/776, C12P1/778, C12P1/780, C12P1/782, C12P1/784, C12P1/786, C12P1/788, C12P1/790, C12P1/792, C12P1/794, C12P1/796, C12P1/798, C12P1/800, C12P1/802, C12P1/804, C12P1

```

; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1

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; LENGTH: 1437
; TYPE: DNA
; ORGANISM: Saccharothrix 44442

```

Query Match 78.2%; Score 17.2; DB 7; Length 1437;  
Best Local Similarity 86.4%; Pred. NO. 2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0

Qy 1 GTCGAACGGAAGGCCCTTTCGG 22  
||| ||| ||| ||| ||| ||| ||| |||  
Db 34 GTCGAGCGGTAAAGGCCCTTTCGG 55

RESULT 46  
US-10-727-643-1  
; Sequence 1, Application US/10727643

; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Fang-Yu  
 ; APPLICANT: Lee, Ming-Liang  
 ; APPLICANT:

```

; APPLICANT: Chiu, Chung-Ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravastatin
; TITLE OF INVENTION: Strains and Isolation Process of (HMG)-COA Reductase
; FILE REFERENCE: 004135.P005

```

; CURRENT FILING DATE: 2003-12-03  
 ; PRIOR APPLICATION NUMBER: US/10/085,871  
 ; PRIOR FILING DATE: 2002-02-27

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1437

```

TYPE: DNA  
ORGANISM: Saccharothrix 44442  
US-10-727-643-1

Query Match 78.2%; Score 17.2; DB 10; Length 1437;  
Best Local Similarity 86.4%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
Db 34 GTCGAGCGGTAAAGGCCCTTCGG 55

RESULT 47  
US-10-085-871C-2  
; Sequence 2, Application US/10085871C  
: Publication No US20030199047A1

; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Fang-Yu  
 ; APPLICANT: Lee, Ming-Liang  
 ; APPLICANT: Anderson, Hong C

; APPLICANT: Chiu, Schung-Ching  
 ; TITLE OF INVENTION: New Strains of Sacchar  
 ; TITLE OF INVENTION: Strains and Isolation  
 ; FILE REFERENCE: 004135.P005

```

; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; CURRENT APPLICATION NUMBER: US/10/085,810

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; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
```

Query Match	78.2%	Score 17.2;	DB 7;	Length 1471;
Best Local Similarity	86.4%	Pred. No. 2e+02;		
Matches 19: Conservative		0: Mismatches	3: Indels	0

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
||||| ||| ||||| |||||  
Db 34 GTCGAGCGGTAAGGCCCTTCGG 55

RESULT 48  
US-10-727-643-2  
; Sequence 2, Application US/10727643  
; Publication No. US20050064566A1

; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Fang-Yu  
 ; APPLICANT: Lee, Ming-Liang  
 ; APPLICANT: Anderson, Hong C

```

; APPLICANT: Chiu, Schung-Ching
;
; TITLE OF INVENTION: New Strain
;
; TITLE OF INVENTION: Strains a
;
; FILE REFERENCE: 004125 P005

```

; CURRENT APPLICATION NUMBER: US/10/727,643  
 ;  
 ; CURRENT FILING DATE: 2003-12-03  
 ;  
 ; PRIOR APPLICATION NUMBER: US/10/085,871  
 ; PRIOR FILING DATE: 2003-02-27

```

; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

```

; TYPE: DNA  
; ORGANISM: Saccharothrix 45494  
US-10-727-643-2

Query Match 78.2%; Score 17.2; DB 10; Length 1471;  
Best Local Similarity 86.4%; Pred. No. 2e+02;  
Matches 19; Conservative 0; Mismatches 3; Indels 0;

Qy 1 GTCGAACGGAAGGCCTTTCGG 22  
||| ||| ||| ||| ||| ||| ||| |||  
pb 34 GTCGAGCGGTAAAGGCCCTTCGG 55

RESULT 49  
US-10-756-683-1  
; Sequence 1, Application US/10756683  
; Publication No. US20040180960A1

```
; GENERAL INFORMATION:
; APPLICANT: Korea Chungang Educational Foundation
; APPLICANT: Hwang, Byong Kook
; APPLICANT: Lee, Jung Yeop
; TITLE OF INVENTION: Thiobactin and Antifungal Composition for Controlling Plant
; TITLE OF INVENTION: Diseases Using the Same
; FILE REFERENCE: 4228-102
; CURRENT APPLICATION NUMBER: US/10/756,683
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015628
; PRIOR FILING DATE: 2003-03-13
; PRIOR APPLICATION NUMBER: KP 10-2003-0015629
; PRIOR FILING DATE: 2003-03-13
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Lechevalieria aerocolonigenes
US-10-756-683-1

Query Match          78.2%; Score 17.2; DB 9; Length 1488;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGCGAAGCCCTTCGG 22
Db 46 GTCGAGCGGTAAGCCCTTCGG 67

RESULT 50
US-10-875-161-2
; Sequence 2, Application US/10875161
; Publication No. US20050009151A1
; GENERAL INFORMATION:
; APPLICANT: Chase, Matthew
; APPLICANT: Clayton, Robert
; APPLICANT: Landis, Bryan
; APPLICANT: Banerjee, Amit
; TITLE OF INVENTION: Methods for the Stereoselective Synthesis and Enantiomeric
; TITLE OF INVENTION: Enrichment of Beta-Amino Acids
; FILE REFERENCE: SO-3262-2-PR-US
; CURRENT APPLICATION NUMBER: US/10/875,161
; CURRENT FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Rhodococcus opacus
; FEATURE:
; NAME/KEY: rRNA
; LOCATION: (1)..(1514)
; OTHER INFORMATION: 16s rRNA gene (rDNA) from Rhodococcus opacus
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: (1)..(1514)
; OTHER INFORMATION: Alignment 0.17% different from 16s rRNA gene (rDNA) of
; OTHER INFORMATION: Rhodococcus opacus
US-10-875-161-2

Query Match          78.2%; Score 17.2; DB 9; Length 1514;
Best Local Similarity 86.4%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGCGAAGCCCTTCGG 22
Db 57 GTCGAGCGGTAAGCCCTTCGG 78

RESULT 51
US-10-831-286A-1517
; Sequence 1517, Application US/10831286A
```

```
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1517
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium diphtheriae
US-10-831-286A-1517

Query Match          77.3%; Score 17; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCT 17
Db 4 GTCGAACGGAAGGCCT 20

RESULT 52
US-10-831-286A-8212
; Sequence 8212, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8212
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Corynebacterium kutscheri
US-10-831-286A-8212

Query Match          74.5%; Score 16.4; DB 11; Length 30;
Best Local Similarity 94.4%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18
Db 4 GTCGAACGGAAGGCCTT 21

RESULT 53
US-10-062-674-613/c
; Sequence 613, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
```



; PRIOR APPLICATION NUMBER: US 09/625,102  
; PRIOR FILING DATE: 2000-07-24  
; NUMBER OF SEQ ID NOS: 2217  
; SOFTWARE: PERL Program  
; SEQ ID NO 613  
; LENGTH: 367  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; NAME/KEY: misc feature  
; OTHER INFORMATION: GenBank ID No. US20040005559A1 g2292157  
US-10-062-674-613

Query Match 73.6%; Score 16.2; DB 7; Length 367;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 22  
Db 39 TTGAATGGAGAGCGCTTTCG 19

## RESULT 54

US-10-767-701-31297  
; Sequence 31297, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 31297  
; LENGTH: 622  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 18066455  
US-10-767-701-31297

Query Match 73.6%; Score 16.2; DB 8; Length 622;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCGCTTTCG 21  
Db 32 GTCGAGAGGAATGGCGCTTTCG 52

## RESULT 55

US-10-425-115-59269  
; Sequence 59269, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 59269  
; LENGTH: 635  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577\_15404C.1  
US-10-425-115-59269

Query Match 73.6%; Score 16.2; DB 9; Length 635;  
Best Local Similarity 85.7%; Pred. No. 6.2e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCG 22  
Db 452 TTGAGCGGAAGGCGCTTTCG 472

## RESULT 56

US-10-831-286A-12801  
; Sequence 12801, Application US/10831286A  
; Publication No. US20060046246A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENG, QIANDONG  
; APPLICANT: CHATELLIER, SONIA  
; APPLICANT: MOIR, DONALD T.  
; APPLICANT: LACROIX, BRUNA  
; APPLICANT: CHILDRESS, DARRELL  
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
; FILE REFERENCE: 032796-174.001  
; CURRENT APPLICATION NUMBER: US/10/831,286A  
; CURRENT FILING DATE: 2004-04-26  
; PRIOR APPLICATION NUMBER: 60/464,955  
; PRIOR FILING DATE: 2003-04-24  
; NUMBER OF SEQ ID NOS: 48788  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12801  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Corynebacterium ulcerans  
US-10-831-286A-12801

Query Match 72.7%; Score 16; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
Db 5 GTCGAACGGAAGGCC 20

## RESULT 57

US-10-831-286A-23905  
; Sequence 23905, Application US/10831286A  
; Publication No. US20060046246A1  
; GENERAL INFORMATION:  
; APPLICANT: ZENG, QIANDONG  
; APPLICANT: CHATELLIER, SONIA  
; APPLICANT: MOIR, DONALD T.  
; APPLICANT: LACROIX, BRUNA  
; APPLICANT: CHILDRESS, DARRELL  
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
; FILE REFERENCE: 032796-174.001  
; CURRENT APPLICATION NUMBER: US/10/831,286A  
; CURRENT FILING DATE: 2004-04-26  
; PRIOR APPLICATION NUMBER: 60/464,955  
; PRIOR FILING DATE: 2003-04-24  
; NUMBER OF SEQ ID NOS: 48788  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23905  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Corynebacterium ulcerans  
US-10-831-286A-23905

Query Match 72.7%; Score 16; DB 11; Length 20;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
| | | | | | | | | | | | | | | |  
Db 4 GTCGAACGGAAGGCC 19

## RESULT 58

US-09-738-274-27  
; Sequence 27, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-27

Query Match 72.7%; Score 16; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
| | | | | | | | | | | | | | | |  
Db 4 GTCGAACGGAAGGCC 19

## RESULT 59

US-10-665-708-27  
; Sequence 27, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-27

Query Match 72.7%; Score 16; DB 10; Length 23;

Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTCGAACGGAAGGCC 16  
| | | | | | | | | | | | | | | |  
Db 4 GTCGAACGGAAGGCC 19

## RESULT 60

US-09-738-274-28  
; Sequence 28, Application US/09738274  
; Publication No. US20030165824A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-09-738-274-28

Query Match 72.7%; Score 16; DB 3; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
| | | | | | | | | | | | | | | |  
Db 1 GTCGAACGGAAGGCC 16

## RESULT 61

US-10-665-708-28  
; Sequence 28, Application US/10665708  
; Publication No. US20050100915A1  
; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 28  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; OTHER INFORMATION: oligonucleotide  
US-10-665-708-28

## US-10-665-708-28

Query Match 72.7%; Score 16; DB 10; Length 26;  
Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
|||||  
Db 1 GTCGAACGGAAGGCC 16

## RESULT 62

US-10-830-943-11  
; Sequence 11, Application US/10830943  
; Publication No. US2005009053A1  
; GENERAL INFORMATION:  
; APPLICANT: Boecker, Sebastien  
; APPLICANT: van den Boom, Dirk  
; TITLE OF INVENTION: FRAGMENTATION-BASED METHODS AND SYSTEMS  
; TITLE OF INVENTION: FOR DE NOVO SEQUENCING  
; FILE REFERENCE: 17082-079001  
; CURRENT APPLICATION NUMBER: US/10/830,943  
; CURRENT FILING DATE: 2004-04-22  
; PRIOR APPLICATION NUMBER: US 60/466,006  
; PRIOR FILING DATE: 2003-04-25  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 80  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: amplicon sequence  
US-10-830-943-11

Query Match 72.7%; Score 16; DB 9; Length 80;  
Best Local Similarity 100.0%; Pred. No. 7.6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
|||||  
Db 54 GTCGAACGGAAGGCC 69

## RESULT 63

US-10-478-633A-24  
; Sequence 24, Application US/10478633A  
; Publication No. US2005005900A1  
; GENERAL INFORMATION:  
; APPLICANT: TAKARA BIO INC.  
; TITLE OF INVENTION: A stabilization method and a preservation method for a reagent for  
; TITLE OF INVENTION: acid amplification or detection reaction  
; FILE REFERENCE: 663232  
; CURRENT APPLICATION NUMBER: US/10/478,633A  
; CURRENT FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: JP 2001-177737  
; PRIOR FILING DATE: 2001-06-12  
; PRIOR APPLICATION NUMBER: JP 2001-249689  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 173  
; SEQ ID NO 24  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Mycobacterium intracellulare  
US-10-478-633A-24

Query Match 72.7%; Score 16; DB 10; Length 560;  
Best Local Similarity 100.0%; Pred. No. 7.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16  
|||||  
Db 46 GTCGAACGGAAGGCC 61

## RESULT 64

US-10-779-543-8365  
; Sequence 8365, Application US/10779543  
; Publication No. US20050227917A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams et al  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II  
; FILE REFERENCE: 2300-21302  
; CURRENT APPLICATION NUMBER: US/10/779,543  
; CURRENT FILING DATE: 2004-02-12  
; PRIOR APPLICATION NUMBER: 10/076,555  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: 09/217,471  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/068,755  
; PRIOR FILING DATE: 1997-12-23  
; PRIOR APPLICATION NUMBER: 60/080,664  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/105,234  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 09/237,648  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: PCT/US99/01619  
; PRIOR FILING DATE: 1999-01-28  
; PRIOR APPLICATION NUMBER: 60/072,910  
; PRIOR FILING DATE: 1998-01-28  
; PRIOR APPLICATION NUMBER: 60/075,954  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/080,114  
; PRIOR FILING DATE: 1998-03-31  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 23767  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8365  
; LENGTH: 935  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 13, 17, 18, 20, 21, 25, 35, 37, 43, 46, 48, 52, 57, 81, 89,  
; LOCATION: 108, 116, 127, 138, 139, 142, 144, 168, 169, 172, 178, 179,  
; LOCATION: 184, 185, 204, 222, 231, 234, 242, 248, 258, 263, 279, 287,  
; LOCATION: 291, 304, 310, 317, 319, 328, 335, 337, 350, 357, 362  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 363, 365, 375, 387, 390, 391, 401, 433, 434, 436, 455, 460,  
; LOCATION: 468, 476, 479, 489, 495, 500, 502, 506, 515, 529, 530, 534,  
; LOCATION: 543, 553, 563, 564, 565, 566, 592, 627, 628, 631, 642, 645,  
; LOCATION: 650, 653, 662, 668, 670, 680, 681, 682, 684, 685, 691  
; OTHER INFORMATION: n = A,T,C or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 696, 703, 707, 741, 745, 752, 756, 763, 767, 770, 771, 779,  
; LOCATION: 795, 823, 824, 829, 830, 846, 850, 854, 855, 873, 874, 878,  
; LOCATION: 887, 890, 894, 907, 910, 920, 922, 929, 935  
; OTHER INFORMATION: n = A,T,C or G  
US-10-779-543-8365

Query Match 72.7%; Score 16; DB 10; Length 935;  
Best Local Similarity 84.2%; Pred. No. 7.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTCGG 22  
|||||  
Db 452 GAAGGAAGCCCTTNGG 470

## RESULT 65

US-10-697-802A-11

```
; Sequence 11, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 11
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Mycobacterium kubicacae
US-10-697-802A-11

Query Match          72.7%; Score 16; DB 10; Length 1321;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCC 16
Db      18 GTCGAACGGAAAGGCC 33

RESULT 66
US-10-697-802A-14
; Sequence 14, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 14
; LENGTH: 1415
; TYPE: DNA
; ORGANISM: Mycobacterium paraffinicum
US-10-697-802A-14

Query Match          72.7%; Score 16; DB 10; Length 1415;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCC 16
Db      19 GTCGAACGGAAAGGCC 34

RESULT 67
US-10-062-777-1
; Sequence 1, Application US/10062777
; Publication No. US20020119514A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/062,777
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/463,618
; PRIOR FILING DATE: 2000-01-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-062-777-1

Query Match          72.7%; Score 16; DB 6; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCC 16
Db      42 GTCGAACGGAAAGGCC 57

RESULT 68
US-10-419-095-1
; Sequence 1, Application US/10419095
; Publication No. US20030162244A1
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: A PROCESS FOR PRODUCING A BRAN PICKLES FLAVORING SOLUTION
; FILE REFERENCE: 11142W0
; CURRENT APPLICATION NUMBER: US/10/419,095
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/463,618
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: H10-166226
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1460
; TYPE: DNA
; ORGANISM: Corynebacterium sp.NK-1
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (166)
; OTHER INFORMATION: n is "a" or "g" or "c" or "t".
US-10-419-095-1

Query Match          72.7%; Score 16; DB 7; Length 1460;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCC 16
Db      42 GTCGAACGGAAAGGCC 57

RESULT 69
US-10-697-802A-16
; Sequence 16, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 16
; LENGTH: 1462
; TYPE: DNA
; ORGANISM: Mycobacterium szulgai
US-10-697-802A-16

Query Match          72.7%; Score 16; DB 10; Length 1462;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAAGGCC 16
Db      24 GTCGAACGGAAAGGCC 39
```

```
RESULT 70
US-10-697-802A-15
; Sequence 15, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 15
; LENGTH: 1484
; TYPE: DNA
; ORGANISM: Mycobacterium simiae
US-10-697-802A-15
Query Match 72.7%; Score 16; DB 10; Length 1484;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 24 GTCGAACGGAAGGCC 39

RESULT 71
US-10-697-802A-8
; Sequence 8, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 8
; LENGTH: 1527
; TYPE: DNA
; ORGANISM: Mycobacterium heckeshornense
US-10-697-802A-8
Query Match 72.7%; Score 16; DB 10; Length 1527;
Best Local Similarity 100.0%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCC 16
Db 48 GTCGAACGGAAGGCC 63

RESULT 72
US-09-738-274-14
; Sequence 14, Application US/09738274
; Publication No. US20030165824A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14
Query Match 71.8%; Score 15.8; DB 10; Length 32;
Best Local Similarity 89.5%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTT 19
Db 5 GTCGAACGGAAGGCTCTCT 23

RESULT 73
US-10-665-708-14
; Sequence 14, Application US/10665708
; Publication No. US20050100915A1
; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; TITLE OF INVENTION: MYCOBACTERIUM SPECIES
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-665-708-14
Query Match 71.8%; Score 15.8; DB 10; Length 32;
Best Local Similarity 89.5%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCCTTT 19
Db 5 GTCGAACGGAAGGCTCTCT 23

RESULT 74
US-10-062-727-254
; Sequence 254, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; TITLE OF INVENTION: for their Use
; FILE REFERENCE: 11000.1006CIP
; CURRENT APPLICATION NUMBER: US/10/062,727
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
```

```
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 170
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
; NAME/KEY: misc feature
; LOCATION: (1)-(170)
; OTHER INFORMATION: n = A,T,C or G
US-10-062-727-254

Query Match          71.8%; Score 15.8; DB 6; Length 170;
Best Local Similarity 89.5%; Pred. No. 9.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAAGCCCTTCGG 22
    ||| ||||| ||||| |||
Db 69 GAAGGAAAGCCCTTTAGG 87

RESULT 75
US-10-062-727-376
; Sequence 376, Application US/10062727
; Publication No. US20030018185A1
; GENERAL INFORMATION:
; APPLICANT: Havukkala, Ilkka
; APPLICANT: Bloksberg, Leonard
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Plant Microsatellite Markers and Methods
; FILE REFERENCE: for their Use
; CURRENT APPLICATION NUMBER: US/10/062,727
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 09/105,307
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 1057
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 376
; LENGTH: 305
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-062-727-376

Query Match          71.8%; Score 15.8; DB 6; Length 305;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAAGCCCTTCGG 22
    ||| ||||| ||||| |||
Db 70 GAAGGAAAGCCCTTTAGG 88

RESULT 76
US-10-450-763-13678/c
; Sequence 13678, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 13678
; LENGTH: 381

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(372)
; OTHER INFORMATION: 100% homologous to Escherichia coli K12 orf, hypothetical
; OTHER INFORMATION: protein, accession number AE000223, Smith-Waterman Score=635.
US-10-450-763-13678

Query Match          71.8%; Score 15.8; DB 10; Length 381;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTT 19
    ||||| ||||| ||||| |||
Db 160 GACGAACGGAAAGCGGTT 142

RESULT 77
US-10-438-774-17
; Sequence 17, Application US/10438774
; Publication No. US20040010504A1
; GENERAL INFORMATION:
; APPLICANT: Hinrichs, Steven
; APPLICANT: Mohammed, Amr
; APPLICANT: Ali, Hesham
; APPLICANT: Kuyper, Dan
; TITLE OF INVENTION: Custom Sequence Databases and Methods of
; FILE OF INVENTION: Use Thereof
; FILE REFERENCE: UNMC.63174-US
; CURRENT APPLICATION NUMBER: US/10/438,774
; CURRENT FILING DATE: 2003-05-14
; PRIOR APPLICATION NUMBER: 60/381,015
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 468
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-438-774-17

Query Match          71.8%; Score 15.8; DB 7; Length 468;
Best Local Similarity 89.5%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAAGCCCTTT 19
    ||||| ||||| ||||| |||
Db 1 GTCGAACGGAAAGGTCCTCT 19

RESULT 78
US-10-450-763-3105
; Sequence 3105, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 3105
; LENGTH: 576
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (419)..(3)
; OTHER INFORMATION: 3% homologous to Santalum album proline rich
; OTHER INFORMATION: protein.accession number AF020261,Smith-Waterman Score=109.
US-10-450-763-3105

Query Match          71.8%; Score 15.8; DB 10; Length 576;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCGCTTCGG 22
Db 512 GAATGGAAGGCTCTTCGG 530

RESULT 79
US-10-301-480-442948
; Sequence 442948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 442948
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-442948

Query Match          71.8%; Score 15.8; DB 12; Length 625;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 275 TGGAAACGGAAGGCTTTC 293

RESULT 80
US-10-301-480-1056357
; Sequence 1056357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1056357
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1056357
```

```
Query Match          71.8%; Score 15.8; DB 12; Length 625;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 275 TGGAAACGGAAGGCTTTC 293

RESULT 81
US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match          71.8%; Score 15.8; DB 4; Length 634;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTC 20
Db 284 TGGAAACGGAAGGCTTTC 302

RESULT 82
US-09-925-065A-373045
; Sequence 373045, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373045
; LENGTH: 634
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-09-925-065A-373045

Query Match      71.8%; Score 15.8; DB 5; Length 634;
Best Local Similarity 89.5%; Pred. No. 9.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCGCTTC 20
      | ||||| ||||| |||||
Db      284 TGGACGGAAGGCTCTTC 302

RESULT 83
US-10-697-802A-17
; Sequence 17, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 17
; LENGTH: 1416
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-697-802A-17

Query Match      71.8%; Score 15.8; DB 10; Length 1416;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
Db      24 GTCGAACGGAAGGCTCT 42

RESULT 84
US-10-697-802A-3
; Sequence 3, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 3
; LENGTH: 1421
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-697-802A-3

Query Match      71.8%; Score 15.8; DB 10; Length 1421;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
Db      24 GTCGAACGGAAGGCTCT 42

RESULT 85
US-10-697-802A-10
; Sequence 10, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
```

```
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 10
; LENGTH: 1463
; TYPE: DNA
; ORGANISM: Mycobacterium kansasii
US-10-697-802A-10

Query Match      71.8%; Score 15.8; DB 10; Length 1463;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
Db      23 GTCGAACGGAAGGCTCT 41

RESULT 86
US-09-726-774-7
; Sequence 7, Application US/09726774
; Patent No. US2002008226A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/09/726,774
; CURRENT FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-726-774-7

Query Match      71.8%; Score 15.8; DB 3; Length 1464;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GTCGAACGGAAGGCGCTTT 19
      | ||||| ||||| |||||
Db      24 GTCGAACGGAAGGCTCT 42

RESULT 87
US-10-719-633-7
; Sequence 7, Application US/10719633
; Publication No. US20040137485A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Antisense Antibacterial Method and
; TITLE OF INVENTION: Composition
; FILE REFERENCE: 0450-0032.30
; CURRENT APPLICATION NUMBER: US/10/719,633
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US/09/726,774
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 60/168,150
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-719-633-7
```



```
Query Match      71.8%; Score 15.8; DB 8; Length 1464;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
   |||||
Db 24 GTCGAACGGAAGGCTCT 42

RESULT 88
US-10-220-212A-34
; Sequence 34, Application US/10220212A
; Publication No. US20040110129A1
; GENERAL INFORMATION:
; APPLICANT: Government of the United States of America as represented by the
; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes
; APPLICANT: Health
; APPLICANT: Beckman Coulter, Inc.
; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen
; FILE REFERENCE: 4239-58135
; CURRENT APPLICATION NUMBER: US/10/220,212A
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/186,840
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-220-212A-34

Query Match      71.8%; Score 15.8; DB 8; Length 1524;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
   |||||
Db 54 GTCGAACGGAAGGCTCT 72

RESULT 89
US-10-029-397A-33
; Sequence 33, Application US/10029397A
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-10-029-397A-33

Query Match      71.8%; Score 15.8; DB 7; Length 1536;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
   |||||
Db 63 GTCGAACGGAAGGCTCT 81

RESULT 90
US-10-029-397A-34
; Sequence 34, Application US/10029397A
```

```
; Publication No. US20030175709A1
; GENERAL INFORMATION:
; APPLICANT: MURPHY, GEORGE L.
; APPLICANT: WHITLEY, J. PENN
; TITLE OF INVENTION: METHOD AND SYSTEM FOR DEPLETING rRNA POPULATIONS
; FILE REFERENCE: AMBI:076US
; CURRENT APPLICATION NUMBER: US/10/029,397A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1536
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-029-397A-34

Query Match      71.8%; Score 15.8; DB 7; Length 1536;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTTT 19
   |||||
Db 63 GTCGAACGGAAGGCTCT 81

RESULT 91
US-10-488-528-3
; Sequence 3, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2896
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1525)
US-10-488-528-3

Query Match      71.8%; Score 15.8; DB 10; Length 2896;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTTTCGG 22
   |||||
Db 1486 GAACGGAAGGCCTTTCGG 1504

RESULT 92
US-10-369-493-35634/c
; Sequence 35634, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
```

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35634
; LENGTH: 2919
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-369-493-35634

Query Match          71.8%; Score 15.8; DB 7; Length 2919;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTT 19
    |||||
Db 2382 GCGCAACGCAAGCCCTTT 2364

RESULT 93
US-10-488-528-1
; Sequence 1, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(1576)
US-10-488-528-1

Query Match          71.8%; Score 15.8; DB 10; Length 3054;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCG 22
    |||||
Db 1540 GAACGGAAGCCCTTTCCG 1558

RESULT 94
US-09-764-877-3363
; Sequence 3363, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3363

Query Match          71.8%; Score 15.8; DB 3; Length 6883;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCG 22
    |||||
Db 478 GAATGGAAGGCTCTTCGG 496

RESULT 95
US-10-242-515-3363
; Sequence 3363, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363

Query Match          71.8%; Score 15.8; DB 7; Length 6883;
Best Local Similarity 89.5%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGCCCTTTCCG 22
    |||||
Db 478 GAATGGAAGGCTCTTCGG 496

RESULT 96
US-10-465-008-10
; Sequence 10, Application US/10465008
; Publication No. US20040016016A1
; GENERAL INFORMATION:
; APPLICANT: MANKIN, LUKE S.
; APPLICANT: DA COSTA E SILVA, OSWALDO
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMPROVING PLANT PERFORMANCE
; FILE REFERENCE: 16313-0232
; CURRENT APPLICATION NUMBER: US/10/465,008
; CURRENT FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: 60/389,982
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21126
; TYPE: DNA
; ORGANISM: Agrobacterium rhizogenes
US-10-465-008-10

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; PRIOR FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: US 60/137,461
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Microsoft Office 97
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; Publication No. US20060046253A1
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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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OM nucleic - nucleic search, using sw model

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Searched: 224314 seqs, 35277956 residues

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Listing first 300 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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7	14.4	65.5	2454	7	US-11-217-529-6038 Sequence 6038, App
8	14.2	64.5	858	7	US-11-217-529-1257 Sequence 1257, App
9	14.2	64.5	858	7	US-11-217-529-77141 Sequence 77141, A
10	14.2	64.5	1260	7	US-11-217-529-5375 Sequence 5375, App
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13	14	63.6	1758	7	US-11-217-529-1422 Sequence 1422, App
14	14	63.6	5900	6	US-10-505-928-182 Sequence 182, App
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19	13.6	61.8	1326	7	US-11-217-529-80747 Sequence 80747, A
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21	13.6	61.8	2952	7	US-11-217-529-4946 Sequence 4946, App
22	13.6	61.8	3102	7	US-11-217-529-82302 Sequence 82302, A
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24	13.4	60.9	599	6	US-10-488-619-2156 Sequence 2156, App
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c 138	12.6	57.3	1737	7	US-11-217-529-82238	Sequence 82238, A	c 211	12.4	56.4	888	7	US-11-217-529-77949	Sequence 77949, A
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C 261 12.4 56.4 11435 7 US-11-264-784-126 Sequence 126, App
C 262 12.4 56.4 11564 6 US-10-505-928-105 Sequence 105, App
C 263 12.4 56.4 13034 7 US-11-254-173-37 Sequence 37, Appl
C 264 12.4 56.4 13034 7 US-11-264-784-116 Sequence 116, App
C 265 12.2 55.5 25 7 US-11-217-529-10285 Sequence 10285, A
C 266 12.2 55.5 25 7 US-11-217-529-36553 Sequence 36553, A
C 267 12.2 55.5 25 7 US-11-217-529-48962 Sequence 48962, A
C 268 12.2 55.5 25 7 US-11-217-529-61824 Sequence 61824, A
C 269 12.2 55.5 25 7 US-11-217-529-103429 Sequence 103429, A
C 270 12.2 55.5 25 7 US-11-217-529-188129 Sequence 188129, A
C 271 12.2 55.5 192 1 US-09-756-097B-88 Sequence 88, Appl
C 272 12.2 55.5 192 1 US-09-756-097B-92 Sequence 92, Appl
C 273 12.2 55.5 366 7 US-11-217-529-77191 Sequence 77191, A
C 274 12.2 55.5 378 7 US-11-301-554-889 Sequence 889, App
C 275 12.2 55.5 390 7 US-11-301-554-1419 Sequence 1419, App
C 276 12.2 55.5 402 7 US-11-217-529-173452 Sequence 173452, A
C 277 12.2 55.5 410 6 US-10-488-619-466 Sequence 466, App
C 278 12.2 55.5 447 6 US-10-473-173-139 Sequence 139, App
C 279 12.2 55.5 462 6 US-10-488-619-319 Sequence 319, App
C 280 12.2 55.5 480 7 US-11-217-529-75552 Sequence 75552, A
C 281 12.2 55.5 573 7 US-11-217-529-81230 Sequence 81230, A
C 282 12.2 55.5 585 7 US-11-217-529-79588 Sequence 79588, A
C 283 12.2 55.5 606 7 US-11-217-529-77702 Sequence 77702, A
C 284 12.2 55.5 883 6 US-10-488-619-2064 Sequence 2064, App
C 285 12.2 55.5 906 7 US-11-217-529-2768 Sequence 2768, App
C 286 12.2 55.5 909 7 US-11-217-529-1523 Sequence 1523, App
C 287 12.2 55.5 933 7 US-11-217-529-4222 Sequence 4222, App
C 288 12.2 55.5 984 7 US-11-217-529-174359 Sequence 174359, A
C 289 12.2 55.5 1029 7 US-11-217-529-81270 Sequence 81270, A
C 290 12.2 55.5 1089 6 US-10-511-937-2916 Sequence 2916, App
C 291 12.2 55.5 1089 7 US-11-217-529-4005 Sequence 4005, App
C 292 12.2 55.5 1143 7 US-11-217-529-3940 Sequence 3940, App
C 293 12.2 55.5 1155 7 US-11-217-529-999 Sequence 999, App
C 294 12.2 55.5 1197 7 US-11-217-529-5027 Sequence 5027, App
C 295 12.2 55.5 1212 7 US-11-217-529-77899 Sequence 77899, A
C 296 12.2 55.5 1344 7 US-11-217-529-4610 Sequence 4610, App
C 297 12.2 55.5 1359 7 US-11-217-529-79910 Sequence 79910, A
C 298 12.2 55.5 1398 7 US-11-217-529-2602 Sequence 2602, App
C 299 12.2 55.5 1410 6 US-10-511-937-447 Sequence 447, App
C 300 12.2 55.5 1422 7 US-11-136-524-69 Sequence 69, Appl
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## ALIGNMENTS

```
RESULT 1
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805
Query Match 70.9%; Score 15.6; DB 7; Length 471;
Best Local Similarity 81.8%; Pred. No. 7.1;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
||| ||||| ||| |||
Db 152 GTCCACGGAAGCCGTCGG 173

RESULT 2
US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254
Query Match 70.9%; Score 15.6; DB 7; Length 2397;
Best Local Similarity 81.8%; Pred. No. 8.5;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGCCCTTCGG 22
||| ||||| ||| |||
Db 400 GTCGACGGAATGCCATTGG 421

RESULT 3
US-11-217-529-110320
; Sequence 110320, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
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; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110320
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match      66.4%; Score 14.6; DB 7; Length 25;
Best Local Similarity 81.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GTCGACGGAAGGCGCTTTTCG 21
   ||||| ||||| ||||| |||||
Db 5 GTCCACGGAAGGCGCGTCG 25

RESULT 4
US-11-217-529-78935
; Sequence 78935, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78935
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match      66.4%; Score 14.6; DB 7; Length 1242;
Best Local Similarity 81.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
   ||||| ||||| ||||| |||||
Db 63 TCGAACAGTAAGGCTTTTTCG 83

RESULT 5
US-11-217-529-79690/c
; Sequence 79690, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79690
; LENGTH: 1824
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79690

Query Match      66.4%; Score 14.6; DB 7; Length 1824;
Best Local Similarity 81.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
   ||||| ||||| ||||| |||||
Db 748 TCGACGGAATGACTTACGG 728

RESULT 6
US-11-217-529-77876
; Sequence 77876, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77876
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77876

Query Match      66.4%; Score 14.6; DB 7; Length 1950;
Best Local Similarity 81.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCGCTTTTCG 22
   ||||| ||||| ||||| |||||
Db 1232 TCGAACTGAAAGGCTTTTCG 1252

RESULT 7
US-11-217-529-6038
; Sequence 6038, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6038
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-6038

; NAME/KEY: modified_base
; LOCATION: (2284)..(2317)
; OTHER INFORMATION: a, c, g, t, unknown, or other
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US-11-217-529-6038

Query Match 65.5%; Score 14.4; DB 7; Length 2454;  
Best Local Similarity 93.8%; Pred. No. 36;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCTTTC 20  
||| ||||| ||||| |||||  
Db 1022 AATGGAAGGCTTTC 1037

RESULT 8

US-11-217-529-1257/c  
; Sequence 1257, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1257  
; LENGTH: 858  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-1257

Query Match 64.5%; Score 14.2; DB 7; Length 858;  
Best Local Similarity 84.2%; Pred. No. 40;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTC 20  
||| ||||| ||||| |||||  
Db 187 TCGAAGGAAGGCTTTC 169

RESULT 9

US-11-217-529-77141/c  
; Sequence 77141, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77141  
; LENGTH: 858  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-77141

Query Match 64.5%; Score 14.2; DB 7; Length 858;  
Best Local Similarity 84.2%; Pred. No. 40;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTC 20  
||| ||||| ||||| |||||  
Db 187 TCGAAGGAAGGCTTTC 169

RESULT 10

US-11-217-529-5375/c  
; Sequence 5375, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5375  
; LENGTH: 1260  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-5375

Query Match 64.5%; Score 14.2; DB 7; Length 1260;  
Best Local Similarity 84.2%; Pred. No. 42;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTT 19  
||| ||||| ||||| |||||  
Db 414 GTGGAACGGAAGCTTT 396

RESULT 11

US-11-217-529-78815  
; Sequence 78815, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 78815  
; LENGTH: 438  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-78815

Query Match 63.6%; Score 14; DB 7; Length 438;  
Best Local Similarity 77.3%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTCG 22  
||| ||||| ||||| |||||  
Db 3 GTCGAAGGAAGGTTTGCTG 24

```
RESULT 12
US-11-217-529-3863
; Sequence 3863, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3863
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3863

Query Match      63.6%; Score 14; DB 7; Length 1224;
Best Local Similarity 77.3%; Pred. No. 53;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 309 GTCGAAAAGGAGGCTTGTGAC 330

RESULT 13
US-11-217-529-1422/c
; Sequence 1422, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1422
; LENGTH: 1758
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1422

Query Match      63.6%; Score 14; DB 7; Length 1758;
Best Local Similarity 77.3%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 288 GTTGAACTGCATGCCCTTTAGG 267

RESULT 14
US-10-505-928-182
; Sequence 182, Application US/10505928
; Publication No. US20060088532A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 182
; LENGTH: 5900
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-182

Query Match      63.6%; Score 14; DB 6; Length 5900;
Best Local Similarity 77.3%; Pred. No. 64;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCCTTTTCGG 22
Db 1001 GTCTACCGGAAGACCTGGCGG 1022

RESULT 15
US-09-949-925-78/c
; Sequence 78, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1212)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-78

Query Match      62.7%; Score 13.8; DB 1; Length 1931;
Best Local Similarity 88.2%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCCTT 18
||| ||| ||| ||| ||| ||| ||| |||
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Db      248 TCGAACGGAAGGCATT 232
RESULT 16
US-09-949-925-12/c
; Sequence 12, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; CURRENT APPLICATION NUMBER: US/09/949,925
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1932
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-949-925-12

Query Match      62.7%; Score 13.8; DB 1; Length 1932;
Best Local Similarity 88.2%; Pred. No. 71;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTT 18
Db      248 TCGAACGGAAGGCATT 232
RESULT 17
US-11-252-080-11/c
; Sequence 11, Application US/11252080
; Publication No. US20060090217A1
; GENERAL INFORMATION:
; APPLICANT: Texas A&M University
; TITLE OF INVENTION: ISOLATION OF SUGARCANE PROTEINS INVOLVED IN POSTTRANSCRIPTIONAL G
; FILE REFERENCE: 017575.0693 (TAMUS 1743)
; CURRENT APPLICATION NUMBER: US/11/252,080
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/10/226,715
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314863
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 829
; TYPE: DNA
; ORGANISM: Saccharum hybrid cultivar CP72-1210
US-11-252-080-11

Query Match      61.8%; Score 13.6; DB 7; Length 829;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      3 CGAACGGAAGGCCTTTCCG 22
Db      589 CGAAGGGAACCCCTTTTGG 570
RESULT 18
US-11-217-529-4440
; Sequence 4440, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4440
; LENGTH: 903
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4440

Query Match      61.8%; Score 13.6; DB 7; Length 903;
Best Local Similarity 80.0%; Pred. No. 83;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTTTTCG 21
Db      268 TCGAACGGAAGACTTTGG 287
RESULT 19
US-11-217-529-80747
; Sequence 80747, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80747
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80747

Query Match      61.8%; Score 13.6; DB 7; Length 1326;
Best Local Similarity 80.0%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 TCGAACGGAAGGCCTTTTCG 21
```

Db  
269 TCCAAC TGAATGGGCTTTTCG 288

RESULT 20

```

RES001 20
US-11-217-529-3010/c
; Sequence 3010, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3010

```

RESULT 21

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US-11-217-529-4946/c
; Sequence 4946, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4946
; LENGTH: 2952
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4946

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RESULT 22

```

US-11-217-529-82302
; Sequence 82302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82302
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82302

```

RESULT 23

```

RES0011 23
US-10-488-619-2075
; Sequence 2075, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2075
; LENGTH: 497
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2075

```

RESULT 24

```

RESULTS 24
US-10-488-619-2156
; Sequence 2156, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
;

```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2156
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2156

Query Match      60.9%; Score 13.4; DB 6; Length 599;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGACGGAAGGC 15
      ||||| ||||| |||||
Db      540 GTCGACGGAAGGC 554

RESULT 25
US-11-217-529-5130/c
; Sequence 5130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5130
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5130

Query Match      60.9%; Score 13.4; DB 7; Length 762;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  AACGGAAGGCCTTT 19
      ||||| ||||| |||||
Db      539 AACGGAAGGCCTTT 525

RESULT 26
US-10-488-619-2155/c
; Sequence 2155, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2155
; LENGTH: 784
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2155

Query Match      60.9%; Score 13.4; DB 6; Length 784;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GTCGACGGAAGGC 15
      ||||| ||||| |||||
Db      394 GTCGACGGAAGGC 380

RESULT 27
US-10-525-126-124/c
; Sequence 124, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 124
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Platichthys stellatus
US-10-525-126-124

Query Match      60.9%; Score 13.4; DB 6; Length 814;
Best Local Similarity 93.3%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5  AACGGAAGGCCTTT 19
      ||||| ||||| |||||
Db      254 AACGGAAGGCCTTT 240

RESULT 28
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matuschek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 649.4
; PRIOR FILING DATE: 2003-09-08
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
```

```
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
;
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4
```

```
Query Match 60.9%; Score 13.4; DB 6; Length 11611;
Best Local Similarity 93.3%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 GAACGGAAGGCCTT 18
Db 8484 GAACGGAAGGCCTT 8498
```

```
RESULT 29
US-11-217-529-173378
; Sequence 173378, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173378
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173378
```

```
Query Match 60.0%; Score 13.2; DB 7; Length 492;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 4 GAACGGAAGGCCTTTCG 21
Db 439 GAGCGGAAGGCCTATTG 456
```

```
RESULT 30
US-11-217-529-76021/c
; Sequence 76021, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
```

```
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76021
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76021
```

```
Query Match 60.0%; Score 13.2; DB 7; Length 498;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 AACGGAAGGCCTTTCGG 22
Db 145 AACGGAAGGCCTTTTGG 128
```

```
RESULT 31
US-10-488-619-2026
; Sequence 2026, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2026
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2026
```

```
Query Match 60.0%; Score 13.2; DB 6; Length 523;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TCGACGGAAGGCCTTT 19
Db 259 TCAAAAGGAAGGACTTT 276
```

```
RESULT 32
US-10-488-619-2939/c
; Sequence 2939, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2939
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2939
```

```
Query Match 60.0%; Score 13.2; DB 6; Length 806;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 TCGAACGGAAGGCCTTT 19
Db 21 TGGGAAGGAAGGCCTTT 4
```

## RESULT 33

US-11-217-529-75628  
 ; Sequence 75628, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED  
 APPLICANT: NAKAO, YOSHIHIRO  
 APPLICANT: NAKAMURA, NORIHISA  
 APPLICANT: KODAMA, YUKIKO  
 APPLICANT: FUJIMURA, TOMOKO  
 APPLICANT: ASHIKARI, TOSHIHIKO  
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 FILE REFERENCE: S-38-285  
 CURRENT APPLICATION NUMBER: US/11/217,529  
 CURRENT FILING DATE: 2005-09-02  
 PRIOR APPLICATION NUMBER: US 10/932,182  
 PRIOR FILING DATE: 2004-09-02  
 NUMBER OF SEQ ID NOS: 197023  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 75628  
 LENGTH: 1242  
 TYPE: DNA  
 ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-75628

Query Match 60.0%; Score 13.2; DB 7; Length 1242;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20

Db 887 CAACGCAACGCGCTTTC 904

## RESULT 34

US-11-217-529-75/c  
 ; Sequence 75, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED  
 APPLICANT: NAKAO, YOSHIHIRO  
 APPLICANT: NAKAMURA, NORIHISA  
 APPLICANT: KODAMA, YUKIKO  
 APPLICANT: FUJIMURA, TOMOKO  
 APPLICANT: ASHIKARI, TOSHIHIKO  
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 FILE REFERENCE: S-38-285  
 CURRENT APPLICATION NUMBER: US/11/217,529  
 CURRENT FILING DATE: 2005-09-02  
 PRIOR APPLICATION NUMBER: US 10/932,182  
 PRIOR FILING DATE: 2004-09-02  
 NUMBER OF SEQ ID NOS: 197023  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 75  
 LENGTH: 1269  
 TYPE: DNA  
 ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-75

Query Match 60.0%; Score 13.2; DB 7; Length 1269;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 AACGGAAGGCCTTCG 22

Db 507 AAGGGAAGGCCTGTAGG 490

## RESULT 35

US-11-217-529-4877/c  
 ; Sequence 4877, Application US/11217529  
 ; Publication No. US20060099612A1

## ; GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED  
 APPLICANT: NAKAO, YOSHIHIRO  
 APPLICANT: NAKAMURA, NORIHISA  
 APPLICANT: KODAMA, YUKIKO  
 APPLICANT: FUJIMURA, TOMOKO  
 APPLICANT: ASHIKARI, TOSHIHIKO  
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 FILE REFERENCE: S-38-285  
 CURRENT APPLICATION NUMBER: US/11/217,529  
 CURRENT FILING DATE: 2005-09-02  
 PRIOR APPLICATION NUMBER: US 10/932,182  
 PRIOR FILING DATE: 2004-09-02  
 NUMBER OF SEQ ID NOS: 197023  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 4877  
 LENGTH: 1377  
 TYPE: DNA  
 ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-4877

Query Match 60.0%; Score 13.2; DB 7; Length 1377;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCCTT 18

Db 85 GTTTAACGGAAGGCCTT 68

## RESULT 36

US-11-217-529-3860  
 ; Sequence 3860, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:

APPLICANT: SUNTORY LIMITED  
 APPLICANT: NAKAO, YOSHIHIRO  
 APPLICANT: NAKAMURA, NORIHISA  
 APPLICANT: KODAMA, YUKIKO  
 APPLICANT: FUJIMURA, TOMOKO  
 APPLICANT: ASHIKARI, TOSHIHIKO  
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 FILE REFERENCE: S-38-285  
 CURRENT APPLICATION NUMBER: US/11/217,529  
 CURRENT FILING DATE: 2005-09-02  
 PRIOR APPLICATION NUMBER: US 10/932,182  
 PRIOR FILING DATE: 2004-09-02  
 NUMBER OF SEQ ID NOS: 197023  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 3860  
 LENGTH: 1611  
 TYPE: DNA  
 ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-3860

Query Match 60.0%; Score 13.2; DB 7; Length 1611;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19

Db 712 TCCAAACGGAAGGCCTTT 729

## RESULT 37

US-11-312-958-13  
 ; Sequence 13, Application US/11312958  
 ; Publication No. US20060100152A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Millennium Pharmaceuticals, Inc.  
 APPLICANT: Rosenfeld, Julie Beth  
 APPLICANT: Silos-Santiago, Inmaculada  
 TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING

;/ TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553.  
;/ TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,  
;/ TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,  
;/ TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR  
;/ TITLE OF INVENTION: 13424 MOLECULES  
;/ FILE REFERENCE: MPI02-027P1RNMNMIM  
;/ CURRENT APPLICATION NUMBER: US/11/312,958  
;/ CURRENT FILING DATE: 2005-12-20  
;/ PRIOR APPLICATION NUMBER: US/10/369,022  
;/ PRIOR FILING DATE: 2003-02-19  
;/ PRIOR APPLICATION NUMBER: US 60/360,495  
;/ PRIOR FILING DATE: 2002-02-28  
;/ PRIOR APPLICATION NUMBER: US 60/370,121  
;/ PRIOR FILING DATE: 2002-04-04  
;/ PRIOR APPLICATION NUMBER: US 60/373,010  
;/ PRIOR FILING DATE: 2002-04-16  
;/ PRIOR APPLICATION NUMBER: US 60/373,908  
;/ PRIOR FILING DATE: 2002-04-19  
;/ PRIOR APPLICATION NUMBER: US 60/377,717  
;/ PRIOR FILING DATE: 2002-05-03  
;/ PRIOR APPLICATION NUMBER: US 60/379,949  
;/ PRIOR FILING DATE: 2002-05-13  
;/ PRIOR APPLICATION NUMBER: US 60/382,409  
;/ PRIOR FILING DATE: 2002-05-21  
;/ PRIOR APPLICATION NUMBER: US 60/385,280  
;/ PRIOR FILING DATE: 2002-06-03  
;/ PRIOR APPLICATION NUMBER: US 60/386,879  
;/ PRIOR FILING DATE: 2002-06-06  
;/ Remaining Prior Application data removed - See File Wrapper or PALM.  
;/ NUMBER OF SEQ ID NOS: 64  
;/ SOFTWARE: Fast-SEQ for Windows Version 4.0  
;/ SEQ ID NO 13  
;/ LENGTH: 1968  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: (73)...(1176)  
US-11-312-958-13

Query Match 60.0%; Score 13.2; DB 7; Length 1968;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTC 20  
Db 1182 CGAAGGAAGGGCTCTC 1199

RESULT 38  
US-10-511-937-440  
;/ Sequence 440, Application US/10511937  
;/ Publication No. US2006008836A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
;/ APPLICANT: Wohlgemuth, Jay  
;/ APPLICANT: Fry, Kirk  
;/ APPLICANT: Woodward, Robert  
;/ APPLICANT: Ly, Ngoc  
;/ APPLICANT: Prentice, James  
;/ APPLICANT: Morris, MacDonald  
;/ APPLICANT: Rosenberg, Steven  
;/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
;/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION  
;/ FILE REFERENCE: 506612000104  
;/ CURRENT APPLICATION NUMBER: US/10/511,937  
;/ CURRENT FILING DATE: 2004-10-19  
;/ PRIOR APPLICATION NUMBER: PCT/US2003/012946  
;/ PRIOR FILING DATE: 2003-04-24  
;/ PRIOR APPLICATION NUMBER: US 10/131,831  
;/ PRIOR FILING DATE: 2002-04-24  
;/ PRIOR APPLICATION NUMBER: US 10/325,899  
;/ PRIOR FILING DATE: 2002-12-20

;/ NUMBER OF SEQ ID NOS: 3117  
;/ SOFTWARE: PatentIn version 3.2  
;/ SEQ ID NO 440  
;/ LENGTH: 2545  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
US-10-511-937-440

Query Match 60.0%; Score 13.2; DB 6; Length 2545;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCTTTC 20  
Db 1826 CGAAGGAAGGGCTTTC 1843

RESULT 39  
US-11-301-554-1900  
;/ Sequence 1900, Application US/11301554  
;/ Publication No. US20060088527A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Henderson, Robert A.  
;/ APPLICANT: Wang, Tongtong  
;/ APPLICANT: Watanabe, Yoshihiro  
;/ APPLICANT: Kalos, Michael D.  
;/ APPLICANT: Sleath, Paul R.  
;/ APPLICANT: Johnson, Jeffrey C.  
;/ APPLICANT: Retter, Marc W.  
;/ APPLICANT: Durham, Margarita  
;/ APPLICANT: Carter, Darick  
;/ APPLICANT: Fanger, Gary R.  
;/ APPLICANT: Vedvick, Thomas S.  
;/ APPLICANT: Bangur, Chaitanya S.  
;/ APPLICANT: McNabb, Andria  
;/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
;/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
;/ FILE REFERENCE: 210121.478C21  
;/ CURRENT APPLICATION NUMBER: US/11/301,554  
;/ CURRENT FILING DATE: 2005-12-13  
;/ PRIOR APPLICATION NUMBER: US 10/283,017  
;/ PRIOR FILING DATE: 2002-10-28  
;/ PRIOR APPLICATION NUMBER: US 10/113,872  
;/ PRIOR FILING DATE: 2002-03-28  
;/ PRIOR APPLICATION NUMBER: US 10/017,754  
;/ PRIOR FILING DATE: 2001-10-29  
;/ PRIOR APPLICATION NUMBER: US 09/902,941  
;/ PRIOR FILING DATE: 2001-07-10  
;/ PRIOR APPLICATION NUMBER: US 09/849,626  
;/ PRIOR FILING DATE: 2001-05-03  
;/ PRIOR APPLICATION NUMBER: US 09/736,457  
;/ PRIOR FILING DATE: 2000-12-13  
;/ PRIOR APPLICATION NUMBER: US 09/702,705  
;/ PRIOR FILING DATE: 2000-10-30  
;/ PRIOR APPLICATION NUMBER: US 09/677,419  
;/ PRIOR FILING DATE: 2000-10-06  
;/ PRIOR APPLICATION NUMBER: US 09/671,325  
;/ PRIOR FILING DATE: 2000-09-26  
;/ PRIOR APPLICATION NUMBER: US 09/658,824  
;/ PRIOR FILING DATE: 2000-09-08  
;/ Remaining Prior Application data removed - See File Wrapper or PALM.  
;/ NUMBER OF SEQ ID NOS: 2157  
;/ SOFTWARE: Fast-SEQ for Windows Version 4.0  
;/ SEQ ID NO 1900  
;/ LENGTH: 2545  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
US-11-301-554-1900

Query Match 60.0%; Score 13.2; DB 7; Length 2545;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;



Qy 3 CGAACGGAAGGCCTTTC 20  
||||| ||||| |||||  
Db 1826 CGAAGGAAGGCCTTTC 1843

## RESULT 40

US-11-217-529-79139/c  
; Sequence 79139, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 79139  
; LENGTH: 2850  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-79139

Query Match 60.0%; Score 13.2; DB 7; Length 2850;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19  
||||| ||||| |||||  
Db 377 TTGAACGTAAGGCATT 360

## RESULT 41

US-11-217-529-78066/c  
; Sequence 78066, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 78066  
; LENGTH: 3267  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-78066

Query Match 60.0%; Score 13.2; DB 7; Length 3267;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19  
||||| ||||| |||||  
Db 440 TTGTATGGAAGGCCTTT 423

RESULT 42  
US-11-217-529-3415  
; Sequence 3415, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3415  
; LENGTH: 3330  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-3415

Query Match 60.0%; Score 13.2; DB 7; Length 3330;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCCTTT 19  
||||| ||||| |||||  
Db 1435 TCTAACAGAAAGGCCTTT 1452

## RESULT 43

US-10-511-937-346  
; Sequence 346, Application US/10511937  
; Publication No. US2006008836A1  
; GENERAL INFORMATION:  
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Ly, Ngoc  
; APPLICANT: Prentice, James  
; APPLICANT: Morris, MacDonald  
; APPLICANT: Rosenberg, Steven  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING  
; FILE REFERENCE: 506612000104  
; CURRENT APPLICATION NUMBER: US/10/511,937  
; CURRENT FILING DATE: 2004-10-19  
; PRIOR FILING DATE: PCT/US2003/012946  
; PRIOR FILING DATE: 2003-04-24  
; PRIOR APPLICATION NUMBER: US 10/131,831  
; PRIOR FILING DATE: 2002-04-24  
; PRIOR APPLICATION NUMBER: US 10/325,899  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 3117  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 346  
; LENGTH: 3655  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-511-937-346

Query Match 60.0%; Score 13.2; DB 6; Length 3655;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAGGCCTTTC 20  
||||| ||||| |||||  
Db 3477 CGAAGGGAATGTCTTTC 3494

```
RESULT 44
US-10-489-730-10/c
; GENERAL INFORMATION: Gennaro
; APPLICANT: Melino, Ian
; APPLICANT: Hayes, Ian
; APPLICANT: de Laurenzi, Vincenzo
; APPLICANT: Barcaroli, Daniela
; APPLICANT: Candi, Eleonora
; APPLICANT: Bernasola, Francesca
; APPLICANT: Tobler, Andreas
; APPLICANT: Novak, Urban
; TITLE OF INVENTION: Human Delta-N p73 Molecules and Uses Thereof
; FILE REFERENCE: 19319-002
; CURRENT APPLICATION NUMBER: US/10/489,730
; CURRENT FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: PCT/GB02/04238
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: US 60/322,436
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 39
; OTHER INFORMATION: reverse complement of exons 14 through 1 as reported in GenBank A
US-10-489-730-10

Query Match      60.8%; Score 13.2; DB 6; Length 138941;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CGAACGGAAAGGCCTTTC 20
Db 106669 CGAATGGAATGCTTTC 106652

RESULT 45
US-11-217-529-91576
; Sequence 91576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-91576

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CGGAAAGGCCTTT 19
Db 9 CGGAAAGGCCTTT 21

RESULT 46
US-11-217-529-132068
; Sequence 132068, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
```

```
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132068
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-132068

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 76.2%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAAGGCCTTTCG 22
Db 3 TCAGACGGAGAGCCCTTTCG 23

RESULT 47
US-11-217-529-152160
; Sequence 152160, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152160

Query Match      59.1%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACGAAAGGCCTT 18
Db 10 ACGAAAGGCCTT 22

RESULT 48
US-11-264-784-222/c
; Sequence 222, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
```

; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 222  
; LENGTH: 95  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer D8-7A  
US-11-264-784-222

Query Match 59.1%; Score 13; DB 7; Length 95;  
Best Local Similarity 76.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22  
|||||  
Db 43 TGGAACTGAATGAGCTTTCGG 23

## RESULT 49

US-11-264-784-223  
; Sequence 223, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 223  
; LENGTH: 95  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer D8-7B  
US-11-264-784-223

Query Match 59.1%; Score 13; DB 7; Length 95;  
Best Local Similarity 76.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22  
|||||  
Db 57 TGGAACTGAATGAGCTTTCGG 77

## RESULT 50

US-11-217-529-4142/c  
; Sequence 4142, Application US/11217529  
; Publication No. US2006009612A1  
; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4142  
; LENGTH: 117  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; OTHER INFORMATION: Saccharomyces pastorianus  
US-11-217-529-4142

Query Match 59.1%; Score 13; DB 7; Length 117;  
Best Local Similarity 76.2%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22  
|||||  
Db 53 TCGAACGTATGACATTTCGG 33

## RESULT 51

US-11-264-784-246/c  
; Sequence 246, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 246  
; LENGTH: 264  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 264 bp XhoI/SacI fragment of pT8(7-9)  
US-11-264-784-246

Query Match 59.1%; Score 13; DB 7; Length 264;  
Best Local Similarity 76.2%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCGCTTTCGG 22  
|||||  
Db 39 TGGAACTGAATGAGCTTTCGG 19

## RESULT 52

US-10-488-619-347/c  
; Sequence 347, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:

```

; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(404)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-347

Query Match      59.1%; Score 13; DB 6; Length 404;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8  GGAAGGCGCTTTCG 21
      |||||
Db      235  GGAAGGCGCTTTCG 222

RESULT 53
US-10-488-619-763/c
; Sequence 763, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 763
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-763

Query Match      59.1%; Score 13; DB 6; Length 411;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2  TCGAACGGAAAGGCGCTTTCG 22
      |||||
Db      286  TCGACTGAAGGCGCGCTCGG 266

RESULT 54
US-10-488-619-762
; Sequence 762, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 762
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-488-619-762
```

```

Query Match      59.1%; Score 13; DB 6; Length 451;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2  TCGAACGGAAAGGCGCTTTCG 22
      |||||
Db      319  TCGCACTGAAGGCGCGCTCGG 339

RESULT 55
US-11-256-428-55/c
; Sequence 55, Application US/11256428
; Publication No. US20060095987A1
; GENERAL INFORMATION:
; APPLICANT: Niblett, Charles L.
; TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and
; FILE REFERENCE: VEN-100
; CURRENT APPLICATION NUMBER: US/11/256,428
; CURRENT FILING DATE: 2005-10-21
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Cercospora zeae-maydis 18s rDNA
US-11-256-428-55

Query Match      59.1%; Score 13; DB 7; Length 536;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2  TCGAACGGAAAGGCGCTTTCG 22
      |||||
Db      324  TCGACAGGCATGCCCTTCGG 304

RESULT 56
US-11-217-529-79746
; Sequence 79746, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORI LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79746
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79746

Query Match      59.1%; Score 13; DB 7; Length 696;
Best Local Similarity 76.2%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2  TCGAACGGAAAGGCGCTTTCG 22
      |||||
Db      421  TCAGACGAGAGCCCTTCGG 441
```

```
RESULT 57
US-11-217-529-81537
; Sequence 81537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81537
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81537
Query Match      59.1%; Score 13; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ACGGAAGGCCTT 18
      |||||
Db      332 ACGGAAGGCCTT 344

RESULT 58
US-10-975-697-7
; Sequence 7, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-21
US-10-975-697-7
Query Match      59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCTTTCG 21
      |||||
Db      1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 59
US-10-975-697-9
; Sequence 9, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
```

```
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-28
US-10-975-697-9
Query Match      59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCTTTCG 21
      |||||
Db      1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 60
US-10-975-697-11
; Sequence 11, Application US/10975697
; Publication No. US20060094099A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Inactivated Enzyme Variants And Associated Process and Reagent
; TITLE OF INVENTION: System
; FILE REFERENCE: 5727-76273
; CURRENT APPLICATION NUMBER: US/10/975,697
; CURRENT FILING DATE: 2004-10-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 1080
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GlucDH variant RC-35
US-10-975-697-11
Query Match      59.1%; Score 13; DB 6; Length 1080;
Best Local Similarity 76.2%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1 GTCGAACGGAAGGCCTTTCG 21
      |||||
Db      1015 GTCGAAGACTGGGCCTTTCG 1035

RESULT 61
US-11-217-529-190860
; Sequence 190860, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 190860
; LENGTH: 1092
```

; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-190860

Query Match 59.1%; Score 13; DB 7; Length 1092;  
Best Local Similarity 76.2%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
|||||  
Db 657 TCCATGGCTAGGCATTTCGG 677

## RESULT 62

US-11-217-529-494  
; Sequence 494, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 494  
; LENGTH: 1098  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus

## US-11-217-529-494

Query Match 59.1%; Score 13; DB 7; Length 1098;  
Best Local Similarity 76.2%; Pred. No. 1.7e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
|||||  
Db 89 TCGAATTGAAAGTCCTTTGGG 109

## RESULT 63

US-11-217-529-998  
; Sequence 998, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 998  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-998

Query Match 59.1%; Score 13; DB 7; Length 1203;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGAACGGGAAG 13  
|||||  
Db 333 GTCGAACGGGAAG 345

## RESULT 64

US-11-217-529-5416  
; Sequence 5416, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5416  
; LENGTH: 1254  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-5416

## Query Match 59.1%; Score 13; DB 7; Length 1254;

Best Local Similarity 76.2%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
|||||  
Db 72 TCGAGCGGTACGGCATTTCGG 92

## RESULT 65

US-11-264-784-255/c  
; Sequence 255, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CU3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 255  
; LENGTH: 1269  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: D8S-3: synthetic delta 8-desaturase gene codon-optimized for  
; OTHER INFORMATION: Yarrowia lipolytica in pDMW261  
US-11-264-784-255

```
Query Match      59.1%; Score 13; DB 7; Length 1269;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTCGG 22
Db      677 TGGAACTGAATGAGCTTCGG 657

RESULT 66
US-11-264-784-209/c
; Sequence 209, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 209
; LENGTH: 1270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-1: Synthetic gene codon-optimized for expression in Yarrowia
; OTHER INFORMATION: lipolytica
US-11-264-784-209

Query Match      59.1%; Score 13; DB 7; Length 1270;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTCGG 22
Db      670 TGGAACTGAATGAGCTTCGG 650

RESULT 67
US-11-264-784-48/c
; Sequence 48, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 1272
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8SF: synthetic delta-8 desaturase (codon-optimized for Yarrowia
; OTHER INFORMATION: lipolytica)
US-11-264-784-48

Query Match      59.1%; Score 13; DB 7; Length 1272;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTCGG 22
Db      678 TGGAACTGAATGAGCTTCGG 658

RESULT 68
US-11-264-784-263/c
; Sequence 263, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 263
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric gene
US-11-264-784-263

Query Match      59.1%; Score 13; DB 7; Length 1272;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCGCTTCGG 22
Db      678 TGGAACTGAATGAGCTTCGG 658

RESULT 69
US-11-217-529-75890/c
; Sequence 75890, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
```

```
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75890
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75890

Query Match          59.1%; Score 13; DB 7; Length 1473;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACGGAAAGCCTTTCCG 22
        ||||| ||||| ||||| |||||
Db       1337 TCGAATGCAAGCCTTTAGG 1317

RESULT 70
US-11-324-517-36
; Sequence 36, Application US/11324517
; Publication No. US20060099221A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, MARY
; TITLE OF INVENTION: METHOD OF SCREENING ANTI-MYCOBACTERIAL MOLECULES
; FILE REFERENCE: 03495.0182-01
; CURRENT APPLICATION NUMBER: US/11/324,517
; CURRENT FILING DATE: 2006-01-04
; PRIOR APPLICATION NUMBER: US/10/914,165
; PRIOR FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US/10/383,675
; PRIOR FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 09/429,370
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/113,375
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/111,813
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/181,934
; PRIOR FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 1600
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (549)..(1562)
US-11-324-517-36

Query Match          59.1%; Score 13; DB 7; Length 1600;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACGGAAAGCCTTTCCG 22
        ||||| ||||| ||||| |||||
Db       1480 TCGACCGGAAGCCGTACGG 1500

RESULT 71
US-11-264-784-250/c
; Sequence 250, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
US-11-264-784-250/c

Query Match          59.1%; Score 13; DB 7; Length 1473;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 250
; LENGTH: 1852
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-1::XPR gene
US-11-264-784-250

Query Match          59.1%; Score 13; DB 7; Length 1852;
Best Local Similarity 76.2%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACGGAAAGCCTTTCCG 22
        ||||| ||||| ||||| |||||
Db       1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 72
US-11-264-784-251/c
; Sequence 251, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 251
; LENGTH: 1898
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric D8S-2::XPR gene
US-11-264-784-251

Query Match          59.1%; Score 13; DB 7; Length 1898;
Best Local Similarity 76.2%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      2 TCGAACGGAAAGCCTTTCCG 22
        ||||| ||||| ||||| |||||
Db       1082 TCGAACTGAATGAGCTTCCG 1062

RESULT 73
US-11-217-529-76130
; Sequence 76130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
```



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; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76130
; LENGTH: 2853
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76130

Query Match          59.1%; Score 13; DB 7; Length 2853;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 CGGAAGGCCTTT 19
        |||||
Db      2501 CGGAAGGCCTT 2513

RESULT 74
US-11-217-529-95
; Sequence 95, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 3078
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-95

Query Match          59.1%; Score 13; DB 7; Length 3078;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCTTTCGG 22
        |||||
Db      936 TCCAACGGAAGAGATTTTGG 956

RESULT 75
US-11-217-529-1369/c
; Sequence 1369, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
```

```
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1369
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-1369

Query Match          59.1%; Score 13; DB 7; Length 3663;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCTTTCGG 22
        |||||
Db      344 TCTAACGTAAGGCTTCTTGG 324

RESULT 76
US-11-217-529-80723
; Sequence 80723, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80723
; LENGTH: 3864
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-80723

Query Match          59.1%; Score 13; DB 7; Length 3864;
Best Local Similarity 76.2%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 TCGAACGGAAGGCCTTTCGG 22
        |||||
Db      2489 TCAACGCGAGAGATTTTCGG 2509

RESULT 77
US-11-217-529-3980/c
; Sequence 3980, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
```

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; SEQ ID NO 3980
; LENGTH: 4005
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3980

Query Match      59.1%; Score 13; DB 7; Length 4005;
Best Local Similarity 76.2%; Pred. No. 2.e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCGCTTTTCG 21
Db 2989 GTTGAAGAGTAAGGGAATTTCG 2969

RESULT 78
US-11-217-529-3246
; Sequence 3246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3246
; LENGTH: 5223
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3246

Query Match      59.1%; Score 13; DB 7; Length 5223;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAAGGCGCTTTTCG 22
Db 322 TTGATCGGAATGCGTTTCG 342

RESULT 79
US-10-520-210-29/c
; Sequence 29, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 6805
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-29

Query Match      59.1%; Score 13; DB 6; Length 6805;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCGCTTTTCG 21
Db 1257 GTCGAAGACTGGGCGCTTTTCG 1237

RESULT 80
US-10-520-210-31/c
; Sequence 31, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 7330
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:plasmid
US-10-520-210-31

Query Match      59.1%; Score 13; DB 6; Length 7330;
Best Local Similarity 76.2%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAAGGCGCTTTTCG 21
Db 1257 GTCGAAGACTGGGCGCTTTTCG 1237

RESULT 81
US-10-520-210-25/c
; Sequence 25, Application US/10520210
; Publication No. US20060099692A1
; GENERAL INFORMATION:
; APPLICANT: Yocum , R. Rogers
; APPLICANT: Patterson, Thomas A.
; APPLICANT: Pero, Janice G.
; APPLICANT: Hermann, Theron
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154US
; CURRENT APPLICATION NUMBER: US/10/520,210
; CURRENT FILING DATE: 2005-01-03
; PRIOR APPLICATION NUMBER: PCT/US2003/021336
; PRIOR FILING DATE: 2003-07-02
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:glyA overexpression
US-10-520-210-25
```

Query Match 59.1%; Score 13; DB 6; Length 7701;  
Best Local Similarity 76.2%; Pred. No. 2.1e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1262 GTCGAAGACTGGGCTTTTCG 1242

## RESULT 82

US-10-520-210-24/c  
; Sequence 24, Application US/10520210  
; Publication No. US20060099692A1  
; GENERAL INFORMATION:  
; APPLICANT: Yocum, R. Rogers  
; APPLICANT: Patterson, Thomas A.  
; APPLICANT: Pero, Janice G.  
; APPLICANT: Hermann, Theron  
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF  
; FILE REFERENCE: BGI-154US  
; CURRENT APPLICATION NUMBER: US/10/520.210  
; CURRENT FILING DATE: 2005-01-03  
; PRIOR APPLICATION NUMBER: PCT/US2003/021336  
; PRIOR FILING DATE: 2003-07-02  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 24  
; LENGTH: 7926  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: sera overexpression  
; FEATURE:  
; OTHER INFORMATION: plasmid  
US-10-520-210-24

Query Match 59.1%; Score 13; DB 6; Length 7926;  
Best Local Similarity 76.2%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GTCGAACGGAAGGCTTTTCG 21  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1262 GTCGAAGACTGGGCTTTTCG 1242

## RESULT 83

US-11-024-544A-129/c  
; Sequence 129, Application US/11024544A  
; Publication No. US20060094086A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
; APPLICANT: Yadav, Narendra  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Zhang, Hongxiang  
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED  
; FILE REFERENCE: CL2717  
; CURRENT APPLICATION NUMBER: US/11/024.544A  
; CURRENT FILING DATE: 2004-12-29  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 129  
; LENGTH: 10448  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pKO2UM36E  
US-11-024-544A-129

Query Match 59.1%; Score 13; DB 7; Length 10448;  
Best Local Similarity 76.2%; Pred. No. 2.2e+02;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTTCGG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1650 TGGAACTGAATGAGCTTTTCGG 1630

## RESULT 84

US-11-190-750-112/c  
; Sequence 112, Application US/11190750  
; Publication No. US20060094089A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours and Company, Inc.  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Yadav, Narendra  
; APPLICANT: Zhang, Hongxiang  
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF  
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS  
; FILE REFERENCE: CL2718  
; CURRENT APPLICATION NUMBER: US/11/190.750  
; CURRENT FILING DATE: 2005-07-27  
; NUMBER OF SEQ ID NOS: 159  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 112  
; LENGTH: 10448  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pKO2UM26E  
US-11-190-750-112

Query Match 59.1%; Score 13; DB 7; Length 10448;  
Best Local Similarity 76.2%; Pred. No. 2.2e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TCGAACGGAAGGCTTTTCGG 22  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1650 TGGAACTGAATGAGCTTTTCGG 1630

## RESULT 85

US-11-264-784-123/c  
; Sequence 123, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264.784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 123  
; LENGTH: 10448  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pDMW297  
US-11-264-784-123

Query Match 59.1%; Score 13; DB 7; Length 10448;  
Best Local Similarity 76.2%; Pred. No. 2.2e+02;

Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
| ||||| ||||| ||||| |||||  
Db 1650 TGGAACTGAATGAGCTTTTCGG 1630

RESULT 86  
US-11-264-784-125  
; Sequence 125, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 125  
; LENGTH: 13295  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pDMW314  
; NAME/KEY: misc feature  
; LOCATION: (10915)..(10918)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (10923)..(10923)  
; OTHER INFORMATION: n is a, c, g, or t  
US-11-264-784-125

Query Match 59.1%; Score 13; DB 7; Length 13295;  
Best Local Similarity 76.2%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
| ||||| ||||| ||||| |||||  
Db 3608 TGGAACTGAATGAGCTTTTCGG 3628

RESULT 87  
US-11-264-784-124  
; Sequence 124, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784

; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 124  
; LENGTH: 15543  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pZP2C16M899  
US-11-264-784-124

Query Match 59.1%; Score 13; DB 7; Length 15543;  
Best Local Similarity 76.2%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
| ||||| ||||| ||||| |||||  
Db 11262 TGGAACTGAATGAGCTTTTCGG 11282

RESULT 88  
US-11-264-784-127  
; Sequence 127, Application US/11264784  
; Publication No. US20060094092A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
; APPLICANT: Damude, Howard Glenn  
; APPLICANT: Gillies, Peter John  
; APPLICANT: Macool, Daniel Joseph  
; APPLICANT: Picataggio, Stephen K.  
; APPLICANT: Pollak, Dana M. Walters  
; APPLICANT: Ragghianti, James John  
; APPLICANT: Xue, Zhixiong  
; APPLICANT: Yadav, Narendra S.  
; APPLICANT: Zhang, Hongxiang  
; APPLICANT: Zhu, Quinn  
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
; FILE REFERENCE: CL3136 USNA  
; CURRENT APPLICATION NUMBER: US/11/264,784  
; CURRENT FILING DATE: 2005-11-01  
; NUMBER OF SEQ ID NOS: 375  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 127  
; LENGTH: 16325  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Plasmid pZKSL5598  
US-11-264-784-127

Query Match 59.1%; Score 13; DB 7; Length 16325;  
Best Local Similarity 76.2%; Pred. No. 2.3e+02;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 TCGAACGGAAGGCTTTTCGG 22  
| ||||| ||||| ||||| |||||  
Db 14741 TGGAACTGAATGAGCTTTTCGG 14761

RESULT 89  
US-10-473-173-32/c  
; Sequence 32, Application US/10473173  
; Publication No. US20060088823A1  
; GENERAL INFORMATION:  
; APPLICANT: VAN ANDEL INSTITUTE  
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell  
; FILE REFERENCE: 38345-170094  
; CURRENT APPLICATION NUMBER: US/10/473,173  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/279,411  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 498

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 37426
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-32

Query Match      59.1%; Score 13; DB 6; Length 37426;
Best Local Similarity 76.2%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCTTTTCG 21
Db      34330  GTTGAACACAAAGGACTTTTG 34310

RESULT 90
US-10-506-549-3/c
; Sequence 3, Application US/10506549
; Publication No. US20060100417A1
; GENERAL INFORMATION:
; APPLICANT: APPLERA CORPORATION
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: CL001361-US
; CURRENT APPLICATION NUMBER: US/10/506,549
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/361,343
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 394191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(394191)
; OTHER INFORMATION: n = A,T,C or G
US-10-506-549-3

Query Match      59.1%; Score 13; DB 6; Length 394191;
Best Local Similarity 76.2%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      1  GTCGAACGGAAGGCTTTTCG 21
Db      388330  GGCAATGGAAAGGCTTTAG 388310

RESULT 91
US-11-529-107378/c
; Sequence 107378, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 107378
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-107378
```

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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-107378

Query Match      58.2%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  TCGAACGGAAGGCTTCG 17
Db      17  TCGAACGGAATGCAT 2

RESULT 92
US-11-217-529-115745/c
; Sequence 115745, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 115745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-115745

Query Match      58.2%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      6  ACGGAAGGCTTTTCG 21
Db      16  ACGGAAGGCTTTTCG 1

RESULT 93
US-11-217-529-152423/c
; Sequence 152423, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152423
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152423

Query Match      58.2%; Score 12.8; DB 7; Length 25;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 18 GAATGCAAGGCCTTT 3

RESULT 94
US-10-488-619-1860/c
; Sequence 1860, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1860
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1860

Query Match 58.2%; Score 12.8; DB 6; Length 617;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 582 GAAAGAAAGGCCTTT 567

RESULT 95
US-10-488-619-1455/c
; Sequence 1455, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1455
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1455

Query Match 58.2%; Score 12.8; DB 6; Length 630;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CGAACGGAAGGCCTT 18
    ||||| ||||| |||
Db 332 CGAACGGAAGGCCTT 317

RESULT 96
US-10-488-619-1859
; Sequence 1859, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
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; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1859
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1859

Query Match 58.2%; Score 12.8; DB 6; Length 711;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GAACGGAAGGCCTTT 19
    ||| | ||||| |||
Db 647 GAAAGAAAGGCCTTT 662

RESULT 97
US-10-473-173-120
; Sequence 120, Application US/10473173
; Publication No. US20060088823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-120

Query Match 58.2%; Score 12.8; DB 6; Length 828;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGAACGGAAGGCC 16
    ||||| ||||| |||
Db 6 GTCGAACGGAAGGAC 21

RESULT 98
US-11-217-529-490/c
; Sequence 490, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-490
```

Query Match 58.2%; Score 12.8; DB 7; Length 996;  
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAAGGGAAGGCCTT 18  
 Db 270 CGAAGGGAAGGCCTT 255

RESULT 99  
 US-11-217-529-76912/c  
 ; Sequence 76912, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 76912  
 ; LENGTH: 1074  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-76912

Query Match 58.2%; Score 12.8; DB 7; Length 1074;  
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CGAAGGGAAGGCCTT 18  
 Db 792 CGTACGCAAGGCCTT 777

RESULT 100  
 US-11-217-529-5765/c  
 ; Sequence 5765, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 5765  
 ; LENGTH: 1098  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-5765

Query Match 58.2%; Score 12.8; DB 7; Length 1098;  
 Best Local Similarity 87.5%; Pred. No. 2.2e+02;  
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GAACGGAAGGCCTT 19

Db 76 GAATGGCAAGGCCTT 61  
 Search completed: May 19, 2006, 05:38:13  
 Job time : 15.6506 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:22:49 ; Search time 223.994 seconds  
(without alignments)  
591.412 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaagccttcgg 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 300 summaries

Database :

N Geneseq 8:\*

1: geneseqn1980s:\*

2: geneseqn1980s:\*

3: geneseqn2000s:\*

4: geneseqn2001bs:\*

5: geneseqn2002as:\*

6: geneseqn2002bs:\*

7: geneseqn2003as:\*

8: geneseqn2003bs:\*

9: geneseqn2003cs:\*

10: geneseqn2003ds:\*

11: geneseqn2004as:\*

12: geneseqn2004bs:\*

13: geneseqn2005as:\*

14: geneseqn2005bs:\*

15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	19	100.0	19	AD11274	Ad11274 Mycobacte
2	19	100.0	19	ADG88355	Adg88355 Mycobacte
3	19	100.0	19	AEA08230	Aea08230 Mycobacte
4	19	100.0	22	AD11273	Ad11273 Mycobacte
5	19	100.0	22	ADG88354	Adg88354 Mycobacte
6	19	100.0	22	AEA08229	Aea08229 Mycobacte
7	18	94.7	24	AD11272	Ad11272 Mycobacte
8	18	94.7	24	ADG88353	Adg88353 Mycobacte
9	18	94.7	24	AEA08228	Aea08228 Mycobacte
10	18	94.7	25	AD11271	Ad11271 Mycobacte
11	18	94.7	25	ADG88352	Adg88352 Mycobacte
12	18	94.7	25	AEA08227	Aea08227 Mycobacte
13	17.4	91.6	25	AA30718	Aa30718 Mycobacte
14	17.4	91.6	25	AA30716	Aa30716 Mycobacte
15	17.4	91.6	500	AD220587	Adz20587 Formaldeh
16	17.4	91.6	1449	AEA22405	Aea22405 Mycobacte
17	17.4	91.6	1455	AEA22412	Aea22412 Mycobacte
18	17.4	91.6	1482	AEA22404	Aea22404 Mycobacte

AA57239	Human CGD	1137	89.5	17	9	AA57239
AAV24413	Target se	23	86.3	16.4	2	AAV24413
AAV13021	Mycobacte	23	86.3	16.4	2	AAV13021
AAV24418	Target se	25	86.3	16.4	2	AAV24418
AAV13026	Mycobacte	25	86.3	16.4	2	AAV13026
ADA68711	Rice gene	765	85.3	16.2	8	ADA68711
AAA02278	Human col	935	84.2	16	3	AAA02278
ADF94057	Microorga	50	83.2	15.8	12	ADF94057
AA32481	Preferred	166	83.2	15.8	3	AA32481
AA31293	Plant mic	170	83.2	15.8	3	AA31293
AA31415	Plant mic	305	83.2	15.8	3	AA31415
AB276674	Microctetr	460	83.2	15.8	8	AB276674
AEB72673	Streptosp	497	83.2	15.8	14	AEB72673
AED64356	Rhodococc	500	83.2	15.8	14	AED64356
AAS67301	DNA encod	576	83.2	15.8	5	AAS67301
ADO80217	Rhodococc	1343	83.2	15.8	12	ADO80217
ADW16264	DNA copy	1390	83.2	15.8	14	ADW16264
ADJ38609	Micromono	1403	83.2	15.8	12	ADJ38609
ADW16290	DNA copy	1427	83.2	15.8	14	ADW16290
ADC61232	Baeyer-Vi	1439	83.2	15.8	10	ADC61232
ADZ35975	Verrucosi	1440	83.2	15.8	14	ADZ35975
AD38843	Microbisp	1443	83.2	15.8	14	AD38843
AEA22406	Mycobacte	1461	83.2	15.8	14	AEA22406
AED35651	Pseudonoc	1483	83.2	15.8	14	AED35651
ADR90327	Rhodococc	1511	83.2	15.8	13	ADR90327
ADR90325	Rhodococc	1511	83.2	15.8	13	ADR90325
AED11327	Aliphatic	1511	83.2	15.8	14	AED11327
ADA41084	coralli	1584	83.2	15.8	10	ADA41084
AEA51361	Mouse gen	1849	83.2	15.8	14	AEA51361
ACC47372	Human lat	2896	83.2	15.8	10	ACC47372
ADL35344	Murine se	2898	83.2	15.8	12	ADL35344
ACC47371	Rat late	3054	83.2	15.8	10	ACC47371
AA136998	Human mus	6883	83.2	15.8	8	AA136998
ABX59986	cDNA enco	6883	83.2	15.8	8	ABX59986
ADJ30736	Human mus	6883	83.2	15.8	12	ADJ30736
AED48445	M. echino	84222	83.2	15.8	14	AED48445
AAC55929	Eucalyptu	455	81.1	15.4	3	AAC55929
AAC57218	M. xanthu	455	81.1	15.4	3	AAC57218
ACL67957	M. xanthu	861	81.1	15.4	14	ACL67957
AB104331	Drosophil	5433	81.1	15.4	4	AB104331
AB104330	Drosophil	7162	81.1	15.4	4	AB104330
ACL64755	M. xanthu	23677	81.1	15.4	14	ACL64755
ADB82110	Human CDN	297	78.9	15	9	ADB82110
ABQ89167	Human pro	331	78.9	15	6	ABQ89167
ACH79967	Human gen	592	78.9	15	12	ACH79967
ADI31363	Human CDN	1429	78.9	15	11	ADI31363
ADS83430	Human lym	1429	78.9	15	13	ADS83430
AAN99589	Human pro	1453	78.9	15	4	AAN99589
ABN59917	Novel hum	2010	78.9	15	6	ABN59917
AAF88159	Human thy	2015	78.9	15	5	AAF88159
AA03044	Human dia	2098	78.9	15	4	AA03044
AAK94562	Human ful	2169	78.9	15	4	AAK94562
ADL31436	Full leng	2169	78.9	15	12	ADL31436
ABA28974	Human tra	2173	78.9	15	5	ABA28974
ADB76868	A. gossyp	2240	78.9	15	10	ADB76868
ABL07155	Drosophil	3003	78.9	15	4	ABL07155
AAS25944	Human CDN	3293	78.9	15	4	AAS25944
ABX73285	Human nov	3293	78.9	15	8	ABX73285
AEE83945	Human CDN	5165	78.9	15	15	AEE83945
ABL07154	Drosophil	8544	78.9	15	4	ABL07154
AAT70787	Stenotic	40	77.9	14.8	2	AAT70787
AAK85278	Motif I f	87	77.9	14.8	2	AAK85278
ADP20374	Pinus rad	365	77.9	14.8	12	ADP20374
ACH95596	Klebsiell	375	77.9	14.8	11	ACH95596
ABD06974	Pseudomon	543	77.9	14.8	11	ABD06974
AAI43438	Probe #12	591	77.9	14.8	4	AAI43438
ABD07046	Pseudomon	600	77.9	14.8	11	ABD07046
ACA27357	Prokaryot	981	77.9	14.8	8	ACA27357
ADW16249	DNA copy	1158	77.9	14.8	14	ADW16249
AZ11765	Maize his	1392	77.9	14.8	2	AZ11765
ADA71495	Rice gene	2000	77.9	14.8	8	ADA71495
ACL36116	Rice stre	2000	77.9	14.8	11	ACL36116
ABL14648	Drosophil	7564	77.9	14.8	4	ABL14648

92	14.8	77.9	7564	4	AAS57142	Aas57142 DNA encod	C 165	14.4	75.8	3764	4	ABL22306	AbL22306 Drosophil
93	14.8	77.9	7564	10	ADC35854	Adc35854 Drosophil	C 166	14.4	75.8	3809	6	ABK95303	Abk95303 Human pro
94	14.8	77.9	19183	4	AAK64938	Aak64938 Human imm	C 167	14.4	75.8	5634	4	ABL28614	AbL28614 Drosophil
95	14.8	77.9	19183	4	AAK36434	Aak36434 Human imm	C 168	14.4	75.8	5832	6	ABQ71069	Abq71069 Listeria
96	14.8	77.9	19183	8	ABX59422	Abx59422 cDNA enco	C 169	14.4	75.8	15419	4	ABL20618	AbL20618 Drosophil
97	14.8	77.9	19183	12	ADJ30172	Adj30172 Human mus	C 170	14.4	75.8	15434	4	ABL20620	AbL20620 Drosophil
98	14.8	77.9	30904	4	AAK75071	Aak75071 Human imm	C 171	14.4	75.8	17794	4	ABL02220	AbL02220 Drosophil
99	14.8	77.9	32249	4	AAK36814	Aak36814 Human car	C 172	14.4	75.8	22958	13	ADT05537	Adt05537 Haemophil
100	14.8	77.9	32249	10	ADe47508	Ade47508 Human car	C 173	14.4	75.8	23615	14	AEC09537	Aec09537 Human Bli
101	14.8	77.9	32249	13	ADT08926	Adt08926 Human car	C 174	14.4	75.8	24281	13	ABD33480	Abd33480 Murine ca
102	14.8	77.9	42104	11	ACN44606	Acn44606 Human gen	C 175	14.4	75.8	24281	14	ADZ13479	Adz13479 Murine ca
103	14.8	77.9	87731	11	ACN44742	Acn44742 Human gen	C 176	14.4	75.8	41685	11	ACN44330	Acn44330 Human gen
104	14.8	77.9	89328	6	ABL61995	AbL61995 Colon ade	C 177	14.4	75.8	105305	11	ACN44760	Acn44760 Mouse gen
105	14.8	77.9	110000	9	ADB12064_02	AdB12064_02	C 178	14.4	75.8	110000	2	AA42063_03	AA42063_03
106	14.8	77.9	110000	9	ADB12064_03	AdB12064_03	C 179	14.4	75.8	110000	6	ABQ69245_03	ABQ69245_03
107	14.8	77.9	110000	12	ADN46845_10	AdN46845_10	C 180	14.4	75.8	110000	6	ABQ67197_02	ABQ67197_02
108	14.8	77.9	110000	12	ADN47591_10	AdN47591_10	C 181	14.4	75.8	110000	6	ABA03041_03	ABA03041_03
109	14.8	77.9	110000	12	ADN46123_10	AdN46123_10	C 182	14.4	75.8	110000	12	ADN46845_13	ADN46845_13
110	14.8	77.9	110000	12	ADN47209_10	AdN47209_10	C 183	14.4	75.8	110000	12	ADN47591_06	ADN47591_06
111	14.8	77.9	110000	12	ADN46464_10	AdN46464_10	C 184	14.4	75.8	110000	12	ADN46123_13	ADN46123_13
112	14.8	77.9	110000	12	ADN47960_10	AdN47960_10	C 185	14.4	75.8	110000	12	ADN47209_06	ADN47209_06
113	14.8	77.9	173115	14	AEB989425	Aeb989425	C 186	14.4	75.8	110000	12	ADN46464_13	ADN46464_13
114	14.4	75.8	27	2	AAV24410	Aav24410 Target se	C 187	14.4	75.8	110000	12	ADN47960_06	ADN47960_06
115	14.4	75.8	27	2	AAV13018	Aav13018 Mycobacte	C 188	14.4	75.8	138839	14	AED18450	Aed18450 Fibrotic
116	14.4	75.8	28	4	AAD11025	Rad11025 Probe #5	C 189	14.4	75.8	161974	15	AEP80153	Aep80153 Cancer-as
117	14.4	75.8	28	4	AAD11018	Rad11018 PCR prime	C 190	14.4	75.8	198161	6	ABK83564	Abk83564 Human CDN
118	14.4	75.8	32	4	AAD11024	Rad11024 Probe #4	C 191	14.4	75.8	198161	12	ADQ17348	Adq17348 Human sof
119	14.4	75.8	32	4	AAD11017	Rad11017 PCR prime	C 192	14.4	75.8	198161	13	ADK52701	Adk52701 Drug ther
120	14.4	75.8	50	2	AAX99195	Aax99195 M. avium	C 193	14.4	75.8	349980	5	AAH41224	Aah41224 Pyrococcu
121	14.4	75.8	50	2	AAX99196	Aax99196 M. fortui	C 194	14.4	75.8	349980	5	AAH41225	Aah41225 Pyrococcu
122	14.4	75.8	50	12	ADP94050	Adf94050 Microorga	C 195	14.4	75.8	349980	13	ADT05648	Adt05648 Haemophil
123	14.4	75.8	209	14	AEB98762	Aeb98762 Mycobacte	C 196	14.2	74.7	142	6	AAS98571	Aas98571 Human neu
124	14.4	75.8	341	4	AAS36010	Aas36010 Human car	C 197	14.2	74.7	159	10	ABZ239038	Abz239038 N. gonorr
125	14.4	75.8	341	4	AAS36011	Aas36011 Human car	C 198	14.2	74.7	193	2	AAT22735	Aat22735 Human gen
126	14.4	75.8	341	10	ADe46704	Ade46704 Human car	C 199	14.2	74.7	301	3	AAA06480	Aaa06480 Human imm
127	14.4	75.8	341	10	ADe46705	Ade46705 Human car	C 200	14.2	74.7	301	4	AAH93596	Aah93596 Human pro
128	14.4	75.8	341	13	ADJ08123	Adj08123 Human car	C 201	14.2	74.7	301	4	AAS63688	Aas63688 Human pro
129	14.4	75.8	341	13	ADJ08122	Adj08122 Human car	C 202	14.2	74.7	301	4	AAH02661	Aah02661 Prostate
130	14.4	75.8	352	4	AAS35269	Aas35269 Human car	C 203	14.2	74.7	301	4	AH84910	Aah84910 Human pro
131	14.4	75.8	352	10	ADe45348	Ade45348 Human car	C 204	14.2	74.7	301	5	ACA59497	Aca59497 Prostate
132	14.4	75.8	352	13	ADJ06766	Adj06766 Human car	C 205	14.2	74.7	301	6	ABU95060	AbU95060 Human PTP
133	14.4	75.8	381	5	AAS77874	AdS77874 DNA encod	C 206	14.2	74.7	301	8	ACC95224	Acc95224 Prostate
134	14.4	75.8	560	10	ADT23571	Adt23571 Stabilisi	C 207	14.2	74.7	301	10	ADB13697	Adb13697 Human pro
135	14.4	75.8	649	4	AAH69025	Aah69025 Human cer	C 208	14.2	74.7	301	10	ADG26113	Adg26113 Human pro
136	14.4	75.8	649	4	AAH69025	Aah69025 Human cer	C 209	14.2	74.7	301	15	AEF66394	Aef66394 Human pro
137	14.4	75.8	981	3	AAC54004	Aac54004 Arabidops	C 210	14.2	74.7	341	14	ADL75211	Adl75211 Human col
138	14.4	75.8	983	3	AAC52885	Aac52885 Arabidops	C 211	14.2	74.7	387	14	ACL67607	Acl67607 M. xanthu
139	14.4	75.8	1158	4	ABL23865	AbL23865 Drosophil	C 212	14.2	74.7	411	8	ABX39805	Abx39805 Bovine ES
140	14.4	75.8	1158	13	ADQ89669	Adq89669 Antagonis	C 213	14.2	74.7	424	4	ABA08574	AbA08574 Human enh
141	14.4	75.8	1296	4	ABL22307	AbL22307 Drosophil	C 214	14.2	74.7	426	10	ADC35700	Adc35700 Rhodococc
142	14.4	75.8	1421	14	AEA22411	Aea22411 Mycobacte	C 215	14.2	74.7	447	14	ADY37634	Ady37634 Leishmani
143	14.4	75.8	1431	12	ADK66476	Adk66476 Corynebac	C 216	14.2	74.7	447	14	ADY37632	Ady37632 Leishmani
144	14.4	75.8	1431	12	ADK66445	Adk66445 Corynebac	C 217	14.2	74.7	447	14	ADY37633	Ady37633 Leishmani
145	14.4	75.8	1431	12	AAV38415	AAv38415 DNA encod	C 218	14.2	74.7	447	14	ADY37631	Ady37631 Leishmani
146	14.4	75.8	1446	2	AAQ37639	Aaq37639 Mycobacte	C 219	14.2	74.7	447	14	ADY37630	Ady37630 Leishmani
147	14.4	75.8	1454	14	AEA22401	Aea22401 Mycobacte	C 220	14.2	74.7	456	10	ABZ239039	Abz239039 N. gonorr
148	14.4	75.8	1465	10	ADB61680	Adb61680 16S rRNA	C 221	14.2	74.7	499	9	ACH13049	Ach13049 Human adu
149	14.4	75.8	1472	13	ADP90572	Adp90572 M avium 1	C 222	14.2	74.7	503	12	ADJ39286	Adj39286 Plant CDN
150	14.4	75.8	1906	13	ADQ85867	Adq85867 Human tum	C 223	14.2	74.7	508	3	AAC59084	Aac59084 Human sec
151	14.4	75.8	1907	4	AAH14960	Aah14960 Human cDN	C 224	14.2	74.7	511	13	AAF08440	Aaf08440 Fusarium
152	14.4	75.8	1907	13	ADX27659	Adx27659 Plant ful	C 225	14.2	74.7	511	13	ADU52481	AdU52481 Fusarium
153	14.4	75.8	1908	13	ADP76376	Adp76376 Novel hum	C 226	14.2	74.7	511	14	ADZ90484	Adz90484 Fusarium
154	14.4	75.8	1908	13	ADP76376	Adp76376 Novel hum	C 227	14.2	74.7	511	14	ADZ90484	Adz90484 Fusarium
155	14.4	75.8	1908	13	ADP56021	Adp56021 Human PRO	C 228	14.2	74.7	523	3	AAQ35675	Aaq35675 Arabidops
156	14.4	75.8	1942	6	ABK34562	Abk34562 Human cDN	C 229	14.2	74.7	526	4	AAH11789	Aah11789 Human CDN
157	14.4	75.8	1972	10	ADD14695	Add14695 Human src	C 230	14.2	74.7	529	10	ADC35702	Adc35702 Rhodococc
158	14.4	75.8	1972	14	AED17806	Aed17806 Fibrotic	C 231	14.2	74.7	535	13	ADS75567	AdS75567 Rhodococc
159	14.4	75.8	1972	15	AEE60944	Aee60944 Human pat	C 232	14.2	74.7	600	3	AAC79222	Aac79222 Human lun
160	14.4	75.8	2400	13	AEE31095	Aee31095 Haemophil	C 233	14.2	74.7	600	4	ADZ23298	Adz23298 Human lun
161	14.4	75.8	2919	13	ADS59960	AdS59960 Bacterial	C 234	14.2	74.7	600	10	ADD66572	Add66572 Human lun
162	14.4	75.8	3231	11	ADM03126	Adm03126 Human cDN	C 235	14.2	74.7	610	13	ACN56868	Acn56868 Cotton gy
163	14.4	75.8	3291	14	AEC86056	Aec86056 Human cDN	C 236	14.2	74.7	624	10	ADC72425	Adc72425 DNA Seq I
164	14.4	75.8	3417	4	ABL23864	AbL23864 Drosophil	C 237	14.2	74.7	633	10	ACF70237	Acf70237 Photorhab

238	14.2	74.7	691	2	AAx20463	Human sec
239	14.2	74.7	691	3	AAa72426	Human nuc
240	14.2	74.7	691	10	ADD90247	Novel hum
241	14.2	74.7	691	10	ADg90066	Human cDN
242	14.2	74.7	691	14	ADy25406	Novel hum
243	14.2	74.7	713	10	ABx95074	Human p11
244	14.2	74.7	713	14	AEd14036	Human cum
245	14.2	74.7	769	6	ABQ56097	Human ova
246	14.2	74.7	776	4	AAi94564	Human neu
247	14.2	74.7	788	3	AAc33114	Arabidops
248	14.2	74.7	798	5	AAH68033	C glutami
249	14.2	74.7	851	4	AAi94024	Human neu
250	14.2	74.7	861	3	AAAD01331	Soybean P
251	14.2	74.7	861	6	ABK34319	Human cDN
252	14.2	74.7	861	10	ABZ39185	N. gonorr
253	14.2	74.7	879	4	AAf71819	Corynebac
254	14.2	74.7	879	4	AAf72312	Corynebac
255	14.2	74.7	891	4	AAH05515	Human cDN
256	14.2	74.7	898	6	ABS70422	Human bon
257	14.2	74.7	928	10	ADD13548	C. glutam
258	14.2	74.7	936	6	ABN74448	Bovine em
259	14.2	74.7	954	6	ABO20284	Oligonuc1
260	14.2	74.7	954	6	ABQ20285	Oligonuc1
261	14.2	74.7	996	10	ACF67845	Phototrab
262	14.2	74.7	1024	6	ABX65639	Helicobac
263	14.2	74.7	1024	6	ABX66177	Helicobac
264	14.2	74.7	1035	6	ABS51363	cDNA enco
265	14.2	74.7	1095	6	ABQ94247	F1011 gen
266	14.2	74.7	1158	4	ABL23865	Drosophil
267	14.2	74.7	1158	13	ADQ96669	Antagonis
268	14.2	74.7	1161	14	ABE66883	Rice geno
269	14.2	74.7	1194	6	ABQ75110	Anopheles
270	14.2	74.7	1194	10	ACF79723	Mosquito
271	14.2	74.7	1236	3	AAc45925	Arabidops
272	14.2	74.7	1315	6	ABL57729	Human sbg
273	14.2	74.7	1329	13	ADU05441	DNA encod
274	14.2	74.7	1332	8	ACA34802	Prokaryot
275	14.2	74.7	1425	10	ADH71201	Human gen
276	14.2	74.7	1437	12	ADF56670	YS-44442
277	14.2	74.7	1437	12	ADG64519	Saccharot
278	14.2	74.7	1437	14	ADY86147	Saccharot
279	14.2	74.7	1443	10	ADB69806	C. neofor
280	14.2	74.7	1471	12	ADF56671	YS-45494
281	14.2	74.7	1471	12	ADG64520	Saccharot
282	14.2	74.7	1471	14	ADY86148	Saccharot
283	14.2	74.7	1477	14	AEa47485	Nocardia
284	14.2	74.7	1484	2	AAV90921	Nucleotid
285	14.2	74.7	1488	13	ADSL7289	Lechevali
286	14.2	74.7	1491	4	AAf77686	Human pro
287	14.2	74.7	1494	6	ABL57728	Human sbg
288	14.2	74.7	1498	13	ADS47642	Bacterial
289	14.2	74.7	1514	14	ADW12667	Rhodococ
290	14.2	74.7	1529	2	AAx14164	H. pylori
291	14.2	74.7	1538	3	AAc36652	Arabidops
292	14.2	74.7	1540	2	AAV90845	Nucleotid
293	14.2	74.7	1540	3	AAc45334	Arabidops
294	14.2	74.7	1555	3	AAAD01326	Soybean P
295	14.2	74.7	1584	6	AAAD28460	Bacillus
296	14.2	74.7	1612	12	ADH71205	Human gen
297	14.2	74.7	1675	4	AAa89283	Brassica
298	14.2	74.7	1677	4	AAa89279	Arabidops
299	14.2	74.7	1691	10	ADB63529	Human cDN
300	14.2	74.7	1695	12	ADO02829	Soybean o

ALIGNMENTS

XX	24-SBP-2001	(first entry)	XX	AAx20463	Human sec
DT	Myobacterium 16S rRNA	amplifying primer #18.	DT	AAa72426	Human nuc
DE	Myobacterium 16S rRNA	amplifying primer #18.	DE	ADD90247	Novel hum
XX	Myobacterium; 16S rRNA; 16S ribosomal RNA; amplification;		XX	ADg90066	Human cDN
KW	Myobacterium other than tuberculosis; MOTT; PCR primer; ss.		KW	ADy25406	Novel hum
XX	Myobacterium sp.		XX	ABx95074	Human p11
OS	WO200144510-A2.		OS	AEd14036	Human cum
PN	21-JUN-2001.		PN	ABQ56097	Human ova
PD	17-DEC-1999; 99WO-US030346.		PD	AAi94564	Human neu
XX	17-DEC-1999; 99WO-US030346.		XX	AAc33114	Arabidops
XX	(GENP-) GEN-PROBE INC.		XX	AAH68033	C glutami
PA	(INMR ) BIOMERIEUX SA.		PA	AAi94024	Human neu
XX	Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;		XX	AAAD01331	Soybean P
XX	WPI; 2001-398170/42.		XX	ABK34319	Human cDN
PS	Detecting Mycobacterium species, involves in vitro amplification of 16S		PS	ABZ39185	N. gonorr
XX	rRNA or DNA encoding RNA in nucleic acid amplification mixture using		XX	AAf71819	Corynebac
PT	specific primers, and detecting the amplified nucleic acid.		PT	AAf72312	Corynebac
XX	Claim 1; Page 36; 44pp; English.		XX	AAH05515	Human cDN
CC	The invention relates to a method of detecting Mycobacterium species,		CC	ABS70422	Human bon
CC	that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA		CC	ADD13548	C. glutam
CC	encoding 16S rRNA in an in vitro nucleic acid amplification mixture		CC	ABN74448	Bovine em
CC	comprising a polymerase, and at least two primers, and then detecting the		CC	ABO20284	Oligonuc1
CC	amplified nucleic acid. The method is relatively simple and useful for		CC	ABQ20285	Oligonuc1
CC	detecting the presence of various Mycobacterium species in a biological		CC	ACF67845	Phototrab
CC	sample, and thus important for diagnosis of infections resulting from		CC	ABX65639	Helicobac
CC	them. The method is especially important for screening opportunistic		CC	ABX66177	Helicobac
CC	infections caused by M. tuberculosis or a Mycobacterium other than		CC	ABS51363	cDNA enco
CC	tuberculosis (MOTT). The present sequence is a PCR primer used for		CC	ABQ94247	F1011 gen
CC	amplifying Mycobacterium 16S rRNA		CC	ABL23865	Drosophil
XX	Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;		XX	ADQ96669	Antagonis
XX	Query Match 100.0%; Score 19; DB 4; Length 19;		XX	ABE66883	Rice geno
XX	Best Local Similarity 100.0%; Pred. No. 5.5;		XX	ABQ75110	Anopheles
XX	Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		XX	ACF79723	Mosquito
Qy	1 GAACGGAAGGCTTCGG 19		Qy	AAc45925	Arabidops
Db	1 GAACGGAAGGCTTCGG 19		Db	ABL57729	Human sbg
RESULT 2			Db	ADU05441	DNA encod
ADG88355			Db	ACA34802	Prokaryot
ID	ADG88355 standard; DNA; 19 BP.		Db	ADH71201	Human gen
XX	ADG88355;		Db	ADF56670	YS-44442
AC	ADG88355;		Db	ADG64519	Saccharot
XX	11-MAR-2004 (first entry)		Db	ADY86147	Saccharot
DT	Myobacterium amplifying PCR primer #24.		Db	ADB69806	C. neofor
XX	In vitro amplification; PCR; primer; ss.		Db	ADF56671	YS-45494
OS	Myobacterium xenopi.		Db	ADG64520	Saccharot
XX	US2003165824-A1.		Db	ADY86148	Saccharot
PN	04-SEP-2003.		Db	AEa47485	Nocardia
XX	15-DEC-2000; 2000US-00738274.		Db	AAV90921	Nucleotid
PD			Db	ADSL7289	Lechevali
PF			Db	AAf77686	Human pro

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XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX
XX Claim 1; SEQ ID NO 24; 20pp; English.
XX
XX The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAACGGAAGGCTTCGG 19
DB 1 GAACGGAAGGCTTCGG 19
XX
RESULT 3
AEA08230 ID AEA08230 standard; DNA; 19 BP.
XX
AC AEA08230;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium xenopi 16S rRNA amplifying non-T7 primer, SEQ ID NO: 24.
XX
KW DNA amplification; microorganism detection; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX
OS Mycobacterium xenopi; ATCC 19250.
XX
PN US2005100915-A1.
XX
XX 12-MAY-2005.
XX
XX 18-SEP-2003; 2003US-00665708.
XX
XX 17-DEC-1999; 99US-0172190P.
XX 15-DEC-2000; 2000US-00738274.
XX
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2005-345392/35.
XX
XX Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample, comprises using in vitro nucleic acid
XX amplification and detection of amplified products.
XX
Claim 1; SEQ ID NO 24; 21pp; English.
XX
The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample. The method involves using in
XX vitro nucleic acid amplification and detection of amplified products. The
XX invention is useful for diagnostic detection of pathogenic bacteria such
XX as Mycobacterium species. The present sequence is the Mycobacterium
XX xenopi (ATCC 19250) 16S ribosomal RNA (16S rRNA) amplifying non-T7 PCR
XX primer.
XX
XX Sequence 19 BP; 5 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GAACGGAAGGCTTCGG 19
DB 1 GAACGGAAGGCTTCGG 19
XX
RESULT 4
AAD11273 ID AAD11273 standard; DNA; 22 BP.
XX
AC AAD11273;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #17.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
XX Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
XX (GENP-) GEN-PROBE INC.
XX (INMR ) BIOMERIEUX SA.
XX
XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
XX
XX Detecting Mycobacterium species, involves in vitro amplification of 16S
XX rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX
XX Claim 1; Page 36; 44pp; English.
XX
XX The invention relates to a method of detecting Mycobacterium species,
XX that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
XX encoding 16S rRNA in an in vitro nucleic acid amplification mixture
XX comprising a polymerase, and at least two primers, and then detecting the
XX amplified nucleic acid. The method is relatively simple and useful for
XX detecting the presence of various Mycobacterium species in a biological
XX sample, and thus important for diagnosis of infections resulting from
XX them. The method is especially important for screening opportunistic
XX infections caused by M. tuberculosis or a Mycobacterium other than
XX tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX
XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 19; DB 4; Length 22;

```

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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
Db 4 GAACGGAAGGCTTCGG 22

RESULT 5
ADG88354
ID ADG88354 standard; DNA; 22 BP.
XX
AC ADG88354;
XX
DT 11-MAR-2004 (first entry)
XX
DE Mycobacterium amplifying PCR primer #23.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 23; 20pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
Db 4 GAACGGAAGGCTTCGG 22

RESULT 6
AEA08229
ID AEA08229 standard; DNA; 22 BP.
XX
AC AEA08229;
XX
DT 14-JUL-2005 (first entry)
XX
DE Mycobacterium celatum 16S rRNA amplifying non-T7 primer, SEQ ID NO: 23.
XX
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KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
OS Mycobacterium celatum.
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 23; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16S rRNA)
CC amplifying non-r7 PCR primer.
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTCGG 19
Db 4 GAACGGAAGGCTTCGG 22

RESULT 7
AAD11272
ID AAD11272 standard; DNA; 24 BP.
XX
AC AAD11272;
XX
DT 24-SEP-2001 (first entry)
XX
DE Mycobacterium 16S rRNA amplifying primer #16.
XX
KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX
OS Mycobacterium sp.
XX
PN WO200144510-A2.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99WO-US030346.
XX
PR 17-DEC-1999; 99WO-US030346.
XX
PA (GENP-) GEN-PROBE INC.
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PA (INMR ) BIOMERIEUX SA.
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2001-398170/42.
DR
XX
PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
PT specific primers, and detecting the amplified nucleic acid.
XX
PS Claim 1; Page 36; 44pp; English.
XX
CC The invention relates to a method of detecting Mycobacterium species
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
CC amplifying Mycobacterium 16S rRNA
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCG 18
Db 7 GAACGGAAAGGCTTTTCG 24

RESULT 8
ADG88353
ID ADG88353 standard; DNA; 24 BP.
XX
AC ADG88353;
XX
DT 11-MAR-2004 (first entry)
DE Mycobacterium amplifying PCR primer #22.
XX
KW In vitro amplification; PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2003165824-A1.
XX
PD 04-SEP-2003.
XX
PF 15-DEC-2000; 2000US-00738274.
XX
PR 17-DEC-1999; 99US-0172190P.
XX
PS (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2003-898044/82.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample comprises performing in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 1; SEQ ID NO 22; 20pp; English.
XX

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CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample comprises performing an in vitro
CC amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
CC detecting the amplified Mycobacterium nucleic acid. The present sequence
CC is Mycobacterium amplifying PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCG 18
Db 7 GAACGGAAAGGCTTTTCG 24

RESULT 9
AEA08228
ID AEA08228 standard; DNA; 24 BP.
XX
AC AEA08228;
XX
DT 14-JUL-2005 (first entry)
DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 22.
XX
KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
KW PCR; primer; ss.
XX
OS Mycobacterium celatum.
XX
PN US2005100915-A1.
XX
PD 12-MAY-2005.
XX
PF 18-SEP-2003; 2003US-00665708.
XX
PR 17-DEC-1999; 99US-0172190P.
PR 15-DEC-2000; 2000US-00738274.
XX
PA (BREN/) BRENTANO S T.
PA (JUCK/) JUCKER M T.
PA (DELG/) DELGADO F D.
PA (CLEU/) CLEUZIAT P.
PA (RODR/) RODRIGUE M.
XX
PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX
DR WPI; 2005-345392/35.
XX
PT Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
PT in a biological sample, comprises using in vitro nucleic acid
PT amplification and detection of amplified products.
XX
PS Claim 8; SEQ ID NO 22; 21pp; English.
XX
CC The present invention relates to a method of detecting Mycobacterium
CC species present in a biological sample. The method involves using in
CC vitro nucleic acid amplification and detection of amplified products. The
CC invention is useful for diagnostic detection of pathogenic bacteria such
CC as Mycobacterium species. The present sequence is the Mycobacterium
CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)
CC amplifying non-T7 PCR primer.
XX
SQ Sequence 24 BP; 7 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 94.7%; Score 18; DB 14; Length 24;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCG 18

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Db          7 GAACGGAAGGCTTTTCG 24
RESULT 10
AAD11271
ID AAD11271 standard; DNA; 25 BP.
XX AC AAD11271;
XX DT 24-SEP-2001 (first entry)
XX DE Mycobacterium 16S rRNA amplifying primer #15.
XX KW Mycobacterium; 16S rRNA; 16S ribosomal RNA; amplification;
KW Mycobacterium other than tuberculosis; MOTT; PCR primer; ss.
XX OS Mycobacterium sp.
XX PN WO200144510-A2.
XX PD 21-JUN-2001.
XX PF 17-DEC-1999; 99WO-US030346.
XX PR 17-DEC-1999; 99WO-US030346.
XX PA (GENP-) GEN-PROBE INC.
PA (INMR ) BIOMERIEUX SA.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX DR WPI; 2001-398170/42.
XX PT Detecting Mycobacterium species, involves in vitro amplification of 16S
PT rRNA or DNA encoding RNA in nucleic acid amplification mixture using
XX specific primers, and detecting the amplified nucleic acid.
XX Claim 1; Page 36; 44pp; English.
XX PS The invention relates to a method of detecting Mycobacterium species,
CC that involves amplifying Mycobacterium 16S ribosomal RNA (rRNA) or DNA
CC encoding 16S rRNA in an in vitro nucleic acid amplification mixture
CC comprising a polymerase, and at least two primers, and then detecting the
CC amplified nucleic acid. The method is relatively simple and useful for
CC detecting the presence of various Mycobacterium species in a biological
CC sample, and thus important for diagnosis of infections resulting from
CC them. The method is especially important for screening opportunistic
CC infections caused by M. tuberculosis or a Mycobacterium other than
CC tuberculosis (MOTT). The present sequence is a PCR primer used for
XX amplifying Mycobacterium 16S rRNA
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25

RESULT 11
ADG88352
ID ADG88352 standard; DNA; 25 BP.
XX AC ADG88352;
XX DT 11-MAR-2004 (first entry)
XX DE Mycobacterium amplifying PCR primer #21.
XX KW In vitro amplification; PCR; primer; ss.

XX Mycobacterium celatum.
XX US2003165824-A1.
XX 04-SEP-2003.
XX 15-DEC-2000; 2000US-00738274.
XX 17-DEC-1999; 99US-0172190P.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
XX PI Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;
XX WPI; 2003-898044/82.
XX DR Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present
XX in a biological sample comprises performing in vitro nucleic acid
XX amplification and detection of amplified products.
XX Claim 1; SEQ ID NO 21; 20pp; English.
XX PS The present invention relates to a method of detecting Mycobacterium
XX species present in a biological sample comprises performing an in vitro
XX amplification of Mycobacterium 16S rRNA or DNA encoding 16S rRNA and
XX detecting the amplified Mycobacterium nucleic acid. The present sequence
XX is Mycobacterium amplifying PCR primer.
XX SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 94.7%; Score 18; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
Db 8 GAACGGAAGGCTTTTCG 25

RESULT 12
AEA08227
ID AEA08227 standard; DNA; 25 BP.
XX AC AEA08227;
XX DT 14-JUL-2005 (first entry)
XX DE Mycobacterium celatum 16SrRNA amplifying non-T7 primer, SEQ ID NO: 21.
XX KW Microorganism detection; DNA amplification; 16s ribosomal RNA; 16s rRNA;
XX PCR; primer; ss.
XX OS Mycobacterium celatum.
XX PN US2005100915-A1.
XX PD 12-MAY-2005.
XX PF 18-SEP-2003; 2003US-00665708.
XX PR 17-DEC-1999; 99US-0172190P.
XX PR 15-DEC-2000; 2000US-00738274.
XX (BREN/) BRENTANO S T.
XX (JUCK/) JUCKER M T.
XX (DELG/) DELGADO F D.
XX (CLEU/) CLEUZIAT P.
XX (RODR/) RODRIGUE M.
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XX Brentano ST, Jucker MT, Delgado FD, Cleuziat P, Rodrigue M;  
 PI WPI; 2005-345392/35.  
 DR  
 CC Detecting Mycobacterium species (e.g. Mycobacterium tuberculosis) present  
 PT in a biological sample, comprises using in vitro nucleic acid  
 PT amplification and detection of amplified products.  
 XX  
 PS Claim 8; SEQ ID NO 21; 21pp; English.  
 XX  
 CC The present invention relates to a method of detecting Mycobacterium  
 CC species present in a biological sample. The method involves using in  
 CC vitro nucleic acid amplification and detection of amplified products. The  
 CC invention is useful for diagnostic detection of pathogenic bacteria such  
 CC as Mycobacterium species. The present sequence is the Mycobacterium  
 CC celatum (ATCC 51130 and ATCC 51131) 16S ribosomal RNA (16SrRNA)  
 CC amplifying non-T7 PCR primer.  
 XX  
 SQ Sequence 25 BP; 7 A; 6 C; 8 G; 4 T; 0 U; 0 Other;  
 Query Match 94.7%; Score 18; DB 14; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 19;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAACGGAAAGGCTTTTCG 18  
 |||||  
 Db 8 GAACGGAAAGGCTTTTCG 25  
 |||||  
 RESULT 13  
 AAS30718  
 ID AAS30718 standard; DNA; 25 BP.  
 XX  
 AC AAS30718;  
 XX  
 XX 06-AUG-2003 (revised)  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Mycobacterium species-specific probe #24.  
 XX  
 KW Mycobacterium; species-specific bacterial identification; primer; ss.  
 XX  
 OS Mycobacterium chelonae.  
 XX  
 PN WO200166797-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US006731.  
 XX  
 PR 03-MAR-2000; 2000US-0186840P.  
 XX  
 PA (BECI ) BECKMAN COULTER INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US NAT INST OF HEALTH.  
 XX  
 PI Fischer SH, Rampal JB, Fahle GA, Conville PS;  
 XX  
 DR WPI; 2001-514847/56.  
 XX  
 XX Species-specific bacterial identification, used particularly to identify  
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or  
 PT specific primers to a sample.  
 XX  
 PS Claim 28; Page 21; 43pp; English.  
 XX  
 CC The invention relates to a method of species-specific bacterial  
 CC identification, comprising hybridising a bacterial genus-selective or  
 CC specific primer to a sample and amplifying nucleic acids. This is  
 CC followed by hybridising the amplified nucleic acid to a solid phase array  
 CC comprising bacterial species specific probe oligonucleotides chemically  
 CC linked to a polymeric support in a predetermined pattern. This method is  
 CC used for species-specific identification of a bacterium, particularly a  
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.  
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid  
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720  
 CC represent Mycobacterium species-specific primers and probes used in the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 91.6%; Score 17.4; DB 4; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 39;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC used for species-specific identification of a bacterium, particularly a  
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.  
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid  
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720  
 CC represent Mycobacterium species-specific primers and probes used in the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 25 BP; 5 A; 6 C; 10 G; 4 T; 0 U; 0 Other;  
 Query Match 91.6%; Score 17.4; DB 4; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 39;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GAACGGAAAGGCTTTTCG 19  
 |||||  
 Db 1 GAACGGAAAGGCTTTTCG 19  
 |||||  
 RESULT 14  
 AAS30716  
 ID AAS30716 standard; DNA; 25 BP.  
 XX  
 AC AAS30716;  
 XX  
 XX 06-AUG-2003 (revised)  
 DT 04-DEC-2001 (first entry)  
 XX  
 DE Mycobacterium species-specific probe #22.  
 XX  
 KW Mycobacterium; species-specific bacterial identification; primer; ss.  
 XX  
 OS Mycobacterium chelonae.  
 XX  
 PN WO200166797-A2.  
 XX  
 PD 13-SEP-2001.  
 XX  
 PF 01-MAR-2001; 2001WO-US006731.  
 XX  
 PR 03-MAR-2000; 2000US-0186840P.  
 XX  
 PA (BECI ) BECKMAN COULTER INC.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (USSH ) US NAT INST OF HEALTH.  
 XX  
 PI Fischer SH, Rampal JB, Fahle GA, Conville PS;  
 XX  
 DR WPI; 2001-514847/56.  
 XX  
 XX Species-specific bacterial identification, used particularly to identify  
 PT Mycobacterium species, involves hybridizing bacterial genus-selective or  
 PT specific primers to a sample.  
 XX  
 PS Claim 28; Page 21; 43pp; English.  
 XX  
 CC The invention relates to a method of species-specific bacterial  
 CC identification, comprising hybridising a bacterial genus-selective or  
 CC specific primer to a sample and amplifying nucleic acids. This is  
 CC followed by hybridising the amplified nucleic acid to a solid phase array  
 CC comprising bacterial species specific probe oligonucleotides chemically  
 CC linked to a polymeric support in a predetermined pattern. This method is  
 CC used for species-specific identification of a bacterium, particularly a  
 CC Mycobacterium, especially M. gordonae, M. intracellulare, M. avium, M.  
 CC tuberculosis, M. marinum, or M. kansasii. The method provides rapid  
 CC identification of multiple species of Mycobacterium. AAS30686-AAS30720  
 CC represent Mycobacterium species-specific primers and probes used in the  
 CC method of the invention. (Updated on 06-AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 25 BP; 6 A; 6 C; 9 G; 4 T; 0 U; 0 Other;  
 Query Match 91.6%; Score 17.4; DB 4; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 39;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



QY 1 GAACGGAAGCCCTTCGG 19  
 |||||  
 Db 1 GAACGGAAGCCCTTCGG 19

RESULT 15  
 ADZ20587  
 ID ADZ20587 standard; DNA; 500 BP.  
 XX  
 AC ADZ20587;  
 DT 16-JUN-2005 (first entry)  
 XX  
 DE Formaldehyde decomposition related Mycobacterium sp. DNA.  
 XX  
 KW decomposition; formaldehyde; ds.  
 XX  
 OS Mycobacterium sp.  
 XX  
 PN JP2003284548-A.  
 XX  
 PD 07-OCT-2003.  
 XX  
 PF 27-MAR-2002; 2002JP-00089307.  
 XX  
 PR 27-MAR-2002; 2002JP-00089307.  
 XX  
 PA (KUMO-) KUMOMOTO KEN PREFECTURE.  
 PA (MITS-) MITSUWA CORP YG.  
 PA (MITS-) MITSUWA BIRO KK.  
 XX  
 DR WPI; 2004-172963/17.  
 XX  
 PT Decomposing formaldehyde by Mycobacterium and/or growth medium of the  
 PT cells.  
 XX  
 PS Example 1; SEQ ID NO 1; 20pp; Japanese.  
 XX  
 CC The invention relates to a novel method for decomposing formaldehyde by  
 CC using microbial cells that belong to Mycobacterium sp. or Fusarium  
 CC oxysporum, and/or the growth medium of the microbial cells. The invention  
 CC further comprises: microbial cells which belong to Mycobacterium sp.  
 CC having the ability to decompose formaldehyde; a formaldehyde  
 CC decomposition agent comprising Mycobacterium sp. and/or the growth medium  
 CC of the microbial cells; and a formaldehyde decomposition agent comprising  
 CC F. oxysporum and/or its growth medium. The method is useful for  
 CC decomposing formaldehyde in sea water by Mycobacterium sp. or F.  
 CC oxysporum that is deposited under FERM P-S18690 or FERM P-18483,  
 CC respectively. This polynucleotide sequence represents the Mycobacterium  
 CC sp. DNA of the invention.  
 XX  
 SQ Sequence 500 BP; 108 A; 119 C; 178 G; 95 T; 0 U; 0 Other;  
 Query Match 91.6%; Score 17.4; DB 13; Length 500;  
 Best Local Similarity 94.7%; Pred. No. 50;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GAACGGAAGCCCTTCGG 19  
 |||||  
 Db 60 GAACGGAAGCCCTTCGG 78

RESULT 16  
 AEA22405  
 ID AEA22405 standard; DNA; 1449 BP.  
 XX  
 AC AEA22405;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX  
 DE Mycobacterium fortuitum 16S rRNA sequence SEQ ID NO:6.  
 XX

KW microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
 XX  
 OS Mycobacterium fortuitum.  
 XX  
 PN US2005130168-A1.  
 XX  
 PD 16-JUN-2005.  
 XX  
 PF 31-OCT-2003; 2003US-00697802.  
 XX  
 PR 31-OCT-2003; 2003US-00697802.  
 XX  
 PA (HANX/) HAN X.  
 PA (PHAM/) PHAM A S.  
 XX  
 PI Han X, Pham AS;  
 XX  
 DR WPI; 2005-424597/43.  
 XX  
 PT Determining a bacterium species comprises providing oligonucleotide  
 PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
 XX  
 PS Disclosure; SEQ ID NO 6; 74pp; English.  
 XX  
 CC The invention relates to a method (M1) for determining a bacterium  
 CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
 CC extracting a genomic nucleotide from the bacterium to provide a  
 CC nucleotide template; (c) annealing a region of a nucleotide template to a  
 CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
 CC complimentary fashion, the primer set designed to provide a product  
 CC having a predetermined size dictated by a complimentary primer set; (d)  
 CC amplifying the region of the nucleotide template to produce the product;  
 CC and (e) determining a species of a bacterium in a nucleotide sequence of  
 CC the product. Also described is an alternative method (M2) for determining  
 CC a bacterium species comprising: (a) providing a specimen or a sample  
 CC having a template; (b) providing a pair of primers selected from: (i) a  
 CC first forward primer having consecutive bases of an AFB-f comprising any  
 CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
 CC or variations and a first reverse primer having consecutive bases of an  
 CC AFB-r comprising any of the 36 sequences of 15-22 bp (AEA22453-AEA22488)  
 CC or their fragments or variations, (ii) a second forward primer having  
 CC consecutive bases of an UB-f comprising any of the 28 sequences of 15-21  
 CC bp (AEA22489-AEA22516) or their fragments or variations and a second  
 CC reverse primer having consecutive bases of an UB-r comprising any of the  
 CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
 CC variations, or (iii) a first forward primer having consecutive bases of  
 CC an AFB-f of AEA22417-AEA22452 or their fragments or variations and a  
 CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
 CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
 CC comparing the product from the specimen with a nucleotide sequence from a  
 CC database to determine the bacterium species present in the specimen. The  
 CC methods are useful for determining a bacterium species. The present  
 CC sequence represents a Mycobacterium fortuitum 16S rRNA nucleotide  
 CC sequence, which is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 1449 BP; 322 A; 342 C; 495 G; 290 T; 0 U; 0 Other;  
 Query Match 91.6%; Score 17.4; DB 14; Length 1449;  
 Best Local Similarity 94.7%; Pred. No. 55;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GAACGGAAGCCCTTCGG 19  
 |||||  
 Db 27 GAACGGAAGCCCTTCGG 45

RESULT 17  
 AEA22412  
 ID AEA22412 standard; DNA; 1455 BP.  
 XX  
 AC AEA22412;  
 XX  
 DT 25-AUG-2005 (first entry)  
 XX

XX Mycobacterium mucogenicum 16S rRNA sequence SEQ ID NO:13.  
DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
KW Mycobacterium mucogenicum.  
OS US2005130168-A1.  
XX 16-JUN-2005.  
XX 31-OCT-2003; 2003US-00697802.  
XX 31-OCT-2003; 2003US-00697802.  
XX (HANX/) HAN X.  
XX (PHAM/) PHAM A S.  
XX Han X, Pham AS;  
XX WPI; 2005-424597/43.  
XX Determining a bacterium species comprises providing oligonucleotide  
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
XX Disclosure; SEQ ID NO 13; 74pp; English.  
XX The invention relates to a method (M1) for determining a bacterium  
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
CC extracting a genomic nucleotide from the bacterium to provide a  
CC nucleotide template; (c) annealing a region of a nucleotide template to a  
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
CC complimentary fashion, the primer set designed to provide a product  
CC having a predetermined size dictated by a complimentary primer set; (d)  
CC amplifying the region of the nucleotide template to produce the product;  
CC and (e) determining a species of a bacterium in a nucleotide sequence of  
CC the product. Also described is an alternative method (M2) for determining  
CC a bacterium species comprising: (a) providing a specimen or a sample  
CC having a template; (b) providing a pair of primers selected from: (i) a  
CC first forward primer having consecutive bases of an APB-f comprising any  
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
CC or variations, and a first reverse primer having consecutive bases of an  
CC bp (AEA22489-AEA22516) or their fragments or variations, and a second  
CC reverse primer having consecutive bases of an UB-r comprising any of the  
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
CC variations, or (iii) a first forward primer having consecutive bases of  
CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a  
CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
CC comparing the product from the specimen with a nucleotide sequence from a  
CC database to determine the bacterium species present in the specimen. The  
CC methods are useful for determining a bacterium species. The present  
CC sequence represents a Mycobacterium mucogenicum 16S rRNA nucleotide  
CC sequence, which is used in the exemplification of the present invention.  
XX SQ Sequence 1455 BP; 321 A; 347 C; 500 G; 287 T; 0 U; 0 Other;  
Query Match 91.6%; Score 17.4; DB 14; Length 1455;  
Best Local Similarity 94.7%; Pred. No. 55;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAACGGAAGGCGCTTCGG 19  
DB 37 GAACGGAAGGCGCTTCGG 55  
RESULT 18  
AEA22404  
ID AEA22404 standard; DNA; 1482 BP.  
XX

AC AEA22404;  
XX 25-AUG-2005 (first entry)  
XX Mycobacterium farcinogenes 16S rRNA sequence SEQ ID NO:5.  
DE microorganism identification; 16S rRNA; 16S ribosomal RNA; ds.  
XX Mycobacterium farcinogenes.  
OS US2005130168-A1.  
XX 16-JUN-2005.  
XX 31-OCT-2003; 2003US-00697802.  
XX 31-OCT-2003; 2003US-00697802.  
XX (HANX/) HAN X.  
XX (PHAM/) PHAM A S.  
XX Han X, Pham AS;  
XX WPI; 2005-424597/43.  
XX Determining a bacterium species comprises providing oligonucleotide  
PT primer set comprising SEQ-FOR and SEQ-REV in a complimentary fashion.  
XX Disclosure; SEQ ID NO 5; 74pp; English.  
XX The invention relates to a method (M1) for determining a bacterium  
CC species. (M1) comprises: (a) culturing a bacterium from a specimen; (b)  
CC extracting a genomic nucleotide from the bacterium to provide a  
CC nucleotide template; (c) annealing a region of a nucleotide template to a  
CC specific oligonucleotide primer set comprising SEQ-FOR and SEQ-REV in a  
CC complimentary fashion, the primer set designed to provide a product  
CC having a predetermined size dictated by a complimentary primer set; (d)  
CC amplifying the region of the nucleotide template to produce the product;  
CC and (e) determining a species of a bacterium in a nucleotide sequence of  
CC the product. Also described is an alternative method (M2) for determining  
CC a bacterium species comprising: (a) providing a specimen or a sample  
CC having a template; (b) providing a pair of primers selected from: (i) a  
CC first forward primer having consecutive bases of an APB-f comprising any  
CC of the 36 sequences of 15-22 bp (AEA22417-AEA22452), or their fragments  
CC or variations, and a first reverse primer having consecutive bases of an  
CC bp (AEA22489-AEA22516) or their fragments or variations, and a second  
CC reverse primer having consecutive bases of an UB-r comprising any of the  
CC 28 sequences of 15-21 bp (AEA22517-AEA22544) or their fragments or  
CC variations, or (iii) a first forward primer having consecutive bases of  
CC an APB-f of AEA22417-AEA22452 or their fragments or variations and a  
CC second reverse primer having consecutive bases of an UB-r of AEA22517-  
CC AEA22544 or their fragments or variations; (c) the specimen; and (d)  
CC comparing the product from the specimen with a nucleotide sequence from a  
CC database to determine the bacterium species present in the specimen. The  
CC methods are useful for determining a bacterium species. The present  
CC sequence represents a Mycobacterium farcinogenes 16S rRNA nucleotide  
CC sequence, which is used in the exemplification of the present invention.  
XX SQ Sequence 1482 BP; 327 A; 353 C; 507 G; 295 T; 0 U; 0 Other;  
Query Match 91.6%; Score 17.4; DB 14; Length 1482;  
Best Local Similarity 94.7%; Pred. No. 55;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAACGGAAGGCGCTTCGG 19  
DB 35 GAACGGAAGGCGCTTCGG 53  
RESULT 19

```
AAD57239/c
ID  AAD57239 standard; cDNA; 1137 BP.
XX
XX  AAD57239;
AC
XX
XX  06-NOV-2003 (first entry)
DT
XX
XX  Human CGDD-19 cDNA.
DE
XX
XX  Human; cell growth, differentiation and death protein; CGDD; leukaemia;
KW  neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW  muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW  diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
KW  systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
KW  gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
KW  cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
KW  transgenic animal; gene therapy; neuroprotective; relaxant; cytosstatic;
KW  dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
KW  antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
KW  protozoacide; nootropic; gene; ss.
XX
XX  Homo sapiens.
OS
XX
XX  Key Location/Qualifiers
FH  112..687
FT  CDS
FT  /*tag= a
FT  /product= "Human CGDD-19 protein"
XX
XX  WO2003050253-A2.
XX
XX  19-JUN-2003.
XX
XX  04-DEC-2002; 2002WO-US039133.
XX
XX  07-DEC-2001; 2001US-0340747P.
XX  20-DEC-2001; 2001US-0342761P.
XX  15-JAN-2002; 2002US-0349705P.
XX  06-FEB-2002; 2002US-0354764P.
XX  12-FEB-2002; 2002US-0356216P.
XX
XX  (INCY-) INCYTE GENOMICS INC.
XX
XX  Griffin JA, Rankumar J, Emerling BM, Kable AE, Elliott VS;
PI  Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
PI  Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
PI  Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
PI  Burrill JD, Blake JJ, Ho A, Zheng W;
XX
XX  WPI; 2003-532903/50.
DR  P-PSDB; AAE37930.
XX
XX  New CGDD polypeptides, useful for diagnosing, preventing, and treating
XX  disorders associated with an abnormal expression or activity of CGDD,
XX  e.g. neuromuscular, immunological, cardiovascular disorders, cancer
XX  and/or infections.
XX
XX  Claim 5; Page 283; 299pp; English.
XX
XX  The present invention relates to novel cell growth, differentiation and
XX  death (CGDD) proteins and polynucleotides encoding them. The sequences of
XX  the invention are useful in diagnosing, preventing and treating disorders
XX  associated with an abnormal expression or activity of CGDD such as
XX  neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
XX  disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
XX  endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
XX  leukaemia, cervical or breast cancers), immunological disorders (e.g.
XX  scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
XX  disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
XX  syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
XX  protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
XX  and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
XX  create humanised animals or transgenic animals to model human diseases.
XX  The invention is also used in gene therapy. The present sequence is human
```

```
CC  CGDD-19 cDNA
XX
XX  Sequence 1137 BP; 317 A; 274 C; 296 G; 250 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 89.5%; Score 17; DB 9; Length 1137;
XX  Best Local Similarity 100.0%; Pred. NO. 88;
XX  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 GAACGGAAGGCGCTTTC 17
QY  |||||
DB  1070 GAACGGAAGGCGCTTTC 1054
XX
XX  RESULT 20
XX  AAV24413
ID  AAV24413 standard; preRNA; 23 BP.
XX
XX  AAV24413;
AC
XX
XX  24-AUG-1998 (first entry)
DT
XX
XX  Target sequence #2 for M. intracellulare specific probe.
DE
XX
XX  Probe; target sequence; hybridisation; mycobacterial cell sensitivity;
KW  antimicrobial agent; pre-rRNA detection; ss.
XX
XX  Synthetic.
OS  Mycobacterium intracellulare.
XX
XX  US5770373-A.
XX
XX  23-JUN-1998.
XX
XX  08-NOV-1996; 96US-00745638.
XX
XX  16-JUN-1994; 94US-00261068.
XX  07-JUN-1995; 95US-00485602.
XX
XX  (BECT ) BECTON DICKINSON & CO.
XX
XX  Cangelosi GA, Britschgi TB;
XX
XX  WPI; 1998-376792/32.
XX
XX  Mycobacterial sensitivity and drug screening assays - involving release
XX  of pre-rRNA by lysis.
XX
XX  Example 4; Col 17-18; 50pp; English.
XX
XX  This sequence represents a target sequence for mycobacterial probes. This
XX  sequence represents a precursor RNA fragment that is released during the
XX  method of the invention. The method is for the determination of
XX  mycobacterial cell sensitivity to an antimicrobial agent, and comprises:
XX  (a) culturing the cells in the presence of the antimicrobial agent; (b)
XX  treating the cells by enzymatic or mechanical means to expose the cell
XX  membrane to lysis reagents, and contacting the cells with a lysis reagent
XX  under conditions such that pre-rRNA is released from the cells but not
XX  degraded; and (c) detecting the pre-rRNA with an oligonucleotide probe
XX  capable of hybridising to a region of the pre-rRNA that is not present in
XX  mature mycobacterial rRNA, where sensitivity to the antimicrobial agent
XX  is indicated by an increase or decrease in pre-rRNA levels for cells
XX  exposed to the antimicrobial agent compared with mycobacterial cells not
XX  exposed to the antimicrobial agent. The lysis method, unlike known
XX  methods, results in detectable levels of pre-rRNA
XX
XX  Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;
SQ
XX
XX  Query Match 86.3%; Score 16.4; DB 2; Length 23;
XX  Best Local Similarity 78.9%; Pred. No. 1.3e+02;
XX  Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX  1 GAACGGAAGGCGCTTCG 19
QY  |||||
```

```

Db      1 GAACGGAAGNCCCUCCG 19

RESULT 21
AAV13021
ID      AAV13021 standard; rRNA; 23 BP.
XX
AC      AAV13021;
XX
DT      18-MAY-1998 (first entry)
XX
DE      Mycobacterium intracellulare mature rRNA target sequence SEQ ID NO:56.
XX
DE      Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
KW      hybridisation; antibiotic resistance; cell lysis; ss.
XX
OS      Mycobacterium intracellulare.
XX
PN      US5712095-A.
XX
PD      27-JAN-1998.
XX
PF      07-JUN-1995; 95US-00485602.
XX
PR      16-JUN-1994; 94US-00261068.
XX
PA      (BECT ) BECTON DICKINSON CO.
XX
PI      Cangelosi GA, Britschgi TB;
XX
DR      WPI; 1998-119975/11.
XX
XX      Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
PT      with specific probes after cell lysis.
XX
PS      Disclosure; Col 18; 54pp; English.
XX
CC      The present sequence represents a mycobacterial mature ribosomal RNA
CC      target sequence. The present invention describes a method for detecting
CC      pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
CC      treating the cells to release pre-rRNA by: (i) pretreating the cells by
CC      enzymatic degradation using both lysozyme and protease until their cell
CC      walls are rendered porous to expose their cell membranes, making the
CC      cells susceptible to lysis; (ii) contacting the pretreated cells with a
CC      combination of a magnesium chelator, a nonionic detergent and an anionic
CC      detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
CC      mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
CC      least one oligonucleotide probe which is capable of selectively
CC      hybridizing to a region of the pre-rRNA that is not present in a mature
CC      mycobacterial rRNA. The probes can be used to identify many Mycobacterium
CC      spp. including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
CC      M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
CC      intracellulare. The probes may also be used to measure mycobacterial
CC      response to inhibitors of RNA and protein synthesis and may therefore be
CC      used to screen new antimycobacterial drugs. Mycobacteria have a slow
CC      growth rate. By using the probes, drug developers can now identify
CC      compounds that are more effective, but less stable than those previously
CC      identified
XX
SQ      Sequence 23 BP; 6 A; 6 C; 7 G; 0 T; 3 U; 1 Other;

Query Match      86.3%; Score 16.4; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY      1 GAACGGAAGCCTTTCCG 19
        ||||| ||| :|||
Db      1 GAACGGAAGNCCCUCCG 19

RESULT 22
AAV24418
ID      AAV24418 standard; preRNA; 25 BP.
XX
XX      Mycobacterium habana mature rRNA target sequence SEQ ID NO:61.
XX      Mycobacterium; pre-rRNA; precursor ribosomal RNA; target sequence; probe;
KW      hybridisation; antibiotic resistance; cell lysis; ss.

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```

XX OS Mycobacterium simiae.
XX PN US5712095-A.
XX PD 27-JAN-1998.
XX PF 07-JUN-1995; 95US-00485602.
XX PR 16-JUN-1994; 94US-00261068.
XX PA (BECT ) BECTON DICKINSON CO.
XX PI Cangelosi GA, Britschgi TB;
XX PR WPI; 1998-119975/11.
XX PT Assay for pre-ribosomal RNA in mycobacterium cells - by hybridisation
XX PS with specific probes after cell lysis.
XX PS Disclosure; Col 18; 54pp; English.
XX CC The present sequence represents a mycobacterial mature ribosomal RNA
XX CC target sequence. The present invention describes a method for detecting
XX CC pre-rRNA in cells of a mycobacterial sample. The method comprises: (a)
XX CC treating the cells to release pre-rRNA by: (i) pretreating the cells by
XX CC enzymatic degradation using both lysozyme and protease until their cell
XX CC walls are rendered porous to expose their cell membranes, making the
XX CC cells susceptible to lysis; (ii) contacting the pretreated cells with a
XX CC combination of a magnesium chelator, a nonionic detergent and an anionic
XX CC detergent; and (iii) heating the cells to 75-99 degrees Celsius until the
XX CC mycobacterial cells are lysed; and (b) detecting the pre-rRNA using at
XX CC least one oligonucleotide probe which is capable of selectively
XX CC hybridizing to a region of the pre-rRNA that is not present in a mature
XX CC mycobacterial RNA. The probes can be used to identify many Mycobacterium
XX CC spp, including M. tuberculosis, M. leprae, M. habana, M. avium, M. bovis,
XX CC M. lufu, M. paratuberculosis, M. marinum, M. simiae and/or M.
XX CC intracellulare. The probes may also be used to measure mycobacterial
XX CC response to inhibitors of RNA and protein synthesis and may therefore be
XX CC used to screen new antimycobacterial drugs. Mycobacteria have a slow
XX CC growth rate. By using the probes, drug developers can now identify
XX CC compounds that are more effective, but less stable than those previously
XX CC identified. (Updated on 17-OCT-2003 to standardise OS field)
XX SQ Sequence 25 BP; 6 A; 7 C; 7 G; 0 T; 3 U; 2 Other;

Query Match 86.3%; Score 16.4; DB 2; Length 25;
Best Local Similarity 78.9%; Pred. No. 1.3e+02;
Matches 15; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Dy 2 GAACGGAAGGCCUCCG 20
    |||||

RESULT 24
ADA68711/C
ID ADA68711 standard; DNA; 765 BP.
XX AC ADA68711;
XX XX
XX 20-NOV-2003 (first entry)
XX DE Rice gene, SEQ ID 2034.
XX PR Plant; bacterial infection; fungal infection; viral infection; rice;
XX KW gene; ds.
XX PR Oryza sativa.
XX OS
XX PN WO2003000898-A1.
XX PD 03-JAN-2003.

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```

XX 22-JUN-2001; 2001WO-IB001105.
XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX PR WPI; 2003-175290/17.
XX PT Identifying at least one gene involved in plant resistance or response to
XX PT pathogenic infection for conferring resistance or tolerance to a plant to
XX PT bacterial, fungal or viral infection by determining or detecting plant
XX PT gene expression.
XX PS Claim 6; SEQ ID NO 2034; 899pp; English.
XX CC The present invention relates to a method (M1) for identifying genes
XX CC involved in plant resistance or response to pathogenic infection. M1
XX CC comprises identifying a gene whose expression is significantly altered in
XX CC the incompatible interaction of plant gene expression relative to
XX CC expression of the gene in an uninfected plant, in a mutant plant that
XX CC does not express a gene associated with response to pathogenic infection,
XX CC or in a corresponding incompatible or compatible interaction. (M1) is
XX CC useful for conferring resistance to resistance or tolerance to a plant to
XX CC bacterial, fungal or viral infection. The present sequence was used to
XX CC illustrate the invention.
XX SQ Sequence 765 BP; 207 A; 171 C; 153 G; 216 T; 0 U; 18 Other;

Query Match 85.3%; Score 16.2; DB 8; Length 765;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTCGG 19
    |||||
Dy 725 GAAVGAARGTCCTTCGR 707
    |||||

RESULT 25
AAA02278
ID AAA02278 standard; cDNA; 935 BP.
XX AC AAA02278;
XX XX
XX 19-MAY-2000 (first entry)
XX DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2269.
XX KW Human; colon cancer; tumour; diagnosis; gene expression product; probe;
XX KW detection; cancerous state; metastasis; identification; breast cancer;
XX KW oestrogen receptor-positive breast cancer; therapy;
XX KW oestrogen receptor-negative breast cancer; lung cancer; ss.
XX OS Homo sapiens.
XX PN WO9958675-A2.
XX PD 18-NOV-1999.
XX PF 13-MAY-1999; 99WO-US010602.
XX PR 14-MAY-1998; 98US-0085426P.
XX PR 15-MAY-1998; 98US-0085537P.
XX PR 15-MAY-1998; 98US-0085696P.
XX PR 21-OCT-1998; 98US-0105234P.
XX PR 27-OCT-1998; 98US-0105877P.
XX PA (CHIR ) CHIRON CORP.
XX PA (HYSE-) HYSEQ INC.
XX XX

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PI Genilloud O, Mellado RP, Parro V, Rodriguez V;  
XX WPI; 1999-229548/19.  
XX  
XX New probes used for detection of maduromycetes bacteria and to  
XX differentiate between maduromycetes and streptomycetes.  
XX  
XX Disclosure; Fig 1; 22pp; English.  
XX  
XX The invention relates to a novel nucleic acid probe hybridises to a  
XX nucleic acid encoding a portion of 16S rRNA of maduromycetes bacteria  
XX under hybridisation conditions, and does not hybridise to nucleic acids  
XX encoding a portion of 16S rRNA of streptomycetes under identical  
XX hybridisation conditions. The probes can be used for detecting the  
XX presence of maduromycetes bacteria in a sample and for differentiating  
XX between maduromycetes and streptomycetes bacteria in a sample. The  
XX present sequence represents a preferred probe of the invention  
XX  
XX Sequence 166 BP; 39 A; 43 C; 55 G; 29 T; 0 U; 0 Other;  
SQ  
Query Match 83.2%; Score 15.8; DB 2; Length 166;  
Best Local Similarity 89.5%; Pred. No. 3.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 GAACGGAAGGCCTTTCGG 19  
Db 63 GAGCGGAAGGCCTTTCGG 81  
RESULT 28  
ID AAA31293 standard; DNA; 170 BP.  
XX  
XX AAA31293;  
XX  
XX 05-JUL-2000 (first entry)  
XX  
XX Plant microsatellite marker #254.  
XX  
XX Plant microsatellite sequence; core repeat sequence; detection; probe;  
XX DNA polymorphism; genome mapping; physical mapping; fingerprinting;  
XX variety identification; genetic variability evaluation; primer; ss.  
XX  
XX Eucalyptus grandis.  
XX  
XX WO9967421-A1.  
XX  
XX 29-DEC-1999.  
XX  
XX 25-JUN-1999; 99WO-NZ000092.  
XX  
XX 25-JUN-1998; 98US-00105307.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FOREST LTD.  
XX  
XX Havukkala IJ, Bloksberg LN, Glenn M;  
XX WPI; 2000-116958/10.  
XX  
XX 29-DEC-1999.  
XX  
XX 25-JUN-1999; 99WO-NZ000092.  
XX  
XX 25-JUN-1998; 98US-00105307.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FOREST LTD.  
XX  
XX Havukkala IJ, Bloksberg LN, Glenn M;  
XX WPI; 2000-116958/10.  
XX  
XX New plant microsatellite markers and associated flanking species for the  
XX detection of polymorphic genetic markers.  
XX  
XX Claim 1; Page 151; 392pp; English.  
XX  
XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences  
XX and associated flanking species. The sequences comprise a central core  
XX repeat sequence, especially selected from the sequences AAA32094-A32096  
XX with left and right flanking sequences. The polynucleotide sequences can  
XX be used in the detection of DNA polymorphisms, in genome mapping, in  
XX physical mapping, in positional cloning of genes, in variety  
XX identification and in evaluation of genetic variability within and  
XX between plant tissues, populations, cultivars, species and species  
XX  
XX Claim 1; Page 151; 392pp; English.  
XX  
XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences  
XX and associated flanking species. The sequences comprise a central core  
XX repeat sequence, especially selected from the sequences AAA32094-A32096  
XX with left and right flanking sequences. The polynucleotide sequences can  
XX be used in the detection of DNA polymorphisms, in genome mapping, in  
XX physical mapping, in positional cloning of genes, in variety  
XX identification and in evaluation of genetic variability within and  
XX between plant tissues, populations, cultivars, species and species

CC groups. They may also be used to design hybridization probes for  
CC oligonucleotide fingerprinting and library screening and to design  
CC primers for microsatellite-primed PCR. Microsatellite markers are useful  
CC to locate specific economically useful genes in plant genomes  
XX  
XX Sequence 170 BP; 44 A; 35 C; 65 G; 22 T; 0 U; 4 Other;  
SQ  
Query Match 83.2%; Score 15.8; DB 3; Length 170;  
Best Local Similarity 89.5%; Pred. No. 3.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 GAACGGAAGGCCTTTCGG 19  
Db 69 GAAGGGAAGGCCTTTCGG 87  
RESULT 29  
ID AAA31415 standard; DNA; 305 BP.  
XX  
XX AAA31415;  
XX  
XX 05-JUL-2000 (first entry)  
XX  
XX Plant microsatellite marker #376.  
XX  
XX Plant microsatellite sequence; core repeat sequence; detection; probe;  
XX DNA polymorphism; genome mapping; physical mapping; fingerprinting;  
XX variety identification; genetic variability evaluation; primer; ss.  
XX  
XX Eucalyptus grandis.  
XX  
XX WO9967421-A1.  
XX  
XX 29-DEC-1999.  
XX  
XX 25-JUN-1999; 99WO-NZ000092.  
XX  
XX 25-JUN-1998; 98US-00105307.  
XX  
XX (GENE-) GENESIS RES & DEV CORP LTD.  
XX (FLET-) FLETCHER CHALLENGE FOREST LTD.  
XX  
XX Havukkala IJ, Bloksberg LN, Glenn M;  
XX WPI; 2000-116958/10.  
XX  
XX New plant microsatellite markers and associated flanking species for the  
XX detection of polymorphic genetic markers.  
XX  
XX Claim 1; Page 187; 392pp; English.  
XX  
XX Sequences AAA31040-A32093 represent novel plant microsatellite sequences  
XX and associated flanking species. The sequences comprise a central core  
XX repeat sequence, especially selected from the sequences AAA32094-A32096  
XX with left and right flanking sequences. The polynucleotide sequences can  
XX be used in the detection of DNA polymorphisms, in genome mapping, in  
XX physical mapping, in positional cloning of genes, in variety  
XX identification and in evaluation of genetic variability within and  
XX between plant tissues, populations, cultivars, species and species  
XX  
XX oligonucleotide fingerprinting and library screening and to design  
XX primers for microsatellite-primed PCR. Microsatellite markers are useful  
XX to locate specific economically useful genes in plant genomes  
XX  
XX Sequence 305 BP; 82 A; 67 C; 121 G; 35 T; 0 U; 0 Other;  
SQ  
Query Match 83.2%; Score 15.8; DB 3; Length 305;  
Best Local Similarity 89.5%; Pred. No. 3.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 GAACGGAAGGCCTTTCGG 19  
||| ||||||||| |||

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Db 70 GAAGGGAAGGCGCTTTAGG 88

RESULT 30
ABZ76674
ID ABZ76674 standard; DNA; 460 BP.
XX AC ABZ76674;
XX DT 30-APR-2003 (first entry)
XX DE Microtetraspora recticatena IFO14525 DNA sequence SEQ ID NO:5.
XX KW Streptomyces sp. TW-7; pravastatin; compactin; hyperlipidaemia;
XX KW antilipaeamic; microorganism; gene; ds.
XX OS Nonomuraea recticatena.
XX PN WO200299109-A1.
XX PD 12-DEC-2002.
XX PF 30-MAY-2002; 2002WO-JP005252.
XX PR 01-JUN-2001; 2001JP-00166412.
XX PA (SAOC ) MERCIAN CORP.
XX PI Fujii T, Hirose S, Aritoku Y, Morimiya T, Johdo O, Ishiki K;
XX WP1; 2003-148672/14.
XX PT Novel Streptomyces sp. produced polypeptide for hydroxylation of
PT compactin at 6beta-position and its encoded DNA, applicable in
PT constructing transformant microbes to synthesize pravastatin for treating
PT hyperlipedemia.
XX PS Disclosure; Page 50-51; 67pp; Japanese.
XX CC The present invention describes a DNA sequence which contains a base
CC sequence from bases 544-1758 in the sequence of (I) with 1992 base pairs,
CC or a DNA hybridisable with the DNA under stringent conditions and
CC encoding a polypeptide with hydroxylase activity on compactin at 6beta-
CC position. Also described: (1) DNA containing base sequences from bases
CC 544-1758 and from bases 1782-1970 in the sequence of (I) or a DNA
CC hybridisable with the DNA under stringent conditions and encoding a
CC polypeptide with hydroxylase activity on compactin at the 6beta-position;
CC (2) a polypeptide encoded by any of the DNA or containing an amino acid
CC sequence based on the polypeptide but with some amino acids deleted,
CC substituted or added and having hydroxylase activity on compactin at the
CC 6beta-position; (3) a recombinant DNA obtained by integrating with any of
CC the DNA; (4) a microorganism transferred with the recombinant DNA; (5) a
CC process for producing pravastatin by culturing the transformant
CC microorganism before isolating the culture liquor or cells, and addition
CC of compactin for reaction to give pravastatin for recovery; and (6)
CC Streptomyces sp. TW-6 (FERM BP-8002) or TW-7 (FERM BP-8003). (I) has
CC antilipaeamic activity. The polypeptide and its encoded DNA are applicable
CC in constructing transformant microorganisms to synthesise pravastatin for
CC treating hyperlipidaemia. With the recombinant microorganisms,
CC pravastatin can be produced efficiently, with much less galpha
CC hydroxylated epimer formed. The present sequence represents a
CC Microtetraspora recticatena IFO14525 nucleotide sequence, which is given
CC in the exemplification of the present invention
XX SQ Sequence 460 BP; 97 A; 119 C; 166 G; 78 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 8; Length 460;
Best Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 37 GAGCGGAAGGCGCTTTTCGG 55

RESULT 31
AEB72673
ID AEB72673 standard; DNA; 497 BP.
XX AC AEB72673;
XX DT 06-OCT-2005 (first entry)
XX DE Streptosporangium sp. AF935 16S rDNA, SEQ ID 2.
XX KW cyclosporin; cyclosporin A; ds.
XX OS Streptosporangium sp.
XX PN JP2005198543-A.
XX PD 28-JUL-2005.
XX PF 15-JAN-2004; 2004JP-00007488.
XX PR 15-JAN-2004; 2004JP-00007488.
XX PA (SAOC ) MERCIAN CORP.
XX PI Ota K, Uematsu H, Kaneko K, Tsuchida T;
XX WP1; 2005-537020/55.
XX PT Producing cyclosporin derivative useful as reference standard for
PT quantitative measurement of cyclosporin A in blood, by incubating
PT cyclosporin A in presence of Dactylosporangium and extracting cyclosporin
PT derivative.
XX PS Disclosure; SEQ ID NO 2; 12pp; Japanese.
XX CC The invention relates to a novel method for producing a cyclosporin
CC derivative. The method involves incubating cyclosporin A in the presence
CC of a strain belonging to Dactylosporangium, Streptomycetes, Nocardia,
CC Pseudonocardia or Streptosporangium or its cultured microbial cells and
CC extracting the cyclosporin derivative from the incubated liquid. The
CC cyclosporin derivative is used as a reference standard for quantitative
CC measurement of cyclosporin A and its metabolite in blood and urine. This
CC polynucleotide represents a Streptosporangium 16S rDNA sequence used in
CC the cyclosporin production method of the invention.
XX SQ Sequence 497 BP; 105 A; 121 C; 178 G; 93 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 497;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 60 GAGCGGAAGGCGCTTTTCGG 78

RESULT 32
AED64356
ID AED64356 standard; DNA; 500 BP.
XX AC AED64356;
XX DT 12-JAN-2006 (first entry)
XX DE Rhodococcus sp. 16S rDNA, SEQ ID 1.
XX KW 16S ribosomal RNA; 16S rRNA; ds.
XX OS Rhodococcus sp.; Z-35-1 strain.
XX PN JP2005304498-A.
```







QY 1 GAACGGAAAGCCCTTCGG 19  
 |||||  
 Db 32 GAGCGGAAAGCCCTTCGG 50

## RESULT 37

ADW16290  
 ID ADW16290 standard; DNA; 1427 BP.

XX AC ADW16290;

DT 07-APR-2005 (first entry)

XX DNA copy of the Actinomycete 16S ribosomal RNA EN47 isolate.

XX 16S ribosomal RNA; ds; 16S rRNA; medicinal plant; plant breeding;  
 KW disease resistance; insect resistance; crop improvement;  
 KW plant growth factor; antibacterial; antimicrobial; fungicide;  
 KW insecticide; nematocide.

XX Actinomycetales.

XX OS Actinomycetales.

XX PN W02005003328-A1.

XX PD 13-JAN-2005.

XX PF 07-JUL-2004; 2004WO-AU000914.

XX PR 07-JUL-2003; 2003US-0485241P.

XX PR 22-SEP-2003; 2003US-0504703P.

XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.

XX PI Franco CMM, Coombs JT;

XX DR WPI; 2005-091806/10.

XX Improving plant productivity comprises introducing into the plant or  
 PT propagation material an endophytic actinomycete that facilitates  
 PT induction of at least one characteristic related to improved  
 PT productivity.

XX Example 18; Fig 19; 235pp; English.

XX This invention relates to a novel method for improving plant  
 CC productivity. Specifically, it refers to introducing into the plant or  
 CC propagation material an endophytic actinomycetes or variant thereof,  
 CC where the actinomycetes facilitate induction of a characteristic related  
 CC to improved productivity. The present invention further describes  
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin  
 CC or cytokinin that are able to induce disease resistance in plants i.e.  
 CC provide disease bio-control capabilities against pathogen infection.  
 CC Accordingly, the method facilitates the improvement of cereal crop  
 CC productivity including increasing germination by up-regulating plant  
 CC growth promoting activities, as well as improving plant vigor or flower  
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is  
 CC useful in the manufacture of a medicament for the therapeutic and/or  
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.  
 CC plant. As such, this method provides plant protectants and plant growth  
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,  
 CC insecticide and nematocide activities. This polynucleotide is the DNA  
 CC sequence of an actinomycetes 16S ribosomal RNA sequence of the invention.

XX Sequence 1427 BP; 326 A; 351 C; 471 G; 277 T; 0 U; 2 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 1427;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19  
 |||||  
 Db 31 GAGCGGAAAGCCCTTCGG 49

## RESULT 38

ADC61232  
 ID ADC61232 standard; DNA; 1439 BP.

XX AC ADC61232;

XX DT 18-DEC-2003 (first entry)

XX Baeyer-Villiger enzyme 16S rDNA gene from Rhodococcus erythropolis AN12.

XX Baeyer-Villiger; BV; monooxygenase; ketone substrate; lactone; ester;  
 KW 16S rDNA; ds.

XX Rhodococcus erythropolis.

XX WO2003020890-A2.

XX PD 13-MAR-2003.

XX PF 29-AUG-2002; 2002WO-US027549.

XX PR 29-AUG-2001; 2001US-0315546P.

XX (DUPO ) DU PONT DE NEMOURS & CO E I.

XX Brامucci MG, Brzostowicz PC, Kostichka KN, Nagarajan V;  
 PI Rouviere PE, Thomas SM;

XX WPI; 2003-313085/30.

XX Novel nucleic acid fragment useful for converting ketone substrates to  
 PT the corresponding lactone or ester, is isolated from Rhodococcus,  
 PT Arthrobacter or Acidovorax, encoding Baeyer-Villiger monooxygenase  
 PT polypeptide.

XX Claim 54; SEQ ID NO 6; 225pp; English.

XX The invention relates to a novel isolated nucleic acid fragment  
 CC comprising a fragment encoding a Baeyer-Villiger (BV) monooxygenase  
 CC polypeptide having a sequence of 542, 541, 439, 518, 462, 523, 493, 539,  
 CC 649, 494, 499, 545, 532 or 538 amino acids defined in the specification;  
 CC a nucleic acid molecule that hybridises with the above sequence under the  
 CC hybridisation conditions; or their complements. The BV monooxygenase  
 CC fragment is useful for obtaining a nucleic acid fragment encoding a BV  
 CC monooxygenase polypeptide, by probing a genomic library with the  
 CC fragment, identifying a DNA clone that hybridises with the fragment, and  
 CC sequencing the genomic fragment that comprises the above identified  
 CC clone, where the sequenced genomic fragment encodes a BV monooxygenase  
 CC polypeptide. The genes and their products are useful for converting  
 CC suitable ketone substrates to the corresponding lactone or ester. This  
 CC polynucleotide sequence represents the 16S rDNA gene from Arthrobacter  
 CC sp. BP2 relating to the Baeyer-Villiger enzymes of the invention.

XX Sequence 1439 BP; 333 A; 357 C; 465 G; 283 T; 0 U; 1 Other;

Query Match 83.2%; Score 15.8; DB 10; Length 1439;  
 Best Local Similarity 89.5%; Pred. No. 3.8e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCCTTCGG 19  
 |||||  
 Db 38 GAGCGGTAAGCCCTTCGG 56

## RESULT 39

ADZ35975  
 ID ADZ35975 standard; DNA; 1440 BP.

XX AC ADZ35975;

XX DT 30-JUN-2005 (first entry)

XX	Verrucosisspora sp. AB-18-032 16S rRNA gene.
DE	
XX	
XX	ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
KW	polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;
KW	vitamin; abyssomicin B; abyssomicin C; abyssomicin D;
KW	Staphylococcus aureus infection; protozoal infection;
KW	Plasmodium infection; Leishmania infection; chagas disease;
KW	Gram positive bacteria infection; mrsa infection .
XX	
OS	Verrucosisspora sp. AB-18-032.
XX	
XX	WO2005033114-A1.
XX	
PD	14-APR-2005.
XX	
XX	23-SEP-2004; 2004WO-EP010661.
XX	
PR	01-OCT-2003; 2003DE-01047472.
PR	11-NOV-2003; 2003DE-01053300.
XX	
PA	(UYTU-) UNIV TUEBINGEN.
XX	
PI	Fiedler H, Suessmuth R, Zaehner H, Bull A;
DR	WFI; 2005-296122/30.
XX	
XX	New abyssomicin polycyclic macrolactone compounds, useful as antibiotics
PT	and antiprotozoal agents effective against multidresistant strains,
PT	prepared using bacteria of genus Verrucosisspora.
XX	
XX	Disclosure; SEQ ID NO 1; 47pp; German.
CC	
CC	This invention describes novel polycyclic macrolactones and their
CC	derivatives , prepared using bacteria of genus Verrucosisspora and
CC	designated abyssomicins. The polycyclic macrolactones have at least one
CC	oxa-bicyclo system as a partial structure and at least one Michael system
CC	as double bond system. The polycyclic macrolactones are prepared by
CC	culturing Verrucosisspora strain AB 18-032, recovering a culture
CC	supernatant from the culture, optionally preparing a culture filtrate and
CC	optionally isolating one or more polycyclic macrolactones from the
CC	supernatant and/or filtrate. Alternatively the microorganism is cultured
CC	followed by isolating one or more polycyclic macrolactones from the
CC	microorganism. The Verrucosisspora strain AB 18-032 was isolated from
CC	marine sediment collected at a depth of 1000m in Sagami bay in the
CC	Japanese Sea and is deposited as DSM No. 15899. The polycyclic
CC	macrolactones inhibit the biosynthesis of p-Aminobenzoic acid, (an
CC	essential component in the biosynthesis of folic acid) from chorismic
CC	acid, thus inhibiting folic acid biosynthesis. The vitamin folic acid is
CC	essential to the life of microorganisms, especially prokaryotes and
CC	protozoa. The polycyclic macrolactones do not inhibit the biosynthesis of
CC	folic acid in mammals (including humans), and thus have no adverse
CC	effects on mammalian cells. Three polycyclic macrolactones are
CC	specifically claimed, i.e. abyssomicin B, abyssomicin C and abyssomicin
CC	D. Abyssomicin C strongly inhibited growth of methicillin-resistant
CC	Staphylococcus aureus strain N315 and vancomycin-resistant Staphylococcus
CC	aureus strain Mu50. The products of the invention are useful as
CC	antibiotics (especially effective against Gram positive bacteria) and
CC	antiprotozoal agents, specifically effective against bacteria and
CC	protozoa resistant (especially multi-resistant) to conventional
CC	antibiotics. Typically polycyclic macrolactones are useful for combating
CC	tropical protozoal diseases (e.g. malaria, leishmaniasis, sleeping
CC	sickness and Chagas disease) and infections caused by resistant Gram
CC	positive bacteria such as methicillin- and vancomycin-resistant
CC	Staphylococcus aureus strains. Polycyclic macrolactones are also useful
CC	as disinfectants (especially in hospitals and other medical
CC	establishments) and as lead structures for the development of further
CC	active agents. This sequence represents the Verrucosisspora strain AB 18-
CC	032 16S rRNA DNA which is used to phylogenically classify the bacterial
XX	strain.
XX	
XX	Sequence 1440 BP; 313 A; 363 C; 500 G; 264 T; 0 U; 0 Other
SQ	

Query Match	83.2%;	Score 15.8;	DB 14;	Length 1440;
Best Local Similarity	89.5%;	Pred. No. 3.8e+02;		
Matches	17;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

Qy	1	GAACGGAAAGCCCTTCGG	19
Db	7	GAGCGGAAAGCCCTTCGG	25

RESULT 40	
ADX38843	
ID	ADX38843 standard; DNA; 1443 BP.
XX	
AC	ADX38843;
XX	
DT	05-MAY-2005 (first entry)
XX	
DE	Microbispora 16S rDNA.
XX	
KW	antibiotic; bacterial infection; animal growth; 16S rDNA; ds;
KW	antibacterial; anabolic.
XX	
OS	Microbispora sp. ATCC PTA-5024.
XX	
PN	WO2005014628-A1.
XX	
PD	17-FEB-2005.
XX	
PF	12-JUL-2004; 2004WO-EF007658.
XX	
PR	18-JUL-2003; 2003EP-00016306.
XX	
PA	(VICU-) VICURON PHARM INC.
XX	
PI	Lazzarini A, Gastaldo L, Candiani G, Ciciliato I, Losi D;
PI	Marinelli F, Selva E, Parenti F;
XX	
DR	WPI; 2005-173079/18.
XX	
PT	New antibiotic 107891 complex comprising Factor A1 and Factor A2 and
PT	having specified physico-chemical characteristics, used to form
PT	medicament for the treatment or prevention of bacterial infections, or
PT	used as animal growth promoter.
XX	
PS	Disclosure; SEQ ID NO 1; 85pp; English.
XX	
CC	The invention relates to an antibiotic 107891 complex comprising Factor
CC	A1 and Factor A2. The antibiotic is used to form a pharmaceutical
CC	composition used as medicament for the treatment or prevention of
CC	bacterial infections, or as animal growth promoter. The present sequence
CC	represents the Microbispora 16S rDNA.
XX	
SQ	Sequence 1443 BP; 308 A; 352 C; 504 G; 279 T; 0 U; 0 Other;

Query Match	83.2%;	Score 15.8;	DB 14;	Length 1443;
Best Local Similarity	89.5%;	Pred. No. 3.8e+02;		
Matches	17;	Conservative	0;	Mismatches 2; Indels 0; Gaps 0;

Qy	1	GAACGGAAAGCCCTTCGG	19
Db	37	GAGCGGAAAGCCCTTCGG	55

RESULT 41	
AEA22406	
ID	AEA22406 standard; DNA; 1461 BP.
XX	
AC	AEA22406;
XX	
DT	25-AUG-2005 (first entry)
XX	
DE	Mycobacterium gordonae 16S rRNA sequence SEQ ID NO:7.
XX	



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Query Match      83.2%; Score 15.8; DB 14; Length 1483;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 38 GAGCGGTAAGGCTTTCGG 56

RESULT 43
ADR90327
ID ADR90327 standard; DNA; 1511 BP.
XX
AC ADR90327;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-15 bioremediation-related 16S rDNA.
XX
KW alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
XX
OS Rhodococcus sp.
XX
PN JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WPI; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
Claim 1; SEQ ID NO 3; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-15 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 342 A; 362 C; 510 G; 297 T; 0 U; 0 Other;

Query Match      83.2%; Score 15.8; DB 13; Length 1511;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 57 GAGCGGTAAGGCTTTCGG 75

RESULT 44
ADR90325
ID ADR90325 standard; DNA; 1511 BP.
XX
AC ADR90325;
XX
DT 16-DEC-2004 (first entry)
XX
DE Rhodococcus sp. M-13 bioremediation-related 16S rDNA.
XX
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```
XX alkane; petroleum; bioremediation; 16S ribosomal RNA; 16S rRNA; ds.
KW Rhodococcus sp.
OS
XX JP2004261126-A.
XX
PD 24-SEP-2004.
XX
PF 03-MAR-2003; 2003JP-00056155.
XX
PR 03-MAR-2003; 2003JP-00056155.
XX
PA (EBAR ) EBARA CORP.
XX
WPI; 2004-665486/65.
XX
Evaluating the ability of an environmental sample to degrade alkanes for
PT providing alkane degrading bacteria, comprises measuring alkane degrading
PT bacteria having high resolving power of alkane present in petroleum.
XX
Claim 1; SEQ ID NO 1; 33pp; Japanese.
XX
CC The invention relates to a novel method for evaluating the ability of an
CC environmental sample to degrade alkanes. The method comprises measuring
CC the number of alkane-degrading bacteria present in the sample, where the
CC bacteria have high resolving power of a type of alkane present in
CC petroleum and gyrB (gyrase beta subunit) DNA and 16S rDNA. The method of
CC the invention may be useful for evaluating the ability of an
CC environmental sample to degrade alkanes and thus, for providing alkane-
CC degrading bacteria to be utilised in bioremediation of an environment
CC contaminated with petroleum. The method is rapid and simple. The current
CC sequence is that of the Rhodococcus sp. M-13 bioremediation-related 16S
CC ribosomal RNA gene (rDNA) of the invention.
XX
SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match      83.2%; Score 15.8; DB 13; Length 1511;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTCGG 19
DB 57 GAGCGGTAAGGCTTTCGG 75

RESULT 45
AED11327
ID AED11327 standard; DNA; 1511 BP.
XX
AC AED11327;
XX
DT 01-DEC-2005 (first entry)
XX
DE Aliphatic hydrocarbon degrading R. erythropolis strain 16S rRNA gene.
XX
KW degradation; aliphatic hydrocarbon; bioremediation; oil degradation;
KW pollutant; degradation; groundwater decontamination; 16S rRNA;
KW 16S ribosomal RNA; gene; ds.
XX
OS Rhodococcus erythropolis.
XX
PN JP2005261218-A.
XX
PD 29-SEP-2005.
XX
PF 16-MAR-2004; 2004JP-00074370.
XX
PR 16-MAR-2004; 2004JP-00074370.
XX
PA (EBAR ) EBARA CORP.
XX
PI Karube M, Tamatsubo K, Miya A;
```

XX WPI; 2005-678804/70.

XX Novel Rhodococcus erythropolis M-13 strain capable of degrading aliphatic

PT hydrocarbon, useful for bioremediation of oil-polluted environment such

PT as river water, underground water, ocean, sea cost.

PS Claim 1; SEQ ID NO 1; 14pp; Japanese.

XX The invention relates to a novel Rhodococcus erythropolis M-13 strain

CC capable of degrading aliphatic hydrocarbons. The invention further

CC provides the 16S rRNA gene of the novel strain showing 98% or more

CC homology with a nucleotide sequence of a fully defined 1511 nucleotide

CC (AED11327) sequence given in specification. The novel strain is useful

CC for the bioremediation of an oil-polluted environment, such as river

CC water, underground water, ocean, sea cost, etc. The novel strain degrades

CC linear or branched aliphatic hydrocarbons efficiently. This

CC polynucleotide sequence represents the DNA of the novel Rhodococcus

CC erythropolis M-13 strain 16S rRNA gene of the invention.

XX

SQ Sequence 1511 BP; 343 A; 367 C; 507 G; 294 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 14; Length 1511;

Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGGCTTTTCGG 19

Db 57 GAGCGGTAGGCTTTTCGG 75

RESULT 46

ADE41084

ID ADE41084 standard; rRNA; 1584 BP.

XX

AC ADE41084;

DT 29-JAN-2004 (first entry)

XX . corallina partial 16s rRNA sequence.

XX

XX Antibiotic; ss; 16s rRNA; MF-BA-1768alpal; MF-BA-1768betal;

KW Staphylococcus; Enterococcus; Streptococcus; Haemophilus; Escherichia;

KW bacterial infection.

XX

OS Microbispora corallina; strain NRRL 30420.

XX

XX US6551591-B1.

XX

PD 22-APR-2003.

XX

XX 07-SEP-2001; 2001US-00949230.

PF

XX 07-SEP-2001; 2001US-00949230.

PR

XX (ESSE-) ESSENTIAL THERAPEUTICS INC.

PA

XX Lee MD;

PI

XX WPI; 2003-895156/82.

DR

XX

XX Novel antibiotics isolated from fermentation broth of novel strain of

PT Microbispora corallina, useful for treating a wide range of bacterial

PT infections.

PT

XX Disclosure; SEQ ID NO 1; 20pp; English.

PS

XX The invention relates to antibiotic MF-BA-1768alpal or MF-BA-1768-betal

CC or its pharmaceutically acceptable salt, having physicochemical

CC characteristics in the non-salt form as detailed in the specification.

CC The antibiotics are isolated from a novel strain of Microbispora

CC corallina designated NRRL 30420. Also included are producing the above

CC antibiotic (by cultivating Microbispora corallina NRRL 30420, or an

CC antibiotic MF- BA-1768alpal or MF-BA-1768betal -producing mutant,

CC variant or its recombinant form, in a culture medium containing

CC assimilable sources of carbon, nitrogen and inorganic salts under aerobic

CC fermentation conditions until the antibiotic is produced and then

CC recovering the antibiotic) and a composition comprising the above

CC antibiotic or its salt. The antibiotics are useful for treating a

CC bacterial infection caused by Staphylococcus (e.g. S.aureus , S.epidermis

CC , S.haemolyticus ), Enterococcus (e.g. E.faecalis , E.faecium ) ,

CC Streptococcus (e.g. S.pneumoniae , S.pyrogenes ) , Haemophilus (e.g.

CC H.influenzae ) or Escherichia (e.g. E.coli ) in a patient. The present

CC sequence is partial 16S rRNA sequence from M. corallina NRRL 30420, which

CC identifies the strain.

XX

SQ Sequence 1584 BP; 339 A; 384 C; 525 G; 320 T; 0 U; 16 Other;

Query Match 83.2%; Score 15.8; DB 10; Length 1584;

Best Local Similarity 89.5%; Pred. No. 3.8e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGGCTTTTCGG 19

Db 131 GAGCGGAAGGCTTTTCGG 149

RESULT 47

AEA51361/c

ID AEA51361 standard; DNA; 1849 BP.

XX

AC AEA51361;

XX

DT 25-AUG-2005 (first entry)

XX

DE Mouse gene expressed during angiogenesis, NOC8009G23.

XX

XX angiogenesis disorder; antiangiogenic; diagnosis; pharmaceutical; cancer;

KW cytostatic; retinopathy; ophthalmological; macular degeneration;

KW corneal ulcer; antitumor; cerebrovascular ischemia; cerebroprotective;

KW vasotropic; ischemic heart disease; cardiac; infertility;

KW antiinfertility; ulcer; scleroderma; dermatological; wound healing;

KW vulnary; ischemia; myocardial infarction; angina; antianginal;

KW unstable angina; coronary arteriosclerosis; antiarteriosclerotic;

KW embolism; thrombolytic; cerebral infarction; chronic inflammation;

KW inflammatory bowel disease; psoriasis; sarcoidosis; rheumatoid arthritis;

KW antiinflammatory; gastrointestinal-gen.; antipsoriatic; antiarthritic;

KW antirheumatic; ds; gene.

XX

OS Mus.

XX

PN WO2005054426-A2.

XX

PD 16-JUN-2005.

XX

XX 06-DEC-2004; 2004WO-SE001814.

PF

XX 05-DEC-2003; 2003SE-00003268.

PR

XX 05-DEC-2003; 2003US-0481741P.

XX

PA (ANGI-) ANGIOGENETICS SWEDEN AB.

XX

XX Hellstroem M, Wallgard E, Kalen M;

PI

XX WPI; 2005-435379/44.

DR

XX New nucleic acid molecule encoding angiogenesis affecting polypeptides,

PT for treating an angiogenesis-related disorder, e.g. cancer, infertility,

PT scleroderma, wound healing, arterial thrombosis, psoriasis, or rheumatoid

PT arthritis.

PT

XX Claim 1; SEQ ID NO 44; 149pp; English.

PS

XX The present invention relates to genes and proteins associated with

CC vasculogenesis and angiogenesis related disorders. Specifically claimed

CC is an isolated nucleic acid encoding an angiogenesis affecting

CC polypeptide. The nucleic acid has the ability to stimulate or inhibit at  
 CC least one biological activity, e.g. vasculogenesis, angiogenesis,  
 CC vascular permeability, endothelial cell proliferation, endothelial cell  
 CC differentiation, endothelial cell migration, or endothelial cell  
 CC survival. Also claimed is an isolated siRNA molecule targeted to the  
 CC nucleic acid, and an antibody with specific reactivity to the nucleic  
 CC acid or peptide, which may further comprise a detectable fluorescent  
 CC label. Described is a method of treating an angiogenesis-related  
 CC condition, and a method of detecting an angiogenesis-related transcript  
 CC in a cell of a patient. The protein or nucleic acid are useful as  
 CC pharmaceuticals for affecting vasculogenesis or angiogenesis. The  
 CC angiogenesis-related disorder is cancer, retinopathy, macular  
 CC degeneration, corneal ulceration, stroke, ischemic heart disease,  
 CC infertility, ulcers, scleroderma, wound healing, ischemia, myocardial  
 CC infarction, myocardosis, angina pectoris, unstable angina, coronary  
 CC arteriosclerosis, arteriosclerosis obliterans, Berger's disease, arterial  
 CC embolism, arterial thrombosis, cerebrovascular occlusion, cerebral  
 CC infarction, cerebral thrombosis, cerebral embolism, rubeosis  
 CC proliferative vitreoretinopathy, chronic inflammation, inflammatory bowel  
 CC disease, psoriasis, sarcoidosis, or rheumatoid arthritis. The present  
 CC sequence is mouse gene N0C8009G23, identified as being expressed during  
 CC angiogenesis based on microarray data.

SQ Sequence 1849 BP; 528 A; 399 C; 369 G; 553 T; 0 U; 0 Other;  
 Query Match 83.2%; Score 15.8; DB 14; Length 1849;  
 Best Local Similarity 89.5%; Pred. No. 3.9e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTCGG 19  
 |||||  
 Db 54 GAATGGAGAGCGCTTCGG 36

RESULT 48  
 ACC47372  
 ID ACC47372 standard; cDNA; 2896 BP.

AC ACC47372;  
 DT 11-AUG-2003 (first entry)  
 DE Human late gestation lung 1 (LGL1) polypeptide encoding cDNA.  
 DE LGL1: late gestation lung 1; bronchodilator; respiratory; gene therapy;  
 KW antisense therapy; vaccine; human; gene; ss.  
 KW Homo sapiens.

OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH 32..1525  
 CDS /\*tag= a  
 FT /product= "LGL1"  
 FT  
 XX WO2003020766-A1.  
 PN  
 XX  
 XX 13-MAR-2003.  
 PD  
 XX  
 XX 04-SEP-2002; 2002WO-CA001350.  
 PF  
 XX  
 XX 04-SEP-2001; 2001CA-02357746.  
 PR  
 PR 05-DEC-2001; 2001US-0336598P.  
 XX  
 XX (UYMC-) UNIV MCGILL.  
 PA (HOSP-) HOSPITAL FOR SICK CHILDREN.  
 XX  
 XX Kaplan F, Swezey NB;  
 PI  
 XX WPI; 2003-290169/28.  
 DR P-PSDB; ABR39981.  
 DR  
 XX Novel late gestation lung 1 polypeptide and lg11 genes encoding the  
 FT polypeptide, useful for preparing a medicament for use in the treatment

PT of a lung disease or disorder e.g. abnormal alveolarization.  
 XX  
 XX Claim 1; Page 128-131; 138pp; English.  
 XX  
 CC The invention relates to late gestation lung (LGL) 1 polypeptides and  
 CC encoding polynucleotides. The LGL1 polypeptides can be expressed by  
 CC standard recombinant methodology. The LGL1 polypeptides, polynucleotides  
 CC and modulators are useful for modulating lung disease, airway branching  
 CC and/or abnormal alveolarization. The lung disease is bronchopulmonary  
 CC dysplasia (BPD), emphysema, New BPD, chronic obstructive pulmonary  
 CC disease (COPD), congenital diaphragmatic hernia (CDH), chronic bronchial  
 CC infection, in a human with a deficiency of alpha-1-antitrypsin. The LGL1  
 CC polypeptide or polynucleotide is useful for the preparation of a  
 CC medicament for use in the treatment of lung disease or disorder. They are  
 CC useful in research, diagnostics and the preparation of therapeutics to  
 CC treat diseases. The present sequence represents a cDNA encoding a human  
 CC LGL1 polypeptide  
 XX  
 SQ Sequence 2896 BP; 636 A; 769 C; 825 G; 666 T; 0 U; 0 Other;

Query Match 83.2%; Score 15.8; DB 10; Length 2896;  
 Best Local Similarity 89.5%; Pred. No. 4e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTCGG 19  
 |||||  
 Db 1486 GAACGGAAAGCGCTTCGG 1504

RESULT 49  
 ADL35344  
 ID ADL35344 standard; cDNA; 2898 BP.

AC ADL35344;  
 XX  
 XX 20-MAY-2004 (first entry)  
 DT  
 DE Murine secreted extracellular matrix 33145 cDNA.

XX extracellular matrix; cytostatic; neuroprotective; tissue regeneration;  
 KW cancer metastatic inhibition; morphogenesis; cell growth;  
 KW differentiation; brain disease; prion; taste bud; murine; mouse; ss;  
 KW gene; 33145.

OS Mus musculus.  
 XX  
 XX Key Location/Qualifiers  
 FH 171..1658  
 CDS /\*tag= a  
 FT /product= "Murine secreted extracellular matrix 33145  
 FT protein"  
 XX  
 XX JP2004008021-A.  
 PN  
 XX  
 XX 15-JAN-2004.  
 PD  
 XX  
 XX 03-JUN-2002; 2002JP-00162211.  
 PF  
 XX  
 XX 03-JUN-2002; 2002JP-00162211.  
 PR

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
 XX (RIKA ) RIKAGAKU KENKYUSHO.  
 PA (DANA-) DANAFOMU KK.  
 PA  
 XX WPI; 2004-085645/09.  
 DR P-PSDB; ADL35345.  
 DR  
 XX Novel extra-cellular matrix protein derived from mouse, useful for tissue  
 PT regeneration in regenerative medicine.  
 PT  
 XX Claim 3; SEQ ID NO 1; 86pp; Japanese.  
 PS  
 XX The invention relates to a novel extracellular matrix protein. The



CC protein of the invention demonstrates cytostatic and neuroprotective  
CC activities and may be useful for tissue regeneration in regenerative  
CC medicine and artificial tissue formation in an external, for metastatic  
CC inhibition of a cancer cell and for diagnosing a disease accompanying  
CC morphogenesis or tissue malformation. Furthermore, the protein may be  
CC useful in the research of physiological functions such as human cell  
CC growth and differentiation, as well as for diagnosing, treating or  
CC relieving a brain disease caused by prion in individual and analyzing  
CC taste bud-specific protein function in the vertebrate. The current  
CC sequence is that of a murine secreted extracellular matrix cDNA of the  
CC invention.

XX Sequence 2898 BP; 634 A; 812 C; 807 G; 645 T; 0 U; 0 Other;  
SQ

Query Match 83.2%; Score 15.8; DB 12; Length 2898;  
Best Local Similarity 89.5%; Pred. No. 4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19  
Db 1619 GAACGGAAAGCCCTTCGG 1637

RESULT 50  
AC47371  
ID ACC47371 standard; cDNA; 3054 BP.  
XX AC ACC47371;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Rat late gestation lung 1 (LGL1) polypeptide encoding cDNA.  
XX  
KW LGL1; late gestation lung 1; bronchodilator; respiratory; gene therapy;  
KW antisense therapy; vaccine; rat; gene; ss.  
XX  
OS Rattus norvegicus.

XX  
FH Key Location/Qualifiers  
FT CDS 86..1579  
FT /\*tag= a  
FT /product= "LGL1"  
XX  
PN WO2003020766-A1.  
XX  
XX 13-MAR-2003.  
XX  
PP 04-SEP-2002; 2002WO-CA001350.  
XX  
PR 04-SEP-2001; 2001CA-02357746.  
PR 05-DEC-2001; 2001US-0336598P.  
XX  
XX (UVMC-) UNIV MCGILL.  
XX (HOSP-) HOSPITAL FOR SICK CHILDREN.  
XX  
XX Kaplan F, Swezey NB;  
XX  
XX WPI; 2003-290169/28.  
XX P-PSDB; ABR39980.  
XX  
PT Novel late gestation lung 1 polypeptide and lg1 genes encoding the  
PT polypeptide, useful for preparing a medicament for use in the treatment  
PT of a lung disease or disorder e.g. abnormal alveolarization.  
XX  
XX Claim 1; Page 124-127; 138pp; English.

XX  
XX The invention relates to late gestation lung (LGL) 1 polypeptides and  
CC encoding polynucleotides. The LGL1 polypeptides can be expressed by  
CC standard recombinant methodology. The LGL1 polypeptides, polynucleotides  
CC and modulators are useful for modulating lung disease, airway branching  
CC and/or abnormal alveolarization. The lung disease is bronchopulmonary  
CC dysplasia (BPD), emphysema, New BPD, chronic obstructive pulmonary  
CC disease (COPD), congenital diaphragmatic hernia (CDH), chronic bronchial

CC infection, in a human with a deficiency of alpha-1-antitrypsin. The LGL1  
CC polypeptide or polynucleotide is useful for the preparation of a  
CC medicament for use in the treatment of lung disease or disorder. They are  
CC useful in research, diagnostics and the preparation of therapeutics to  
CC treat diseases. The present sequence represents a cDNA encoding a rat  
CC LGL1 polypeptide

XX  
SQ Sequence 3054 BP; 691 A; 817 C; 856 G; 690 T; 0 U; 0 Other;  
SQ

Query Match 83.2%; Score 15.8; DB 10; Length 3054;  
Best Local Similarity 89.5%; Pred. No. 4.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19  
Db 1540 GAACGGAAAGCCCTTCGG 1558

RESULT 51  
AAL36998  
ID AAL36998 standard; DNA; 6883 BP.  
XX  
AC AAL36998;  
XX  
DT 08-JAN-2002 (first entry)  
XX  
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3363.  
XX  
KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
KW neurological disease; infection; human; secreted protein;  
KW musculoskeletal system; ds.  
XX  
OS Homo sapiens.

XX  
PN WO200155367-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001338.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 14-JUL-2000; 2000US-0217496P.  
PR 26-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
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PR 14-AUG-2000; 2000US-0225213P.  
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PR 14-AUG-2000; 2000US-0225266P.  
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PR 18-AUG-2000; 2000US-0226279P.  
 PR 22-AUG-2000; 2000US-0226681P.  
 PR 23-AUG-2000; 2000US-0226868P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 03-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0232633P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 26-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241809P.  
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 PR 01-NOV-2000; 2000US-0244517P.  
 PR 08-NOV-2000; 2000US-0246474P.  
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 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
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 PR 08-NOV-2000; 2000US-0246523P.  
 PR 08-NOV-2000; 2000US-0246524P.  
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 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
 PR 08-NOV-2000; 2000US-0246532P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
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PR 08-NOV-2000; 2000US-0246613P.  
 PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
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 PR 17-NOV-2000; 2000US-0249210P.  
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 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 06-DEC-2000; 2000US-0256719P.  
 PR 08-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-451937/48.  
 DR  
 XX  
 PT Isolated polypeptide for treating, preventing and/ or prognosing  
 PT disorders related to the musculoskeletal system including musculoskeletal  
 PT cancers and also for testing and detection e.g. diagnosis.  
 XX  
 PS Example 2; SEQ ID NO 3363; 781pp + Sequence Listing; English.  
 XX  
 CC The invention relates to novel genes (AAL34669-AAL37666) and proteins  
 CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for  
 CC preventing, treating or ameliorating medical conditions e.g. by protein  
 CC or gene therapy. The genes are isolated from a range of human tissues  
 CC disclosed in the specification. The nucleic acids, proteins, antibodies  
 CC and (ant)agonists are useful in the diagnosis, treatment and prevention  
 CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as  
 CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.  
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,  
 CC bacterial, fungal and parasitic infections. Note: The sequence data for  
 CC this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 6883 BP; 1921 A; 1341 C; 1311 G; 2310 T; 0 U; 0 Other;  
 Query Match 83.2%; Score 15.8; DB 4; Length 6883;  
 Best Local Similarity 89.5%; Pred. No. 4.4e+02;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GAACGGAAAGGCGCTTTCGG 19  
 ||| ||||| ||||| ||||| |||||



RESULT 53	PR	08-SEP-2000;	2000US-0232081P.
ADJ30736	PR	12-SEP-2000;	2000US-0231968P.
ID ADJ30736 standard; DNA; 6883 BP.	PR	14-SEP-2000;	2000US-0232397P.
XX	PR	14-SEP-2000;	2000US-0232398P.
AC ADJ30736;	PR	14-SEP-2000;	2000US-0232399P.
XX	PR	14-SEP-2000;	2000US-0232400P.
DT	PR	14-SEP-2000;	2000US-0232401P.
XX	PR	14-SEP-2000;	2000US-0233063P.
DT	PR	14-SEP-2000;	2000US-0233064P.
XX	PR	14-SEP-2000;	2000US-0233065P.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3363.	PR	21-SEP-2000;	2000US-0234223P.
XX	PR	21-SEP-2000;	2000US-0234274P.
KW musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;	PR	25-SEP-2000;	2000US-0234997P.
XX gene therapy; vaccine; human; ds.	PR	25-SEP-2000;	2000US-0234998P.
XX	PR	26-SEP-2000;	2000US-0235484P.
OS Homo sapiens.	PR	27-SEP-2000;	2000US-0235834P.
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XX	PR	29-SEP-2000;	2000US-0236367P.
PD	PR	29-SEP-2000;	2000US-0236368P.
XX	PR	29-SEP-2000;	2000US-0236369P.
XX	PR	29-SEP-2000;	2000US-0236370P.
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XX	PR	02-OCT-2000;	2000US-0237037P.
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PR 16-MAR-2000; 2000US-0189874P.	PR	13-OCT-2000;	2000US-0239937P.
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PR 07-JUN-2000; 2000US-0209467P.	PR	20-OCT-2000;	2000US-0241786P.
PR 28-JUN-2000; 2000US-0214886P.	PR	20-OCT-2000;	2000US-0241787P.
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PR 07-JUL-2000; 2000US-0216647P.	PR	20-OCT-2000;	2000US-0241809P.
PR 07-JUL-2000; 2000US-0216880P.	PR	20-OCT-2000;	2000US-0241826P.
PR 11-JUL-2000; 2000US-0217487P.	PR	01-NOV-2000;	2000US-0244617P.
PR 11-JUL-2000; 2000US-0217496P.	PR	08-NOV-2000;	2000US-0246474P.
PR 14-JUL-2000; 2000US-0218290P.	PR	08-NOV-2000;	2000US-0246475P.
PR 26-JUL-2000; 2000US-0220963P.	PR	08-NOV-2000;	2000US-0246476P.
PR 26-JUL-2000; 2000US-0220964P.	PR	08-NOV-2000;	2000US-0246477P.
PR 14-AUG-2000; 2000US-0224518P.	PR	08-NOV-2000;	2000US-0246478P.
PR 14-AUG-2000; 2000US-0224519P.	PR	08-NOV-2000;	2000US-0246523P.
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PR 14-AUG-2000; 2000US-0225214P.	PR	08-NOV-2000;	2000US-0248525P.
PR 14-AUG-2000; 2000US-0225266P.	PR	08-NOV-2000;	2000US-0248526P.
PR 14-AUG-2000; 2000US-0225267P.	PR	08-NOV-2000;	2000US-0248527P.
PR 14-AUG-2000; 2000US-0225268P.	PR	08-NOV-2000;	2000US-0248528P.
PR 14-AUG-2000; 2000US-0225270P.	PR	08-NOV-2000;	2000US-0248532P.
PR 14-AUG-2000; 2000US-0225447P.	PR	08-NOV-2000;	2000US-0248609P.
PR 14-AUG-2000; 2000US-0225757P.	PR	08-NOV-2000;	2000US-0248610P.
PR 14-AUG-2000; 2000US-0225758P.	PR	08-NOV-2000;	2000US-0248611P.
PR 14-AUG-2000; 2000US-0225759P.	PR	08-NOV-2000;	2000US-0248613P.
PR 18-AUG-2000; 2000US-0226279P.	PR	17-NOV-2000;	2000US-0249207P.
PR 22-AUG-2000; 2000US-0226681P.	PR	17-NOV-2000;	2000US-0249208P.
PR 22-AUG-2000; 2000US-0226686P.	PR	17-NOV-2000;	2000US-0249209P.
PR 23-AUG-2000; 2000US-0227182P.	PR	17-NOV-2000;	2000US-0249210P.
PR 23-AUG-2000; 2000US-0227009P.	PR	17-NOV-2000;	2000US-0249211P.
PR 30-AUG-2000; 2000US-0228924P.	PR	17-NOV-2000;	2000US-0249212P.
PR 01-SEP-2000; 2000US-0229287P.	PR	17-NOV-2000;	2000US-0249213P.
PR 01-SEP-2000; 2000US-0229343P.	PR	17-NOV-2000;	2000US-0249214P.
PR 01-SEP-2000; 2000US-0229344P.	PR	17-NOV-2000;	2000US-0249215P.
PR 01-SEP-2000; 2000US-0229345P.	PR	17-NOV-2000;	2000US-0249216P.
PR 05-SEP-2000; 2000US-0229509P.	PR	17-NOV-2000;	2000US-0249217P.
PR 05-SEP-2000; 2000US-0229513P.	PR	17-NOV-2000;	2000US-0249218P.
PR 06-SEP-2000; 2000US-0230437P.	PR	17-NOV-2000;	2000US-0249244P.
PR 06-SEP-2000; 2000US-0230438P.	PR	17-NOV-2000;	2000US-0249245P.
PR 08-SEP-2000; 2000US-0231242P.	PR	17-NOV-2000;	2000US-0249264P.
PR 08-SEP-2000; 2000US-0231243P.	PR	17-NOV-2000;	2000US-0249265P.
PR 08-SEP-2000; 2000US-0231244P.	PR	17-NOV-2000;	2000US-0249297P.
PR 08-SEP-2000; 2000US-0231413P.	PR	17-NOV-2000;	2000US-0249299P.
PR 08-SEP-2000; 2000US-0231414P.	PR	17-NOV-2000;	2000US-0249300P.
PR 08-SEP-2000; 2000US-0232080P.	PR		

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PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 03-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-090458/09.
XX
XX New nucleic acid molecule, useful for preparing a medicament for
XX preventing, treating or ameliorating a medical condition e.g., cancer of
XX musculoskeletal tissues or osteoporosis.
XX
XX Disclosure; SEQ ID NO 3363; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-
XX associated nucleic acid molecule. The nucleic acid of the invention
XX demonstrates cytoskeletal and osteopathic activities and may be useful for
XX preparing a medicament for preventing, treating or ameliorating a medical
XX condition such as cancer of the musculoskeletal tissues or osteoporosis,
XX possibly via gene therapy or vaccine production. The current sequence is
XX that of the human musculoskeletal system-associated genomic DNA of the
XX invention. The current sequence is not shown within the specification per
XX se but is available on the USPTO web-site
XX http://seqdata.uspto.gov/sequence.html?DocID=20040009488.
XX
XX SQ Sequence 6883 BP; 1921 A; 1341 C; 1311 G; 2310 T; 0 U; 0 Other;
XX
XX Query Match 83.2%; Score 15.8; DB 12; Length 6883;
XX Best Local Similarity 89.5%; Pred. No. 4.4e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1 GAACGGAAAGCGCTTTCGG 19
Db |||||
478 GAATGGAAGGCTTTCGG 496

RESULT 54
AED48445/c
ID AED48445 standard; DNA; 84222 BP.
XX
XX AED48445;
XX
XX 15-DEC-2005 (first entry)
XX
XX M. echinospora gentamycin biosynthetic gene cluster DNA.
XX
XX ds, gene; antibiotic; virucide; aminoglycoside; bacterial infection;
XX viral infection; gentamycin; genP; gmrB; genB1; genQ; genD3; genM1; gmrA;
XX genS1; genC; genD2; genM2; genD1; genS2; genW; genB4; genJ; genB3; genK;
XX genB2; genX; genU; genT; genE; genY; genA; genF; genG; genI; genJ;
XX genL; genN; DNA polymerase beta chain; integral membrane protein;
XX agglutinin; esterase; Trp-tRNA ligase;
XX queuine/archaeosine tRNA-ribosyltransferase; ribosomal methyltransferase;
XX gentamicin (hexosaminyl-6-)aminotransferase I; gentamicin oxidoreductase;
XX (N-acetyl-) hexosaminyltransferase; ribosomal methyltransferase;
XX L-glutamine:ketocyclitol; 2-deoxy-scylo-inosose synthase;
XX gentamicin glycosyltransferase II; gentamicin aminotransferase II;
XX gentamicin production protein; gentamicin aminotransferase IV;
XX aminoglycoside 3'-phosphotransferase; gentamicin aminotransferase III;
XX gentamicin C-methyltransferase; gentamicin aminotransferase II;
```

---

```
KW gentamicin exporter; aminocyclitol 1-dehydrogenase; cation transporter;
KW gentamicin methyltransferase; two-component system histidine kinase;
KW two-component system response regulator; serine protease;
KW DNA polymerase III epsilon subunit; RNA polymerase sigma factor;
KW subtilase; transcriptional regulator; acetyltransferase;
KW ATP-binding protein; ABC-transporter; permease component.
XX
XX Micromonospora echinospora.
XX
XX Key Location/Qualifiers
XX CDS 191..1264
XX /tag= a
XX /product= "putative DNA polymerase beta chain"
XX /note= "ORF MecP21.15 "
XX complement(1347..2321)
XX /tag= b
XX /product= "putative integral membrane protein"
XX /note= "ORF MecP21.16c"
XX 2374..2847
XX /tag= c
XX /product= "hypothetical protein"
XX /note= "ORF MecP21.17"
XX 2847..4517
XX /tag= d
XX /product= "hypothetical protein"
XX /note= "ORF MecP21.18"
XX complement(4571..5590)
XX /tag= e
XX /product= "putative plus agglutinin"
XX /note= "ORF MecP21.19c"
XX complement(5628..6206)
XX /tag= f
XX /product= "hypothetical protein"
XX /note= "ORF MecP21.20c"
XX complement(6297..6899)
XX /tag= g
XX /product= "putative esterase"
XX /note= "ORF MecP21.21c"
XX 7683..9389
XX /tag= h
XX /product= "hypothetical protein"
XX /note= "ORF MecP21.22"
XX complement(9518..10144)
XX /tag= i
XX /product= "hypothetical protein"
XX /note= "ORF MecP21.23c"
XX 16081..16620
XX /tag= j
XX /product= "hypothetical protein"
XX /note= "ORF MecE04.1"
XX 16711..17790
XX /tag= k
XX /product= "putative Trp-tRNA ligase"
XX /note= "ORF MecE04.2"
XX 17857..19014
XX /tag= l
XX /product= "queuine/archaeosine tRNA-ribosyltransferase"
XX /gene= "genP"
XX 19121..19939
XX /tag= m
XX /gene= "gmrB"
XX /product= "putative ribosomal methyltransferase"
XX complement(19953..21206)
XX /tag= n
XX /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
XX /gene= "genB1"
XX complement(21238..22761)
XX /tag= o
XX /gene= "genQ"
XX /product= "gentamicin (hexosaminyl-6-)aminotransferase I"
XX complement(22934..23743)
XX /tag= p
XX /product= "putative gentamicin oxidoreductase"
XX
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FT /gene= "genD3"  
FT complement (23758. .25005)  
FT /*tag= q  
FT /gene= "genM1"  
FT /product= "putative (N-acetyl-) hexosaminyltransferase"  
FT complement (25042. .25866)  
FT /*tag= r  
FT /product= "putative ribosomal methyltransferase"  
FT /gene= "gmrA"  
FT 26161. .27423  
FT /*tag= s  
FT /gene= "genS1"  
FT /product= "putative L-glutamine:ketocyclitol"  
FT 27558. .28751  
FT /*tag= t  
FT /product= "2-deoxy-scylo-inosose synthase"  
FT /gene= "genC"  
FT 28744. .29769  
FT /*tag= u  
FT /gene= "genD2"  
FT /product= "putative gentamicin oxidoreductase"  
FT 29858. .31030  
FT /*tag= v  
FT /product= "putative gentamicin glycosyltransferase II"  
FT /gene= "genM2"  
FT 31032. .33011  
FT /*tag= w  
FT /gene= "genD1"  
FT /product= "putative gentamicin oxidoreductase"  
FT 33011. .34267  
FT /*tag= x  
FT /product= "putative gentamicin aminotransferase II"  
FT /gene= "genS2"  
FT 34275. .34646  
FT /*tag= y  
FT /gene= "genW"  
FT /product= "putative gentamicin production protein"  
FT complement (34741. .36078)  
FT /*tag= z  
FT /product= "putative gentamicin aminotransferase IV"  
FT /gene= "genB4"  
FT complement (36137. .36943)  
FT /*tag= aa  
FT /gene= "genJ"  
FT /product= "biosynthetic aminoglycoside 3'-  
FT phosphotransferase"  
FT complement (36981. .38453)  
FT /*tag= ab  
FT /product= "putative gentamicin aminotransferase III"  
FT /gene= "genB3"  
FT complement (38969. .40885)  
FT /*tag= ac  
FT /gene= "genK"  
FT /product= "putative gentamicin C-methyltransferase"  
FT 41135. .42379  
FT /*tag= ad  
FT /product= "putative gentamicin aminotransferase II"  
FT /gene= "genB2"  
FT complement (42465. .42977)  
FT /*tag= ae  
FT /gene= "genX"  
FT /product= "putative gentamicin production protein"  
FT complement (43032. .43967)  
FT /*tag= af  
FT /product= "putative gentamicin production protein"  
FT /gene= "genU"  
FT complement (44162. .45568)  
FT /*tag= ag  
FT /gene= "genT"  
FT /product= "putative gentamicin exporter"  
FT complement (45861. .46883)  
FT /*tag= ah  
FT /product= "putative aminocyclitol 1-dehydrogenase"
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FT /gene= "genE"  
FT 47364. .48878  
FT /*tag= ai  
FT /gene= "genY"  
FT /product= "putative cation antiporter"  
FT 49000. .49737  
FT /*tag= aj  
FT /product= "putative gentamicin production protein"  
FT /gene= "genA"  
FT 49734. .50381  
FT /*tag= ak  
FT /gene= "genF"  
FT /product= "putative gentamicin production protein"  
FT 50381. .50734  
FT /*tag= al  
FT /product= "putative gentamicin production protein"  
FT /gene= "genG"  
FT complement (50813. .54229)  
FT /*tag= am  
FT /product= "putative gentamicin exporter "  
FT /gene= "genH"  
FT complement (54226. .56163)  
FT /*tag= an  
FT /gene= "genI"  
FT /product= "putative gentamicin exporter "  
FT complement (56689. .57627)  
FT /*tag= ao  
FT /gene= "genJ"  
FT /product= "putative gentamicin production protein"  
FT 58121. .58741  
FT /*tag= ap  
FT /product= "putative gentamicin production protein"  
FT
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Query Match 83.2%; Score 15.8; DB 14; Length 84222;  
Best Local Similarity 89.5%; Pred. No. 5.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCGCTTTCGG 19

Db 15389 GAGCGAAAGGCGCTTTCGG 15371

RESULT 55

AAC55929

ID AAC55929 standard; DNA; 455 BP.

XX AAC55929;

XX 25-JAN-2001 (first entry)

DE Eucalyptus grandis transcription factor DNA sequence #60.  
XX

KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;  
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;  
KW type 2 Cys2His2; CCAAT box element; MYB; ss.

XX Eucalyptus grandis.

OS WO200053724-A2.

PN 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US006112.

XX 11-MAR-1999; 99US-00266513.

PR 18-AUG-1999; 99US-0149485P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.

XX Wood M, McGrath A, Shenk MA, Glenn M;

XX WPI; 2000-579369/54.  
XX New isolated polynucleotide encoding a plant transcription factor for  
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
PT having modified gene expression or modified activity of a polypeptide.  
XX  
PS Claim 1; Page 60; 747pp; English.  
XX  
XX The present invention relates to novel plant transcription factors from  
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding  
CC sequence for one such transcription factor. The transcription factor may  
CC be used to produce a plant having modified gene expression such as a  
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or  
CC mahogany species or to modify the activity of a polypeptide in a plant.  
CC The transcription factors of the present invention are members from the  
CC following families of regulatory proteins: bZIP, bZIP family of G-box  
CC binding factors, basic helix-loop-helix zipper,  
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2  
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and  
CC MYB  
XX  
SQ Sequence 455 BP; 156 A; 75 C; 113 G; 111 T; 0 U; 0 Other;  
Query Match 81.1%; Score 15.4; DB 3; Length 455;  
Best Local Similarity 94.1%; Pred. No. 5.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGCGCTTTC 17  
||| ||||| ||||| |||||  
Db 27 GACCGGAAAGCGCTTTC 43  
RESULT 56  
AAC57218  
ID AAC57218 standard; DNA; 455 BP.  
XX  
AC AAC57218;  
XX  
DT 25-JAN-2001 (first entry)  
XX  
DE Eucalyptus grandis transcription factor DNA sequence #724.  
XX  
KW Plant; transcription factor; gene expression; eucalyptus; pine; acacia;  
KW poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;  
KW basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;  
KW homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;  
KW type 2 Cys2His2; CCAAT box element; MYB; SE.  
XX  
OS Eucalyptus grandis.  
XX  
PN WO200053724-A2.  
XX  
PD 14-SEP-2000.  
XX  
PF 09-MAR-2000; 2000WO-US006112.  
XX  
PR 11-MAR-1999; 99US-00266513.  
XX  
PR 18-AUG-1999; 99US-0149485P.  
XX  
PA (GENE-) GENESIS RES & DEV CORP LTD.  
XX  
PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.  
XX  
PI Wood M, McGrath A, Shenk MA, Glenn M;  
XX  
DR WPI; 2000-579369/54.  
XX  
PT New isolated polynucleotide encoding a plant transcription factor for  
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,  
PT having modified gene expression or modified activity of a polypeptide.  
XX  
PS Claim 1; Page 620; 747pp; English.

CC The present invention relates to novel plant transcription factors from  
CC Eucalyptus grandis or Pinus radiata. The present sequence is the coding  
CC sequence for one such transcription factor. The transcription factor may  
CC be used to produce a plant having modified gene expression such as a  
CC woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or  
CC mahogany species or to modify the activity of a polypeptide in a plant.  
CC The transcription factors of the present invention are members from the  
CC following families of regulatory proteins: bZIP, bZIP family of G-box  
CC binding factors, basic helix-loop-helix zipper,  
CC homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2  
CC and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and  
CC MYB  
XX  
SQ Sequence 455 BP; 156 A; 75 C; 113 G; 111 T; 0 U; 0 Other;  
Query Match 81.1%; Score 15.4; DB 3; Length 455;  
Best Local Similarity 94.1%; Pred. No. 5.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGCGCTTTC 17  
||| ||||| ||||| |||||  
Db 27 GACCGGAAAGCGCTTTC 43  
RESULT 57  
ACL67957  
ID ACL67957 standard; DNA; 861 BP.  
XX  
AC ACL67957;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE M. xanthus gene sequence, seq id 4420.  
XX  
KW Transgenic plant; DNA replication; gene regulation; gene expression;  
KW gene; ds.  
XX  
OS Myxococcus xanthus.  
XX  
PN US6833447-B1.  
XX  
PD 21-DEC-2004.  
XX  
PF 10-JUL-2001; 2001US-00902540.  
XX  
PR 10-JUL-2000; 2000US-0217883P.  
XX  
PA (MONS ) MONSANTO TECHNOLOGY LLC.  
XX  
PI Goldman BS, Hinkle GU, Slater SC, Wiegand RC;  
XX  
XX WPI; 2005-028716/03.  
XX  
DR New substantially purified Myxococcus xanthus nucleic acid molecule  
PT encoding a nitrite reductase, useful for determining gene expression,  
PT identifying mutations in a gene of interest, and for constructing  
PT mutations in a gene of interest.  
XX  
PS Example 2; SEQ ID NO 4420; 25pp; English.  
XX  
CC The invention relates to a substantially purified nucleic acid molecule  
CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
CC recombinant DNA construct for expression of a nitrite reductase gene in a  
CC plant cell, and a plant cell comprising the recombinant DNA construct.  
CC The nucleic acid is useful for determining gene expression, identifying  
CC mutations in a gene of interest, and for constructing mutations in a gene  
CC of interest. Sequences given in records for SEQ IDs 1850-9691 represent a  
CC set of about 7842 genes or partial genes from the genome of the bacterium  
CC Myxococcus xanthus. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from USPTO  
XX  
SQ Sequence 861 BP; 155 A; 316 C; 283 G; 107 T; 0 U; 0 Other;

AC	ABL04330;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster expressed polynucleotide SEQ ID NO 7472.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical; gene; ss.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001WO-US009231.
XX	
PR	23-MAR-2000; 2000US-0191637P.
PR	11-JUL-2000; 2000US-00614150.
XX	
PA	(PEKE ) PE CORP NY.
OS	
XX	Venter JC, Adams M, Li PWD, Myers EW;
PI	WPI; 2001-656860/75.
DR	P-PSDB; ABB60227.
DR	
XX	
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signaling and cell-cell
PT	interactions.
XX	
PS	Claim 1; SEQ ID NO 7472; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC	ABB72072). The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 7162 BP; 1502 A; 1777 C; 1860 G; 2023 T; 0 U; 0 Other;
	Query Match 81.1%; Score 15.4; DB 4; Length 7162;
	Best Local Similarity 94.1%; Pred.No. 7.1e+02;
	Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	2 AACGGAAAGGCGTTTCG 18 
Db	4182 AACGTAAAGGCGTTTCG 4166 
RESULT 60	
ACL64755/c	ID
XX	ACL64755 standard; DNA; 23677 BP.
XX	
AC	ACL64755;
XX	
DT	02-JUN-2005 (first entry)
XX	
DE	M. xanthus DNA fragment, seq id 1218.
XX	
KW	Transgenic plant; DNA replication; gene regulation; gene expression; ds.
XX	
OS	Myxococcus xanthus.
XX	
PN	US6833447-B1.
XX	
PD	21-DEC-2004.
XX	



PF 10-JUL-2001; 2001US-00902540.  
 PR 10-JUL-2000; 2000US-0217883P.  
 XX (MONS ) MONSANTO TECHNOLOGY LLC.  
 XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;  
 XX WPI; 2005-028716/03.  
 XX New substantially purified Myxococcus xanthus nucleic acid molecule  
 PT encoding a nitrite reductase, useful for determining gene expression,  
 PT identifying mutations in a gene of interest, and for constructing  
 PT mutations in a gene of interest.  
 XX Example 1; SEQ ID NO 1218; 25pp; English.  
 PS  
 CC The invention relates to a substantially purified nucleic acid molecule  
 CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a  
 CC recombinant DNA construct for expression of a nitrite reductase gene in a  
 CC plant cell, and a plant cell comprising the recombinant DNA construct.  
 CC The nucleic acid is useful for determining gene expression, identifying  
 CC mutations in a gene of interest, and for constructing mutations in a gene  
 CC of interest. Sequences given in records for SEQ IDs 1-1849 represent a  
 CC set of 1849 contig and singleton sequences comprising coding sequences,  
 CC DNA replication elements, promoters and other regulatory elements from  
 CC the genome of the bacterium Myxococcus xanthus. Note: The sequence data  
 CC for this patent did not form part of the printed specification, but was  
 CC obtained in electronic format directly from USPTO  
 XX  
 SQ Sequence 23677 BP; 3557 A; 7986 C; 8412 G; 3722 T; 0 U; 0 Other;  
 Query Match 81.1%; Score 15.4; DB 14; Length 23677;  
 Best Local Similarity 94.1%; Pred. No. 7.8e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 GAACGGAAGGCTTTC 17  
 Db 23339 GAACGGAAGGCTTTC 23323  
 RESULT 61  
 ADB82110/c  
 ID ADB82110 standard; cDNA; 297 BP.  
 XX  
 AC ADB82110;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Human cDNA sequence useful for the treatment of cancer (SeqID 422).  
 XX  
 DE human; prostate; cancer; cytostatic; gene therapy; vaccine;  
 KW immune response; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO2003050236-A2.  
 PN  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 04-SEP-2002; 2002WO-US028214.  
 XX  
 XX 07-DEC-2001; 2001US-00012697.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;  
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;  
 PI Garcia V, Jones LW, Stache-Crain B, Scott EM;  
 XX WPI; 2003-513972/48.  
 DR  
 XX

PT New polynucleotides derived from human prostate, useful for modulating  
 XX immune response to prevent or treat cancer.  
 PS Claim 1; SEQ ID NO 422; 188pp; English.  
 XX  
 CC This invention relates to novel isolated polynucleotides of human origin,  
 CC particularly isolated from the human prostate. Specifically, it refers to  
 CC the diagnostics and therapeutics comprising these novel human  
 CC polynucleotides, and includes the derived probes, antisense  
 CC oligonucleotides and antibodies thereof. The identification of these  
 CC human prostate genes that can inhibit tumour growth is useful for  
 CC understanding the progression and nature of complex diseases such as  
 CC cancer, and hence they are important in the drug discovery process. The  
 CC present invention describes these polynucleotides and encoded  
 CC polypeptides as exhibiting cytostatic activity, and through gene therapy  
 CC and/or vaccines they can be used to modulate the immune response for the  
 CC prevention or treatment of cancers, particularly of the prostate, but  
 CC also for breast, lung and colon cancer. This polynucleotide sequence is a  
 CC human cDNA sequence useful for the treatment of cancer, used in an  
 CC exemplification of the invention. NOTE: These sequences are not given in  
 CC the specification but are provided on the WIPO website.  
 XX  
 SQ Sequence 297 BP; 56 A; 72 C; 76 G; 72 T; 0 U; 21 Other;  
 Query Match 78.9%; Score 15; DB 9; Length 297;  
 Best Local Similarity 100.0%; Pred. No. 8.7e+02;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 5 GGAAGGCGCTTTCGG 19  
 Db 75 GGAAGGCGCTTTCGG 61  
 RESULT 62  
 ABQ89167/c  
 ID ABQ89167 standard; cDNA; 331 BP.  
 XX  
 AC ABQ89167;  
 XX  
 DT 27-SEP-2002 (first entry)  
 XX  
 DE Human prostate expressed polynucleotide SEQ ID NO 423.  
 XX  
 DE Human; prostate; cytostatic; tumour; cancer; vaccine; gene therapy; gene;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200255700-A2.  
 XX  
 PD 18-JUL-2002.  
 XX  
 PF 07-DEC-2001; 2001WO-US047349.  
 XX  
 XX 07-DEC-2000; 2000US-0254648P.  
 PR 13-MAR-2001; 2001US-0275688P.  
 XX  
 PA (CHIR ) CHIRON CORP.  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Escobedo J, Garcia PD, Kassam A, Lamson G, Drmanac R;  
 PI Crkvenjakov R, Dickson M, Drmanac S, Labat I, Leshkowitz D, Kita D;  
 PI Garcia V, Jones WL, Stache-Crain B, Scott EM;  
 XX WPI; 2002-557824/59.  
 DR  
 XX New genes and gene products isolated from human prostate, useful for  
 PT treating or diagnosing tumor or cancer (e.g. prostate cancer or breast  
 PT cancer), or as vaccines for treating or preventing these diseases.  
 XX  
 PS Claim 1; SEQ ID NO 423; 186pp + Sequence Listing; English.  
 XX  
 XX The invention relates to an isolated polynucleotide comprising any of

CC 1477 sequences or its fragment, degenerate variant, antisense or  
CC complement. The polynucleotides and gene products are useful for treating  
CC or diagnosing tumour or cancer (e.g. prostate cancer, breast cancer, lung  
CC cancer or medullary carcinoma) in a subject (e.g. cattle, dogs, cats,  
CC rabbits, horse or human). The polynucleotides and polypeptides are also  
CC useful as vaccines for treating or preventing these diseases. The  
CC polynucleotides are useful for gene therapy. The present sequence is that  
CC of one of a group of polynucleotides (ABQ88745-ABQ90015) disclosed  
CC electronically as sequences of the invention. However only 1271  
CC polynucleotide sequences are given, whereas 1477 polynucleotides and 91  
CC proteins are claimed. Note: The sequence data for this patent did not  
CC form part of the printed specification, but was obtained in electronic  
CC format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequence  
XX  
SQ Sequence 331 BP; 74 A; 77 C; 85 G; 74 T; 0 U; 21 Other;  
  
Query Match 78.9%; Score 15; DB 6; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GGAAGGCCTTCGG 19  
Db 100 GGAAGGCCTTCGG 86  
  
RESULT 63  
ACH79967  
ID ACH79967 standard; DNA; 592 BP.  
AC ACH79967;  
XX  
XX  
XX 29-JUL-2004 (first entry)  
DE Human genome derived single exon probe #13162.  
XX  
XX Human; probe; ss; gene expression; single exon probe; microarray;  
KW alternative splicing event; genomic alteration.  
XX  
XX Homo sapiens.  
XX  
XX US2003194704-A1.  
XX  
XX 16-OCT-2003.  
XX  
XX 03-APR-2002; 2002US-00029386.  
XX  
XX 03-APR-2002; 2002US-00029386.  
PR  
XX (PENN/) PENN S G.  
XX PA (RANK/) RANK D R.  
XX PA (HANZ/) HANZEL D K.  
XX  
XX Penn SG, Rank DR, Hanzel DK;  
XX  
XX WPI; 2004-119264/12.  
XX  
XX New human genome-derived single exon nucleic acid probes useful for human  
PT gene expression analysis, for identifying or characterizing alternative  
PT splicing events, for assessing genomic alterations or as tools for  
PT surveying tissues.  
XX  
XX Claim 15; SEQ ID NO 13162; 80pp; English.  
PS  
XX The invention relates to a nucleic acid probe for measuring human gene  
CC expression, comprising any of the 27,400 fully defined nucleotide  
CC sequences in the specification, or their complements or fragments, and  
CC encoding at least 8 amino acids of any of the 6888 amino acid sequences  
CC fully defined in the specification. The probe is a single exon probe that  
CC hybridises under high stringency conditions to a nucleic acid molecule  
CC expressed in human cells or tissues. Also included are a spatially-  
CC addressable set of single exon nucleic acid probes for measuring human  
CC gene expression (comprising a plurality of single exon nucleic acid  
CC probes cited above, where each of the plurality of probes is separately

CC and addressably isolatable or amplifiable from the plurality), a single  
CC exon microarray for measuring human gene expression, a method of  
CC measuring human gene expression, a vector comprising the single exon  
CC probe cited above, an ORF-encoded peptide comprising at least 8  
CC contiguous amino acids of any of the above-mentioned amino acid  
CC sequences (optionally with conservative amino acid substitutions), an  
CC isolated antibody that binds specifically to a peptide cited above,  
CC methods of selling and/or licensing single exon probes or microarrays to  
CC a customer desiring to measure gene expression, a method of providing  
CC human gene expression data by subscription, and a computer-readable  
CC storage medium which contains a database having a plurality of records  
CC (each record including data on the expression of a single exon probe  
CC cited above. The probe, methods and apparatus are useful in gene  
CC expression analysis. The probes may be used as tools for surveying  
CC tissues to detect the presence of expressed messages that contain their  
CC specific exon, or in constructing genome-derived single exon microarrays.  
CC In addition, the probes are used in identifying and characterising  
CC alternative splicing events, in detecting and characterising gross  
CC alterations in the genomic locus that includes their exon, in assessing  
CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
CC or in expressing the ORF-encoded peptide. The present sequence is a human  
CC single exon probe of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030194704  
XX  
XX Sequence 592 BP; 201 A; 114 C; 140 G; 137 T; 0 U; 0 Other;  
SQ  
  
Query Match 78.9%; Score 15; DB 12; Length 592;  
Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 GGAAGGCCTTCGG 19  
Db 532 GGAAGGCCTTCGG 546  
  
RESULT 64  
AD131363  
ID AD131363 standard; cDNA; 1429 BP.  
XX  
XX AC AD131363;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX DE Human cDNA #689.  
XX  
XX Human; gene; ss; immunological response; immunopathological condition;  
KW Crohn's disease; asthma; ulcerative colitis; hyperesinophilia;  
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;  
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;  
KW osteopathic; antiarthritic; antirheumatic; antineumatic; cytostatic.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US6607879-B1.  
XX  
XX 19-AUG-2003.  
XX  
XX 09-FEB-1998; 98US-00023655.  
XX  
XX 09-FEB-1998; 98US-00023655.  
XX  
XX (INCY-) INCYTE CORP.  
XX  
XX Cocks BG, Stuart SG, Seilhamer JJ;  
XX  
XX WPI; 2003-895307/82.  
XX  
XX A composition comprising a plurality of cDNAs, useful for detecting  
PT altered expression of genes in an immunological response or for  
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma  
PT or osteoarthritis.



```
XX
DR WPI; 2001-457603/49.
DR P-PSDB; AAM25648.
PT Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection.
XX
PS Claim 1; Page 516-517; 1217pp; English.
XX
CC AAH99166 to AAH99904 encode the human proteins given in AM25225 to
CC AM25963. The proteins can have activities based on the tissues and cells
CC they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnarary;
CC antitumor; osteopathic; dermatological; antiallergic; antistatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders
XX
SQ Sequence 1453 BP; 340 A; 366 C; 312 G; 435 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 4; Length 1453;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGAAGGCGCTTCGG 19
Db 1173 GGAAGGCGCTTCGG 1159
RESULT 67
ABN59917
ID ABN59917 standard; cDNA; 2010 BP.
XX
AC ABN59917;
XX
DT 28-JUN-2002 (first entry)
XX
DE Novel human coding sequence SEQ ID NO: 328.
XX
KW Human; antianaemic; vulnarary; antiinflammatory; immunomodulatory;
KW antiinfertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
KW neuroprotective; antiparkinsonian; protein therapy; EST;
KW expressed sequence tag; gene; ss.
XX
OS Homo sapiens.
XX
FN WO200222660-A2.
XX
PD 21-MAR-2002.
XX
PF 10-SEP-2001; 2001WO-US026015.
XX
PR 11-SEP-2000; 2000US-00659671.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
DR WPI; 2002-292408/33.
XX
P-PSDB; ABB97504.
An isolated polynucleotide for treating diseases associated with its
encoded polypeptide such as cancer and multiple sclerosis.
Claim 1; SEQ ID NO 328; 509pp; English.
The present invention provides the protein and coding sequences of 444
novel human proteins. These were isolated from expressed sequences tags
(ESTs). They can be used to stimulate cell growth, to regulate
haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
e.g. in burn treatment, to regulate the immune system e.g. to treat
multiple sclerosis, to regulate activin or inhibin e.g. to treat
infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke
and cancer, to screen for drugs, to treat inflammatory conditions e.g.
rheumatoid arthritis, and to treat nervous system disorders e.g.
Parkinson's disease. The present sequence is a coding sequence of the
invention
SQ Sequence 2010 BP; 585 A; 446 C; 527 G; 452 T; 0 U; 0 Other;
Query Match 78.9%; Score 15; DB 6; Length 2010;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGAAGGCGCTTCGG 19
Db 1043 GGAAGGCGCTTCGG 1057
RESULT 68
AAF88159
ID AAF88159 standard; cDNA; 2015 BP.
XX
AC AAF88159;
XX
DT 17-JUL-2001 (first entry)
XX
DE Human thyroid malfunction-associated protein RITA encoding cDNA.
XX
KW KRAB domain; hyperplasia; thyroid; tumor; zinc finger motif; cytostatic;
KW antithyroid; gene therapy; chromosome 19; 19q13; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 187..1578
FT /tag= a
FT /product= "RITA"
XX
PN WO200127265-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-DE003600.
XX
PR 12-OCT-1999; 99DE-01049179.
XX
PA (UYBR-) UNIV BREMEN.
XX
PI Bullerdiek J, Rippe V, Meiboom M, Belge G;
XX
DR WPI; 2001-290723/30.
DR P-PSDB; AAB86115.
XX
PT New nucleic acid useful for the diagnosis and treatment of thyroid
PT disorders, e.g. tumors.
XX
PS Claim 2; Page 52-54; 59pp; German.
XX
CC This invention describes a novel nucleic acid (N1) encoding a polypeptide
CC which comprises a KRAB-domain and/or at least one zinc finger motif. The
CC products of the invention have cytostatic and antithyroid activity and
```

CC can be used in gene therapy. Nucleic acids, polypeptides, and antibodies  
 CC of the invention may be used in the diagnosis and/or the therapy of the  
 CC malfunction of the thyroid and/or hyperplasias of the thyroid and/or  
 CC thyroid tumors. They may also be used in the production of medicaments.  
 CC (NI) can also be used to diagnose thyroid tumors which are located on  
 CC chromosome 19 at band 19q13. This sequence encodes the thyroid  
 CC malfunction-associated protein, RITA which is described in the method of  
 CC the invention  
 XX  
 SQ Sequence 2015 BP; 601 A; 444 C; 503 G; 467 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 5; Length 2015;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAAGGCGCTTTCGG 19  
 Db 847 GGAAAGGCGCTTTCGG 861  
 |||||

RESULT 69  
 AAS03044  
 ID AAS03044 standard; cDNA; 2098 BP.

AC AAS03044;

XX 29-AUG-2001 (first entry)

XX Human diagnostic and therapeutic (dithp) cDNA sequence #33.

XX Human diagnostic and therapeutic molecule; dithp; gene therapy;  
 KW thalassemia; cardiovascular disorder; cell proliferative disorder;  
 KW cancer; neurodegenerative disorder; autoimmune disorder;  
 KW infectious disorder; inflammatory disorder; developmental disorder;  
 KW Incyte ID number 9027913dec; transcription factor molecule; ss.

XX Homo sapiens.

XX WO200121836-A2.

XX 29-MAR-2001.

XX 19-SEP-2000; 2000WO-US025643.

XX 23-SEP-1999; 99US-0155760P.

XX 24-SEP-1999; 99US-0155939P.

XX 24-SEP-1999; 99US-0156294P.

XX 28-SEP-1999; 99US-0156565P.

XX 28-SEP-1999; 99US-0156624P.

XX 28-SEP-1999; 99US-0156625P.

XX 24-NOV-1999; 99US-0167410P.

XX 24-NOV-1999; 99US-0167517P.

XX 24-NOV-1999; 99US-0167520P.

XX 24-NOV-1999; 99US-0167521P.

XX 24-NOV-1999; 99US-0167522P.

XX 24-NOV-1999; 99US-0167542P.

XX 24-NOV-1999; 99US-0167543P.

XX 29-NOV-1999; 99US-0167943P.

XX 29-NOV-1999; 99US-0167945P.

XX 30-NOV-1999; 99US-0168197P.

XX 30-NOV-1999; 99US-0168265P.

XX 30-NOV-1999; 99US-0168432P.

XX 30-NOV-1999; 99US-0168432P.  
 XX 01-DEC-1999; 99US-0168468P.  
 XX 01-DEC-1999; 99US-0168599P.  
 XX 02-DEC-1999; 99US-0168611P.  
 XX 02-DEC-1999; 99US-0168613P.  
 XX 02-DEC-1999; 99US-0168857P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA  
 XX Hodgson DW, Lincoln SE, Russo FD, Spiro PA, Banville SC;  
 XX Bratcher SR, Dufour GE, Cohen HJ, Rosen BH, Shah P, Chalup MS;

PI Hillman JL, Jones AL, Yu JY, Greenawalt LB, Panzer SR, Roseberry AM;  
 PI Wright RJ, Chen W, Liu TF, Yap PE, Stockdreher TK, Amshey S;  
 PI Fong WT;  
 XX  
 XX WPI; 2001-281607/29.  
 XX  
 XX Novel diagnostic and therapeutic polynucleotides, used in disease  
 PT diagnosis and for gene therapy of conditions such as cancer and  
 PT thalassemia.  
 XX  
 XX Claim 1; Page 271; 299pp; English.

XX The present sequence for human diagnostic and therapeutic (dithp) cDNA  
 CC sequence #33 is 1 of 71 (AAS03012-AAS03082) novel sequences described in  
 CC the invention. The present sequence (Incyte ID No: 9027913dec) encodes a  
 CC transcription factor molecule. The dithp polynucleotides may be used to  
 CC diagnose a condition disease or disorder associated with human molecules.  
 CC They can be used to identify the presence of similar nucleic acids. Dithp  
 CC polynucleotides may be used to generate hybridisation probes for use in  
 CC chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to  
 CC screen for molecules which bind to them and modulate their activity.  
 CC Dithp polynucleotides can be used for gene therapy of disorders such as  
 CC severe combined immunodeficiency syndrome (SCID), cystic fibrosis,  
 CC thalassemia, haemophilia resulting from Factor VIII or IX deficiencies,  
 CC cardiovascular disorders e.g familial hypercholesterolaemia (FH), cell  
 CC proliferative disorders e.g. cancers, neurodegenerative disorders,  
 CC autoimmune/inflammatory disorders, infectious disorders and developmental  
 CC disorders. The antibodies can be used to analyse protein expression  
 CC levels

XX SQ Sequence 2098 BP; 610 A; 467 C; 537 G; 484 T; 0 U; 0 Other;

Query Match 78.9%; Score 15; DB 4; Length 2098;

Best Local Similarity 100.0%; Pred. No. 1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAAGGCGCTTTCGG 19  
 Db 933 GGAAAGGCGCTTTCGG 947  
 |||||

RESULT 70

AAK94562

ID AAK94562 standard; cDNA; 2169 BP.

AC AAK94562;

XX 06-NOV-2001 (first entry)

XX Human full-length cDNA, SEQ ID NO: 3469.

XX Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

XX Homo sapiens.

XX EPI130094-A2.

XX 05-SEP-2001.

XX 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.

XX 11-JAN-2000; 2000JP-00118774.

XX 02-MAY-2000; 2000JP-00183765.

XX (HELI-) HELIX RES INST.

XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

XX WPI; 2001-524255/58.

XX P-PSDB; AAM93629.

PT 830 Primers useful for synthesizing full length cDNA clones and their use  
PT in genetic manipulation.  
PS  
XX Claim 8; SEQ ID NO 3469; 1380pp + Sequence Listing; English.  
XX  
CC The invention relates to primers for synthesizing full length cDNA  
CC clones. 830 cDNA molecules encoding a human protein have been isolated  
CC and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have  
CC been determined. Primers for synthesizing the full length cDNA are useful  
CC for clarifying the function of the protein encoded by the cDNA. The full  
CC length clones were obtained by construction of full length enriched cDNA  
CC libraries that were synthesised by the oligo-capping method. The primers  
CC enable the production of the full length cDNA easily without any special  
CC methods. The present sequence is a full length human cDNA of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in CD-ROM format directly  
CC from EPO  
XX  
SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;  
Query Match 78.9%; Score 15; DB 4; Length 2169;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GGAAGGCGCTTTCGG 19  
|||||||  
Db 1004 GGAAGGCGCTTTCGG 1018  
RESULT 71  
ADL31436  
ID ADL31436 standard; cDNA; 2169 BP.  
XX  
AC ADL31436;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Full length human cDNA clone SegID 3469.  
DE  
DE human; medicine; signal transduction; glycoprotein; transcription;  
KW oligo-capping method; ss; gene.  
KW  
XX Homo sapiens.  
XX  
XX EP1396543-A2.  
XX  
XX 10-MAR-2004.  
XX  
XX 07-JUL-2000; 2003EP-00025638.  
XX  
XX 08-JUL-1999; 99JP-00194486.  
PR 11-JAN-2000; 2000JP-00118774.  
PR 02-MAY-2000; 2000JP-00183865.  
PR 07-JUL-2000; 2000EP-00114089.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
PA  
XX Ora T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
PI Wakanatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
XX  
XX WPI; 2004-204755/20.  
DR P-PSDB; ADL31437.  
XX  
PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full  
PT length human cDNAs.  
XX  
XX Example 1; SEQ ID NO 3469; 1340pp; English.  
PS  
XX This invention relates to a novel primers useful for synthesizing full  
XX length cDNA molecules that encode human proteins. Specifically, it refers  
CC to secretory or membrane proteins that are potential therapeutic agents/  
CC target molecules in the field of medicine, and in particular genes  
CC encoding proteins that are associated with signal transduction,  
CC

CC glycoproteins and transcription. The present invention describes a method  
CC for efficiently cloning a full length human cDNA from both the 5' and 3',  
CC ends using the oligo-capping method. This polynucleotide sequence is a  
CC full length human cDNA clone of the invention.  
XX  
SQ Sequence 2169 BP; 633 A; 485 C; 560 G; 491 T; 0 U; 0 Other;  
Query Match 78.9%; Score 15; DB 12; Length 2169;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GGAAGGCGCTTTCGG 19  
|||||||  
Db 1004 GGAAGGCGCTTTCGG 1018  
RESULT 72  
ABA82974  
ID ABA82974 standard; DNA; 2173 BP.  
XX  
XX ABA82974;  
XX  
DT 05-FEB-2002 (first entry)  
XX  
DE Human transcription factor TRFX-1 coding sequence.  
DE  
DE Human; transcription factor; TRFX; cell proliferative disease;  
KW autoimmune disease; inflammation; cancer; AIDS; infection; cytostatic; anti-HIV;  
KW neuroprotective; antiinflammatory; gene therapy; ds.  
KW  
XX Homo sapiens.  
XX  
XX WO200172777-A2.  
XX  
XX 04-OCT-2001.  
XX  
XX 13-MAR-2001; 2001WO-US008117.  
XX  
XX 13-MAR-2000; 2000US-0188986P.  
PR  
XX (INCY-) INCYTE GENOMICS INC.  
PA  
XX Hillman JL, Baughn MR, Yue H, Lal P, Lu DAM, Patterson C;  
PI Azimzai Y, Bandman O, Tang YT, Mathur P, Shah P, Au-Young J;  
PI Reddy R;  
XX  
XX WPI; 2001-570896/64.  
DR P-PSDB; ABB50150.  
DR  
XX Novel transcription factor polypeptides, used to treat diseases  
PT associated with altered activity and expression of TRFX, and to screen  
PT for agents capable of modulating its activity.  
XX  
XX Claim 11; Page 252; 327pp; English.  
PS  
XX The present sequence is the coding sequence for a human transcription  
CC factor. The transcription factor and its coding sequence are useful in  
CC the diagnosis, treatment and prevention of diseases associated with  
CC altered expression of the transcription factor e.g. cell proliferative,  
CC autoimmune/inflammatory, neurological and developmental disorders. A  
CC number of specific disorders/diseases are given in the specification,  
CC including: arteriosclerosis, cirrhosis, hepatitis, cancers, AIDS,  
CC allergies, anaemia, asthma, autoimmune thyroiditis, bronchitis, atopic  
CC dermatitis, diabetes mellitus, emphysema, Goodpasture's syndrome, gout,  
CC Grave's disease, multiple sclerosis, osteoarthritis, pancreatitis,  
CC psoriasis, rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
CC colitis, uveitis, Alzheimer's disease, Huntington's disease, Parkinson's  
CC disease, stroke, and viral, bacterial, fungal and protozoal infections  
XX  
SQ Sequence 2173 BP; 648 A; 482 C; 555 G; 488 T; 0 U; 0 Other;  
Query Match 78.9%; Score 15; DB 5; Length 2173;

Best Local Similarity 100.0%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Query 5 GGAAGGCGCTTCGG 19  
|||||  
Db 989 GGAAGGCGCTTCGG 1003  
|||||

RESULT 73  
ADB76868/c  
ID ADB76868 standard; DNA; 2240 BP.  
XX AC ADB76868;  
XX XX  
XX 04-DEC-2003 (first entry)  
XX XX  
XX A. gossypii metabolism associated oligo 178 DNA SEQ ID 22.  
XX XX  
XX metabolism; Vitamin B2 production; food supplement; oligo 178; gene; ds.  
XX XX  
XX Erethothecium gossypii.  
XX XX  
XX Key Location/Qualifiers  
XX CDS 394..2019  
FT /\*tag= a  
FT /product= "oligo 178 derived protein SEQ ID 23"  
XX XX  
XX WO2003018813-A2.  
XX XX  
XX 06-MAR-2003.  
XX XX  
XX 23-AUG-2002; 2002WO-EP009454.  
XX XX  
XX 23-AUG-2001; 2001DE-01041267.  
XX 23-AUG-2001; 2001DE-01041268.  
XX 23-AUG-2001; 2001DE-01041280.  
XX 23-AUG-2001; 2001DE-01041281.  
XX 23-AUG-2001; 2001DE-01041282.  
XX 23-AUG-2001; 2001DE-01041283.  
XX 23-AUG-2001; 2001DE-01041284.  
XX 23-AUG-2001; 2001DE-01041288.  
XX 23-AUG-2001; 2001DE-01041289.  
XX 23-AUG-2001; 2001DE-01041290.  
XX 23-AUG-2001; 2001DE-01041291.  
XX 06-MAR-2002; 2002DE-01009829.  
XX 11-APR-2002; 2002DE-01016027.  
XX 11-APR-2002; 2002DE-01016031.  
XX 11-APR-2002; 2002DE-01016032.  
XX 16-MAY-2002; 2002DE-01021912.  
XX 16-MAY-2002; 2002DE-01021914.  
XX 16-MAY-2002; 2002DE-01021917.  
XX 16-MAY-2002; 2002DE-01021920.  
XX 16-MAY-2002; 2002DE-01021927.  
XX 21-JUN-2002; 2002DE-01027797.  
XX 21-JUN-2002; 2002DE-01027798.  
XX (BADI ) BASF AG.  
XX XX  
XX Karos M, Althoefer H, Kroeger B, Revuelta Doval JL;  
XX WPI; 2003-332833/31.  
XX P-PSDB; ADB76869.  
XX XX  
XX New polynucleotide from Ashbya gossypii, useful for increasing microbial  
XX production of Vitamin B2, encodes protein involved in metabolism.  
XX XX  
XX Claim 4; Page 100-102; 141pp; German.  
XX XX  
XX This invention describes novel Ashbya gossypii (also called Erethothecium  
XX gossypii) metabolism associated proteins and their encoding nucleic  
XX acids. Modulating the metabolism of cells improves microbial production  
XX of Vitamin B2, a human and animal food supplement. This sequence  
XX represents Oligo 178 which encodes an A. gossypii metabolism associated

CC protein. Oligo 178 encodes a homologue of a Saccharomyces cerevisiae  
CC phosphoenolpyruvate carboxykinase.  
XX XX  
SQ Sequence 2240 BP; 520 A; 597 C; 645 G; 478 T; 0 U; 0 Other;  
Query Match 78.9%; Score 15; DB 10; Length 2240;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 GGAAGGCGCTTCGG 19  
|||||  
Db 76 GGAAGGCGCTTCGG 62  
|||||

RESULT 74  
ABL07155  
ID ABL07155 standard; cDNA; 3003 BP.  
XX XX  
XX ABL07155;  
XX AC  
XX 26-MAR-2002 (first entry)  
XX DT  
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 15947.  
DE Drosophila; developmental biology; cell signalling; insecticide;  
XX KW  
XX pharmaceutical; gene; ss.  
XX KW  
XX Drosophila melanogaster.  
XX OS  
XX WO200171042-A2.  
XX PN  
XX 27-SEP-2001.  
XX PD  
XX 23-MAR-2001; 2001WO-US009231.  
XX PF  
XX 23-MAR-2000; 2000US-0191637P.  
XX PR  
XX 11-JUL-2000; 2000US-00614150.  
XX PR  
XX (PEKE ) PE CORP NY.  
XX PA  
XX Venter JC, Adams M, Li PWD, Myers EW;  
XX PI  
XX WPI; 2001-656860/75.  
XX DR  
XX P-PSDB; ABB63052.  
XX DR  
XX New isolated nucleic acid detection reagent for detecting 1000 or more  
XX genes from Drosophila and for elucidating cell signaling and cell-cell  
XX interactions.  
XX PT  
XX Claim 1; SEQ ID NO 15947; 21pp + Sequence Listing; English.  
XX PS  
XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of  
XX insecticides, therapeutics and pharmaceutical drugs. The invention  
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
XX ABB72072). The sequence data for this patent did not form part of the  
XX printed specification, but was obtained in electronic format directly  
XX from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX XX  
SQ Sequence 3003 BP; 698 A; 798 C; 889 G; 618 T; 0 U; 0 Other;  
Query Match 78.9%; Score 15; DB 4; Length 3003;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGGCCTT 15  
|||||  
Db 2424 GAACGGAAAGGCCTT 2438  
|||||

RESULT 75  
AAS25944  
ID AAS25944 standard; cDNA; 3293 BP.  
XX  
AC AAS25944;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
XX Human cDNA encoding a novel secreted protein, Seq ID 123.  
DE  
XX  
XX Human; immunosuppressive; antiarthritic; ss; antirheumatic; cytostatic;  
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;  
KW antibacterial; virucide; fungicide; opthalmological; vulnery;  
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;  
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischaemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; skin ageing; food additive;  
KW preservative; antiproliferative.  
XX  
OS Homo sapiens.  
XX  
XX WO20015322-A2.  
PN  
XX  
XX 02-AUG-2001.  
PD  
XX  
XX 17-JAN-2001; 2001WO-US001341.  
PF  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.  
PR 14-AUG-2000; 2000US-0224519P.  
PR 14-AUG-2000; 2000US-0225213P.  
PR 14-AUG-2000; 2000US-0225214P.  
PR 14-AUG-2000; 2000US-0225266P.  
PR 14-AUG-2000; 2000US-0225267P.  
PR 14-AUG-2000; 2000US-0225268P.  
PR 14-AUG-2000; 2000US-0225270P.  
PR 14-AUG-2000; 2000US-0225447P.  
PR 14-AUG-2000; 2000US-0225757P.  
PR 14-AUG-2000; 2000US-0225758P.  
PR 14-AUG-2000; 2000US-0225759P.  
PR 18-AUG-2000; 2000US-0226279P.  
PR 22-AUG-2000; 2000US-0226681P.  
PR 22-AUG-2000; 2000US-0226686P.  
PR 22-AUG-2000; 2000US-0227182P.  
PR 23-AUG-2000; 2000US-0227009P.  
PR 30-AUG-2000; 2000US-0228924P.  
PR 01-SEP-2000; 2000US-0229287P.  
PR 01-SEP-2000; 2000US-0229343P.  
PR 01-SEP-2000; 2000US-0229344P.  
PR 01-SEP-2000; 2000US-0229345P.  
PR 05-SEP-2000; 2000US-0229509P.  
PR 05-SEP-2000; 2000US-0229513P.  
PR 06-SEP-2000; 2000US-0230437P.  
PR 06-SEP-2000; 2000US-0230438P.  
PR 08-SEP-2000; 2000US-0231242P.  
PR 08-SEP-2000; 2000US-0231243P.  
PR 08-SEP-2000; 2000US-0231244P.  
PR 08-SEP-2000; 2000US-0231413P.  
PR 08-SEP-2000; 2000US-0231414P.  
PR 08-SEP-2000; 2000US-0232080P.  
PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.  
PR 14-SEP-2000; 2000US-0232397P.  
PR 14-SEP-2000; 2000US-0232398P.  
PR 14-SEP-2000; 2000US-0232399P.  
PR 14-SEP-2000; 2000US-0232400P.  
PR 14-SEP-2000; 2000US-0232401P.  
PR 14-SEP-2000; 2000US-0233063P.  
PR 14-SEP-2000; 2000US-0233064P.  
PR 14-SEP-2000; 2000US-0233065P.  
PR 21-SEP-2000; 2000US-0234223P.  
PR 21-SEP-2000; 2000US-0234274P.  
PR 25-SEP-2000; 2000US-0234997P.  
PR 25-SEP-2000; 2000US-0234998P.  
PR 26-SEP-2000; 2000US-0235484P.  
PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235836P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.



PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 05-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 11-DEC-2000; 2000US-0251990P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX  
 XX WPI; 2001-488783/53.  
 DR P-PSDB; AAU15957.  
 XX  
 XX New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives.  
 XX  
 XX Claim 1; SEQ ID NO 123; 980pp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used  
 CC in diagnosing a pathological condition or susceptibility to a  
 CC pathological condition. Antibodies to the proteins can also be used in  
 CC alleviating symptoms associated with the disorders and in diagnostic  
 CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbent assays  
 CC (ELISA). Disorders which are diagnosed or treated include autoimmune  
 CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.  
 CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac  
 CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,  
 CC nervous system disorders e.g. Alzheimer's disease, infections caused by  
 CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,  
 CC and many other disorders listed in the specification. The polypeptides  
 CC can also be used to aid wound healing and epithelial cell proliferation,  
 CC to prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence encodes a novel secreted protein of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 Query Match 78.9%; Score 15; DB 4; Length 3293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 GGAAAGGCTTTCGG 19  
 Db 892 GGAAAGGCTTTCGG 906  
 RESULT 76  
 ABX73285  
 ID ABX73285 standard; DNA; 3293 BP.  
 XX  
 AC ABX73285;  
 XX  
 DT 18-MAR-2003 (first entry)

XX Human novel polynucleotide #113.  
 XX  
 KW Human; gene; ds; neural disorder; immune system disorder; renal disorder;  
 KW muscular disorder; respiratory disease; reproductive disorder;  
 KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;  
 KW hyperproliferative disorder; inflammatory disease; allergic reaction;  
 KW blood related disorder; cancer; immunosuppressive; antiinflammatory;  
 KW cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;  
 KW haemostatic; antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002132753-A1.  
 XX  
 XX 19-SEP-2002.  
 XX  
 XX 17-JAN-2001; 2001US-00764864.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 07-JUL-2000; 2000US-0216647P.  
 PR 07-JUL-2000; 2000US-0216880P.  
 PR 11-JUL-2000; 2000US-0217487P.  
 PR 11-JUL-2000; 2000US-0217496P.  
 PR 14-JUL-2000; 2000US-0218290P.  
 PR 26-JUL-2000; 2000US-0220963P.  
 PR 26-JUL-2000; 2000US-0220964P.  
 PR 14-AUG-2000; 2000US-0224518P.  
 PR 14-AUG-2000; 2000US-0224519P.  
 PR 14-AUG-2000; 2000US-0225267P.  
 PR 14-AUG-2000; 2000US-0225268P.  
 PR 14-AUG-2000; 2000US-0225270P.  
 PR 14-AUG-2000; 2000US-0225447P.  
 PR 14-AUG-2000; 2000US-0225757P.  
 PR 14-AUG-2000; 2000US-0225758P.  
 PR 22-AUG-2000; 2000US-0226868P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 21-SEP-2000; 2000US-0234223P.  
 PR 21-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-0236367P.  
 PR 29-SEP-2000; 2000US-0236368P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0236370P.  
 PR 02-OCT-2000; 2000US-0236802P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237039P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-0239935P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241809P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.



```
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR P-PSDB; ABB63051.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Claim 1; SEQ ID NO 15944; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 8544 BP; 2263 A; 2022 C; 2092 G; 2167 T; 0 U; 0 Other;
SQ
Query Match 78.9%; Score 15; DB 4; Length 8544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAACGGAAAGGCCTT 15
DB 6899 GAACGGAAAGGCCTT 6913
RESULT 79
AAT70787/c
ID AAT70787 standard; RNA; 40 BP.
AC AAT70787;
XX
XX 30-JUL-1997 (first entry)
XX
XX Stenotic carotid artery binding ligand Civ19.
XX
XX Ligand; peripheral blood mononuclear cell; fibrin clot; carotid artery;
XX systematic evolution of ligands by exponential enrichment method; PBMC;
XX epitope; macromolecule; tissue SELEX method; cancer screening; therapy;
XX AIDS monitoring; localisation of thrombi; atherosclerosis; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..40
XX /*tag= a
XX /mod_base= all C's are 2-fluorine-C
XX modified_base 1..40
XX /*tag= b
XX /mod_base= all U's are 2-fluorine-U
XX
XX WO9634874-A1.
XX
XX 07-NOV-1996.
XX
XX 01-MAY-1996; 96WO-US006059.
XX
XX 03-MAY-1995; 95US-00433124.
XX
XX 03-MAY-1995; 95US-00433126.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX (SCHD ) SCHERING AG.
XX
XX Stephens A, Gold L, Speck U;
XX
XX Stephens A, Schneider DJ, Gold L, Speck U;
XX WPI; 1996-506091/50.
XX
XX Nucleic acid ligands used in cancer screening, AIDS monitoring etc. -
XX bind to peripheral blood mononuclear cells, fibrin clots or carotid
XX arteries.
XX
XX Claim 23; Page 58; 138pp; English.
XX
XX AAT70705-T70803 represent the random regions from a degenerate ssDNA
XX library based on the sequence represented by AAT72819. These sequences
XX are all ligands specific for fibrin clots identified using the method of
XX the invention. The method of the invention is for identifying nucleic
XX acid (NA) ligands and NA ligand sequences to a tissue target selected
XX from peripheral blood mononuclear cells (PBMC's) (such as the ligands
XX represented by AAT70584-T70616), fibrin clots (such as the ligands
XX represented by AAT70617-T70704), and carotid arteries (such as these
XX ligands). The method comprises preparing a candidate mixture of NA
XX sequences, and contacting these with the tissue, whereby NAs having an
XX increased affinity to the tissue relative to the candidate mixture may be
XX partitioned from the remainder of the candidate mixture. The increased
XX affinity NAs are then partitioned from the remainder of the candidate
XX mixture, and are amplified to yield a mixture of NAs enriched for NA
XX sequences with a relatively higher affinity and specificity for binding
XX to the tissue, whereby NA ligands of the tissue may be identified. The
XX method represents a tissue SELEX (systematic evolution of ligands by
XX exponential enrichment) method. The NA ligands and epitopes and
XX macromolecules identified using the ligands can be used in diagnostic and
XX therapeutic applications. In particular, they can be used for e.g. cancer
XX screening, AIDS monitoring, detection and localisation of thrombi or
XX atherosclerosis diagnosis and therapy
XX
XX Sequence 40 BP; 9 A; 13 C; 8 G; 0 T; 10 U; 0 Other;
SQ
Query Match 77.9%; Score 14.8; DB 2; Length 40;
Best Local Similarity 88.9%; Pred. No. 9.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 AACGGAAGGCCTTCGG 19
DB 27 ATCGTAAGGCCTTCGG 10
RESULT 80
AAX85278/c
ID AAX85278 standard; RNA; 87 BP.
XX
XX AAX85278;
XX
XX 06-AUG-1999 (first entry)
XX
XX Motif I final cluster oligonucleotide SEQ ID NO:221.
XX
XX Nucleic acid ligand; high-affinity; tissue target; blood vessel;
XX atherosclerotic plaque; carotid artery; WHHL; diagnosis; therapy;
XX watanabe heritable hyperlipidaemia; ss.
XX
XX Synthetic.
XX
XX WO9927138-A1.
XX
XX 03-JUN-1999.
XX
XX 19-NOV-1998; 98WO-US025006.
XX
XX 21-NOV-1997; 97US-00976413.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX (SCHD ) SCHERING AG.
XX
XX Stephens A, Gold L, Speck U;
XX
```

XX WPI; 1999-357856/30.  
 XX Identifying nucleic acid ligands to blood vessels.  
 XX Example 3; Page 69; 210pp; English.  
 XX The present invention describes a new method of identifying nucleic acid  
 CC ligands to blood vessels. The method comprises contacting and  
 CC partitioning nucleic acid sequences having increased affinity to the  
 CC blood vessels and amplifying enriched sequences. The nucleic acid ligands  
 CC are capable of binding specifically to tissues which are macromolecules  
 CC in a heterogeneous environment, such as whole cells or substructures,  
 CC aggregates of cells, collections of cells, or aggregates of  
 CC macromolecules. The ligands can be used to identify and purify epitopes  
 CC and macromolecules. The products can be used as diagnostic and  
 CC therapeutic agents. AAX85058 to AAX85497 represent oligonucleotides used  
 CC in the exemplification of the present invention  
 XX  
 SQ Sequence 87 BP; 27 A; 23 C; 21 G; 0 T; 16 U; 0 Other;  
 Query Match 77.9%; Score 14.8; DB 2; Length 87;  
 Best Local Similarity 88.9%; Pred. No. 1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AACGGAAGGCGCTTCGG 19  
 Db 50 ATCGTAAGGCGCTTCGG 33  
 RESULT 81  
 ADP20374/c  
 ID ADP20374 standard; DNA; 365 BP.  
 AC ADP20374;  
 DT 26-AUG-2004 (first entry)  
 XX Pinus radiata alpha expansin regulatory sequence SEQ ID NO:63.  
 DE  
 XX vascular-preferred polynucleotide transcription; plant;  
 KW lignin regulation; cell wall development regulation; wood;  
 KW vascular-preferred gene expression; lignin biosynthesis; lignin;  
 KW cellulose; Pinus radiata; regulatory sequence;  
 KW vascular-preferred promoter; promoter; gene; ds.  
 XX  
 OS Pinus radiata.  
 XX  
 XX WO2004048595-A2.  
 XX  
 XX 10-JUN-2004.  
 XX  
 XX 21-NOV-2003; 2003WO-US037412.  
 XX  
 XX 22-NOV-2002; 2002US-0428287P.  
 XX  
 XX (ARBO-) ARBORGEN LLC.  
 XX  
 XX Phillips J, Puthigae S, Yao J, Flinn B, Forster RS, Eagleton C;  
 PI  
 XX WPI; 2004-480352/45.  
 XX  
 XX New nucleic acid molecule that is capable of conferring vascular-  
 PT preferred polynucleotide transcription, useful for regulating  
 PT biosynthesis of lignin, and for controlling the lignin content in plant  
 PT cell walls.  
 XX  
 XX Claim 2; SEQ ID NO 63; 90pp; English.  
 PS  
 XX The present invention describes an isolated nucleic acid molecule (I)  
 CC comprising a polynucleotide that is capable of conferring vascular-  
 CC preferred polynucleotide transcription. Also described: (1) an isolated  
 CC polynucleotide having a sequence selected from: (a) sequences  
 CC complementary to any of the sequences of SEQ ID NO:1 to 85 (S1, ADP20312  
 CC to ADP20396); (b) sequences that are reverse complements of any one of  
 CC (S1); and (c) sequences comprising at least 20 contiguous bases, which  
 CC hybridises to any one of (a) or (b); (2) a plant cell (II) comprising at  
 CC least one polynucleotide sequence that has (S1) and a desired gene, where  
 CC the polynucleotide and the desired gene are operably linked; (3) a plant  
 CC (III) comprising (II); (4) regulating the lignin content of a plant,  
 CC which involves cultivating (III); (5) regulating cell wall development in  
 CC a plant, which involves cultivating (III); (6) a transgenic plant  
 CC comprising a polynucleotide sequence chosen from (S1) and its functional  
 CC variants; and (7) obtaining (MI) wood, which involves introducing into a  
 CC plant cell of a woody plant a DNA construct comprising a promoter having  
 CC (S1) or its functional variants and a desired nucleic acid, where a  
 CC promoter regulates the expression of the desired nucleic acid, culturing  
 CC the transformed plant cell under condition that promote growth of a plant  
 CC and obtaining wood from the plant. (I) is useful for conferring vascular-  
 CC preferred gene expression, for regulating biosynthesis of lignin, for  
 CC controlling the lignin content plant cell walls, cellulose content, size  
 CC or cell wall development of a plant, cellulose. The present sequence  
 CC represents a Pinus radiata regulatory sequence, which is a vascular-  
 CC preferred promoter from the present invention.  
 XX  
 SQ Sequence 365 BP; 112 A; 79 C; 79 G; 95 T; 0 U; 0 Other;  
 Query Match 77.9%; Score 14.8; DB 12; Length 365;  
 Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AACGGAAGGCGCTTCGG 19  
 Db 158 AACGGACGGCGCTTCGG 141  
 RESULT 82  
 ACH95596  
 ID ACH95596 standard; DNA; 375 BP.  
 AC ACH95596;  
 XX  
 XX 29-JUL-2004 (first entry)  
 DT  
 XX Klebsiella pneumoniae polynucleotide seqid 1391.  
 DE  
 KW Recombinant expression vector; transcription regulatory element;  
 KW Klebsiella pneumoniae protein; antibacterial; Vaccine; gene; ds.  
 XX  
 XX Klebsiella pneumoniae.  
 OS  
 XX US6610836-B1.  
 XX  
 XX 26-AUG-2003.  
 XX  
 XX 27-JAN-2000; 2000US-00489039.  
 XX  
 XX 29-JAN-1999; 99US-0117747P.  
 XX  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 XX  
 XX Breton GL, Osborne M;  
 PI  
 XX WPI; 2003-895346/82.  
 DR  
 XX P-PSDB; ABO62045.  
 XX  
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
 PT preparing a vaccine composition against Klebsiella pneumoniae.  
 XX  
 XX Disclosure; SEQ ID NO 1391; 932pp; English.  
 PS  
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition

CC against Klebsiella pneumoniae. This sequence encodes a Klebsiella  
CC pneumoniae polypeptide of the invention  
XX  
SQ Sequence 375 BP; 71 A; 82 C; 113 G; 109 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 11; Length 375;  
Best Local Similarity 88.9%; Pred. No. 1.1e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18  
|||||  
DB 333 GAACGGAAGGCTTTTCG 350

RESULT 83  
ABD06974

ID ABD06974 standard; DNA; 543 BP.

XX

AC ABD06974;

DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polynucleotide #5578.

XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;

KW antibacterial.

XX Pseudomonas aeruginosa.

OS US6551795-B1.

PN

XX 22-APR-2003.

XX 18-FEB-1999; 99US-00252991.

XX 18-FEB-1998; 98US-0074788P.

PR 27-JUL-1998; 98US-0094190P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX Rubenfield MJ, Nollong J, Deloughery C, Bush D;

PI WPI; 2003-615309/58.

DR P-PSDB; ABO73403.

XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.

PS Disclosure; SEQ ID NO 5578; 455pp; English.

CC The invention relates to Pseudomonas aeruginosa polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-P. aeruginosa drugs, as templates for recombinant  
CC production of P. aeruginosa-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of P. aeruginosa-caused  
CC infection, and in detection of P. aeruginosa sequences or other sequences  
CC of Pseudomonas species using biochip technology. Sequences ABD01397-  
CC ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html

XX Sequence 543 BP; 125 A; 174 C; 147 G; 97 T; 0 U; 0 Other;

Query Match

Best Local Similarity 77.9%; Score 14.8; DB 11; Length 543;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18  
|||||  
DB 145 GAACGATAGGCTGTCTG 162

RESULT 84

AAI43438/C

ID AAI43438 standard; DNA; 591 BP.

XX

AC AAI43438;

DT 17-OCT-2001 (first entry)

XX Probe #12124 used to measure gene expression in human placenta sample.

DE Probe; microarray; human; placenta; antenatal diagnosis;

XX genetic disorder; ss.

OS Homo sapiens.

XX WO200157272-A2.

PN 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000663.

XX 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX gene expression in human placenta.

XX Claim 25; SEQ ID NO 12124; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP).  
XX The present sequence is one such probe. The probes are useful for  
XX producing a microarray for predicting, measuring and displaying gene  
XX expression in samples derived from human placenta. The probes are useful  
XX for antenatal diagnosis of human genetic disorders

XX Sequence 591 BP; 122 A; 171 C; 156 G; 142 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 4; Length 591;

Best Local Similarity 88.9%; Pred. No. 1.2e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18  
|||||

DB 266 GATGGGAAGGCTTTTCG 249

RESULT 85

ABD07046/C

ID ABD07046 standard; DNA; 600 BP.

XX

AC ABD07046;

DT 29-JUL-2004 (first entry)

XX Pseudomonas aeruginosa polynucleotide #5650.

KW	Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;	
KW	antibacterial.	
XX		
OS	Pseudomonas aeruginosa.	
XX		
PN	US6551795-B1.	
XX		
PD	22-APR-2003.	
XX		
PF	18-FEB-1999; 99US-00252991.	
XX		
PR	18-FEB-1998; 98US-0074788P.	
PR	27-JUL-1998; 98US-0094190P.	
XX		
PA	(GENO-) GENOME THERAPEUTICS CORP.	
XX		
PI	Rubenfield MJ, Nolling J, Deloughery C, Bush D;	
XX		
DR	WPI; 2003-615309/58.	
DR	P-PSDB; ABO73475.	
XX		
PT	Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,	
PT	useful as molecular targets for diagnostics, prophylaxis and treatment of	
PT	pathological conditions resulting from bacterial infection.	
XX		
PS	Disclosure; SEQ ID NO 5650; 455pp; English.	
XX		
CC	The invention relates to Pseudomonas aeruginosa polypeptides and the	
CC	polynucleotides encoding them. The sequences are useful in diagnosis and	
CC	therapy of pathological conditions, as molecular targets for diagnostics,	
CC	prophylaxis and treatment of pathological conditions resulting from a	
CC	bacterial infection, for evaluating a compound, such as a polypeptide,	
CC	for the ability to bind a P. aeruginosa nucleic acid, as components of	
CC	effective antibacterial targets, as targets for antibacterial drugs,	
CC	including anti-P. aeruginosa drugs, as templates for recombinant	
CC	production of P. aeruginosa-derived peptides or polypeptides, as target	
CC	components for diagnosis and/or treatment of P. aeruginosa-caused	
CC	infection, and in detection of P. aeruginosa sequences or other sequences	
CC	of Pseudomonas species using biochip technology. Sequences ABD01397-	
CC	ABD17967 represent P. aeruginosa polynucleotides of the invention. Note:	
CC	The sequence data for this patent did not form part of the printed	
CC	specification but was obtained in electronic format from USPTO at	
CC	seqdata.uspto.gov/sequence.html	
XX		
SQ	Sequence 600 BP; 108 A; 167 C; 189 G; 136 T; 0 U; 0 Other;	
	Query Match 77.9%; Score 14.8; DB 11; Length 600;	
	Best Local Similarity 88.9%; Pred. No. 1.2e+03;	
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GAACGGAAGGCCTTTCG 18	
Db	468 GAACGGATAGGCCTGTCG 451	
	RESULT 86	
	ACA27357	
ID	ACA27357 standard; DNA; 981 BP.	
XX		
AC	ACA27357;	
XX		
DT	19-JUN-2003 (first entry)	
DE	Prokaryotic essential gene #9014.	
XX		
KW	Antisense; ds; prokaryotic essential gene; cell proliferation;	
KW	drug design; gene.	
OS	Bordetella pertussis.	
XX		
PN	WO200277183-A2.	
XX		
PD	03-OCT-2002.	
XX		
PF	21-MAR-2002; 2002WO-US009107.	
XX		
PR	21-MAR-2001; 2001US-00815242.	
PR	06-SEP-2001; 2001US-00948993.	
PR	25-OCT-2001; 2001US-0342923P.	
PR	08-FEB-2002; 2002US-00072851.	
PR	06-MAR-2002; 2002US-0362699P.	
XX		
PA	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;	
PI	Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;	
XX		
DR	WPI; 2003-029926/02.	
DR	P-PSDB; ABU23487.	
XX		
PT	New antisense nucleic acids, useful for identifying proteins or screening	
PT	for homologous nucleic acids required for cellular proliferation to	
PT	isolate candidate molecules for rational drug discovery programs.	
XX		
PS	Claim 14; SEQ ID NO 15227; 1765pp; English.	
XX		
CC	The invention relates to an isolated nucleic acid comprising any one of	
CC	the 6213 antisense sequences given in the specification where expression	
CC	of the nucleic acid inhibits proliferation of a cell. Also included are:	
CC	(1) a vector comprising a promoter operably linked to the nucleic acid	
CC	encoding a polypeptide whose expression is inhibited by the antisense	
CC	nucleic acid; (2) a host cell containing the vector; (3) an isolated	
CC	polypeptide or its fragment whose expression is inhibited by the	
CC	antisense nucleic acid; (4) an antibody capable of specifically binding	
CC	the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular	
CC	proliferation or the activity of a gene in an operon required for	
CC	proliferation; (7) identifying a compound that influences the activity of	
CC	the gene product or that has an activity against a biological pathway	
CC	required for proliferation, or that inhibits cellular proliferation; (8)	
CC	identifying a gene required for cellular proliferation or the biological	
CC	pathway in which a proliferation-required gene or its gene product lies	
CC	or a gene on which the test compound that inhibits proliferation of an	
CC	organism acts; (9) manufacturing an antibiotic; (10) profiling a	
CC	compound's activity; (11) a culture comprising strains in which the gene	
CC	product is overexpressed or underexpressed; (12) determining the extent	
CC	to which each of the strains is present in a culture or collection of	
CC	strains; or (13) identifying the target of a compound that inhibits the	
CC	proliferation of an organism. The antisense nucleic acids are useful for	
CC	identifying proteins or screening for homologous nucleic acids required	
CC	for cellular proliferation to isolate candidate molecules for rational	
CC	drug discovery programs, or for screening homologous nucleic acids	
CC	required for proliferation in cells other than S. aureus, S. typhimurium,	
CC	K. pneumoniae or P. aeruginosa. The present sequence is one of the target	
CC	prokaryotic essential genes. Note: The sequence data for this patent did	
CC	not form part of the printed specification, but was obtained in	
CC	electronic format directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences	
XX		
SQ	Sequence 981 BP; 189 A; 306 C; 353 G; 133 T; 0 U; 0 Other;	
	Query Match 77.9%; Score 14.8; DB 8; Length 981;	
	Best Local Similarity 88.9%; Pred. No. 1.2e+03;	
	Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 GAACGGAAGGCCTTTCG 18	
Db	169 GAACGGAAGGCCTGCG 186	
	RESULT 87	
	ADW16249	
ID	ADW16249 standard; DNA; 1158 BP.	
XX		
AC	ADW16249;	
XX		
DT	07-APR-2005 (first entry)	

XX DNA copy of the Microbispora 16s ribosomal RNA EN2 isolate Seq 1.  
 DE 16s ribosomal RNA; ds; 16s rRNA; medicinal plant; plant breeding;  
 KW disease resistance; insect resistance; crop improvement;  
 KW plant growth factor; antibacterial; antimicrobial; fungicide;  
 KW insecticide; nematocide.  
 XX Microbispora.  
 OS WO2005003328-A1.  
 PN 13-JAN-2005.  
 XX 07-JUL-2004; 2004WO-AU000914.  
 XX 07-JUL-2003; 2003US-0485241P.  
 PR 22-SEP-2003; 2003US-0504703P.  
 XX (FLIN-) FLINDERS TECHNOLOGIES PTY LTD.  
 PA Franco CMM, Coombs JT;  
 XX WPI; 2005-091806/10.  
 DR Improving plant productivity comprises introducing into the plant or  
 PT propagation material an endophytic actinomycete that facilitates  
 PT induction of at least one characteristic related to improved  
 PT productivity.  
 XX Claim 1; SEQ ID NO 1; 235pp; English.  
 PS This invention relates to a novel method for improving plant  
 XX productivity. Specifically, it refers to introducing into the plant or  
 CC propagation material an endophytic actinomycetes or variant thereof,  
 CC where the actinomycetes facilitate induction of a characteristic related  
 CC to improved productivity. The present invention further describes  
 CC metabolites of the actinomycetes microorganism such as auxin, gibberellin  
 CC or cytokinin that are able to induce disease resistance in plants i.e.  
 CC provide disease bio-control capabilities against pathogen infection.  
 CC Accordingly, the method facilitates the improvement of cereal crop  
 CC productivity including increasing germination by up-regulating plant  
 CC growth promoting activities, as well as improving plant vigor or flower  
 CC and fruit yield. Furthermore, the new actinomycete or metabolite is  
 CC useful in the manufacture of a medicament for the therapeutic and/or  
 CC prophylactic treatment of a mammalian or non-mammalian subject i.e.  
 CC plant. As such, this method provides plant protectants and plant growth  
 CC stimulants that exhibit antibacterial, antimicrobial, fungicide,  
 CC insecticide and nematocide activities. This polynucleotide is the DNA  
 CC sequence of an actinomycetes 16s ribosomal RNA sequence of the invention.  
 XX Sequence 1158 BP; 247 A; 265 C; 379 G; 234 T; 0 U; 33 Other;  
 SQ Query Match 77.9%; Score 14.8; DB 14; Length 1158;  
 Best Local Similarity 88.9%; Pred. No. 1.2e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AACGGAAGGCTTCGG 19  
 Db 19 AGCGGAAGGCTTCGG 36  
 RESULT 88  
 AAZ11765  
 ID AAZ11765 standard; DNA; 1392 BP.  
 XX AAZ11765;  
 AC 15-NOV-1999 (first entry)  
 XX Maize histone H2B promoter.  
 DE Promoter; constitutive expression; transgenic plant; maize;  
 XX

KW genetic modification; ds.  
 XX Zea mays.  
 PH Location/Qualifiers  
 FT TATA\_signal 871..876  
 FT /tag= a  
 FT /note= "Approximately 25 bases upstream of  
 FT transcriptional start site"  
 XX WO9943797-A2.  
 PN 02-SEP-1999.  
 XX 25-FEB-1999; 99WO-US004203.  
 XX 26-FEB-1998; 98US-0076075P.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 PA Rice DA;  
 PI WPI; 1999-518854/43.  
 DR New constitutive promoter sequences from maize, useful in genetic  
 PT manipulation of plants.  
 XX Claim 1; Page 39; 53pp; English.  
 PS This sequence represents a maize histone H2B constitutive promoter. Maize  
 XX H2B histones are constitutively expressed at a high level in meristematic  
 CC tissue. This promoter was isolated and amplified from a maize seedling  
 CC genomic library using an APL primer (AAZ11775) and a gene-specific  
 CC primer, histone H2B gsp-1 (AAZ11776). The DNA from this first round of  
 CC PCR was diluted and used as a template for a second round of PCR, this  
 CC time using an AP2 primer (AAZ06802) and a second gene-specific primer,  
 CC histone H2B gsp-2 (AAZ06803). The amplified DNA was sequenced for  
 CC verification, cloned into the TA vector pCR2.1, miniprep and subjected  
 CC to a third round of PCR using the AP2 primer and a third gene-specific  
 CC primer, histone H2B gsp-3 (AAZ06810). This sequence, and other  
 CC constitutive plant promoters (AAZ11766-Z11774), are capable of initiating  
 CC constitutive expression in plant cells and have potential for use in  
 CC vectors used to introduce and express heterologous DNA sequences in  
 CC plants. Such a vector would comprise the heterologous DNA sequence  
 CC operably linked to the promoter. The vector could then be used to  
 CC transform a plant cell. A stably transformed plant could then be  
 CC regenerated from the transformed plant cell. The heterologous sequences  
 CC that could be linked to these constitutive promoters might include a  
 CC pathogen-resistance gene, enabling pathogen-resistance proteins to be  
 CC continuously expressed throughout the plant's tissues. Alternatively,  
 CC antisense DNA could be used to inhibit the expression of a native gene to  
 CC produce a desired phenotype. The antisense RNA transcript would bind to  
 CC native mRNA and interfere with translation  
 XX Sequence 1392 BP; 394 A; 280 C; 259 G; 459 T; 0 U; 0 Other;  
 SQ Query Match 77.9%; Score 14.8; DB 2; Length 1392;  
 Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AACGGAAGGCTTCGG 19  
 Db 1143 AAAGGAAGGCTTCGG 1160  
 RESULT 89  
 ADA71495  
 ID ADA71495 standard; DNA; 2000 BP.  
 XX ADA71495;  
 AC 20-NOV-2003 (first entry)  
 XX

XX Rice gene, SEQ ID 4818.  
DE  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
XX  
OS Oryza sativa.  
XX  
XX  
PN WC2003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
XX  
XX  
PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
XX WPI; 2003-175290/17.  
XX  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
XX Claim 27; SEQ ID NO 4818; 899pp; English.  
XX  
XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
XX Sequence 2000 BP; 684 A; 323 C; 365 G; 627 T; 0 U; 1 Other;  
SQ  
Query Match 77.9%; Score 14.8; DB 8; Length 2000;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 AACGGAAGGCGCTTCGG 19  
DB 949 AACGGAAGGCGCTTCGG 966  
RESULT 90  
ACL36116/c  
ID ACL36116 standard; cDNA; 2000 BP.  
XX  
AC ACL36116;  
XX  
XX 02-JUN-2005 (first entry)  
XX  
DE Rice stress-regulated promoter SEQ ID NO:14679.  
XX  
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
KW agriculture.  
XX  
OS Oryza sativa.  
XX  
XX WO2003008540-A2.  
PN  
XX  
XX 30-JAN-2003.  
PD  
XX  
XX 21-JUN-2002; 2002WO-US019668.  
PF  
XX

PR 22-JUN-2001; 2001US-0300112P.  
PR 24-AUG-2001; 2001US-0314662P.  
PR 26-SEP-2001; 2001US-0325277P.  
PR 21-NOV-2001; 2001US-0332132P.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Kreps J Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,  
PI Moughamer T, Provart N, Ricke D, Zhu T;  
XX  
XX WPI; 2003-248011/24.  
XX  
XX New stress-responsive nucleic acid, useful for altering the  
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.  
XX  
XX Claim 48; SEQ ID NO 14679; 89pp; English.  
XX  
XX The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the  
CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention  
XX  
XX Sequence 2000 BP; 626 A; 426 C; 367 G; 581 T; 0 U; 0 Other;  
SQ  
Query Match 77.9%; Score 14.8; DB 11; Length 2000;  
Best Local Similarity 88.9%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGAAGGCGCTTCG 18  
DB 1299 GAACGGAAGGCGCTTCG 1282  
RESULT 91  
ABL14648  
ID ABL14648 standard; cDNA; 7564 BP.  
XX  
AC ABL14648;  
XX  
XX 26-MAR-2002 (first entry)  
XX  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38426.  
XX  
XX Drosophila; developmental biology; cell signalling; insecticide;  
KW pharmaceutical; gene; ss.  
XX  
XX Drosophila melanogaster.  
XX  
XX WO200171042-A2.  
PN  
XX  
XX 27-SEP-2001.  
PD  
XX  
XX 23-MAR-2001; 2001WO-US009231.  
PF  
XX  
XX 23-MAR-2000; 2000US-0191637P.  
PR  
XX 11-JUL-2000; 2000US-00614150.  
XX  
XX (PEKE ) PE CORP NY.  
PA  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
PI  
XX WPI; 2001-656860/75.  
DR



DR P-PSDB; ABB70545.

PT New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from *Drosophila* and for elucidating cell signaling and cell-cell

PT interactions.

XX

XX Claim 1; SEQ ID NO 38426; 2lpp + Sequence Listing; English.

PS

CC The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA

CC sequences (AB101840-AB116175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX

XX Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

Qy Query Match 77.9%; Score 14.8; DB 4; Length 7564;

Db Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTCGG 19

Db 4458 AACGGAAGGCTTTCGG 4475

RESULT 92

AAS57142

ID AAS57142 standard; DNA; 7564 BP.

XX

AC AAS57142;

XX

DT 16-JAN-2002 (first entry)

XX

DE DNA encoding *Drosophila* G-protein coupled receptor, GPCR #36.

XX

XX *Drosophila*; G-protein coupled receptor; GPCR; insecticide; diagnostic;

XX mutation detection; ds.

XX

XX *Drosophila melanogaster*.

XX

XX WO200170980-A2.

XX

XX 27-SEP-2001.

XX

XX 23-MAR-2001; 2001WO-US009341.

XX

XX 23-MAR-2000; 2000US-0191638P.

XX

XX 18-JUL-2000; 2000US-00618893.

XX

XX (PEKE ) PE CORP NY.

PA

XX Cravchik A;

PI

XX WPI; 2001-616405/71.

DR P-PSDB; AAU38958.

DR

XX Sixty six *Drosophila melanogaster* G-protein coupled receptors (GPCR),

PT useful in the treatment and diagnosis of GPCR-related conditions and for

PT identifying GPCR modulators for use as insecticides.

XX

XX Claim 4; Page 182-184; 392pp; English.

XX

CC The invention relates to sixty six novel isolated *Drosophila melanogaster*

CC G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids

CC are useful in the treatment and diagnosis of GPCR-related conditions. The

CC GPCR proteins and nucleic acids are also useful for identifying

CC modulators of GPCR proteins for use as insecticides. The nucleic acid can

CC also be used to detect mutations in GPCR genes and gene expression

CC products such as mRNA. AAS57072-AAS57203 represent *D. melanogaster* G-

CC coupled protein receptor genomic and coding sequences of the invention

XX

XX Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

Qy Query Match 77.9%; Score 14.8; DB 4; Length 7564;

Db Best Local Similarity 88.9%; Pred. No. 1.5e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTCGG 19

Db 4458 AACGGAAGGCTTTCGG 4475

RESULT 93

ADC35854

ID ADC35854 standard; DNA; 7564 BP.

XX

AC ADC35854;

XX

DT 18-DEC-2003 (first entry)

XX

XX *Drosophila* G protein coupled receptor genomic DNA seq id 36.

DE

XX G-protein coupled receptor; GPCR; insecticide; drug screening;

XX insecticide screening; insecticidal activity; insecticidal tolerance;

XX fruit fly; gene; ds.

XX

XX *Drosophila melanogaster*.

XX

XX US2003092124-A1.

XX

XX 15-MAY-2003.

XX

XX 15-OCT-2002; 2002US-00270333.

XX

XX 03-DEC-1999; 99US-0168677P.

PR 12-JAN-2000; 2000US-0175691P.

PR 23-MAR-2000; 2000US-0191638P.

PR 18-JUL-2000; 2000US-00618893.

XX

XX (APPL-) APPLERA CORP.

PA

XX Cravchik A;

PI

XX WPI; 2003-765480/72.

DR P-PSDB; ADC35856.

DR

XX New isolated G-protein coupled receptor useful for identifying modulators

PT as potential insecticides, to determine the biological activity of the

PT protein and for identifying compounds that modulate receptor activity.

XX

XX Claim 4; SEQ ID NO 106; 130pp; English.

XX

CC The invention describes an isolated protein (I) consisting or comprising

CC an amino acid sequence selected from fully defined 66 G-protein coupled

CC receptor amino acid sequences (S1), as given in the specification, an

CC allelic variant of (S1), an orthologue of (S1) or fragment of (S1). (I)

CC is useful for identifying an agent that binds to (I) which comprises

CC contacting the protein with an agent and assaying the contacted mixture

CC to determine whether a complex is formed with the agent bound to the

CC protein. (I) is useful for identifying modulators as potential

CC insecticides, to determine the biological activity of the protein (a

CC panel of multiple proteins for high-throughput screening), as targets for

CC identifying agents for use in human drugs and for identifying compounds

CC that modulate receptor activity. An antibody (II) that selectively binds

CC to (I) is useful for assessing normal and aberrant subcellular

CC localisation of cells and monitoring a treatment modality. A nucleic acid

CC (III) encoding (I) is useful for drug/insecticide screening to identify

CC compounds that modulate G-protein coupled receptor (GPCR) nucleic acid

CC expression, diagnostic assays for qualitative changes in GPCR nucleic

CC acid that lead to insecticidal activity/tolerance, to detect mutations in

CC GPCR genes and gene expression products such as mRNA, and as

CC hybridisation probes for determining the presence, level, form and  
 CC distribution of nucleic acid expression. A host cell comprising a vector  
 CC containing (III) is useful for conducting cell-based assays involving the  
 CC GPCR protein or its fragments, and identifying GPCR protein mutants. This  
 CC sequence encodes a fruit fly G-protein coupled receptor (GPCR).

XX  
 SQ Sequence 7564 BP; 2230 A; 1694 C; 1619 G; 2021 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 10; Length 7564;  
 Best Local Similarity 88.9%; Pred. No. 1.5e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCTTCG 19  
 ||||| |||||  
 Db 4458 AACGGAATGGCTTCG 4475

RESULT 94  
 AAK64938  
 ID AAK64938 standard; DNA; 19183 BP.

XX AC AAK64938;

DT 06-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:19750.

DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytosstatic; gene therapy; vaccine; metastasis; db.

XX Homo sapiens.

XX WC200157182-A2.

XX PD 09-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001354.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225133P.

PR 14-AUG-2000; 2000US-0225214P.

PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
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 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0232398P.  
 PR 14-SEP-2000; 2000US-0232399P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234223P.  
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 PR 25-SEP-2000; 2000US-0234997P.  
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 PR 26-SEP-2000; 2000US-0234984P.  
 PR 27-SEP-2000; 2000US-0235834P.  
 PR 27-SEP-2000; 2000US-0235836P.  
 PR 29-SEP-2000; 2000US-0236327P.  
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 PR 02-OCT-2000; 2000US-0237040P.  
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 PR 08-NOV-2000; 2000US-0246526P.  
 PR 08-NOV-2000; 2000US-0246527P.  
 PR 08-NOV-2000; 2000US-0246528P.  
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 PR 08-NOV-2000; 2000US-0246610P.  
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 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
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PR 17-NOV-2000; 2000US-0249211P.  
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 PR 17-NOV-2000; 2000US-0249216P.  
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 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249219P.  
 PR 17-NOV-2000; 2000US-0249220P.  
 PR 17-NOV-2000; 2000US-0249221P.  
 PR 17-NOV-2000; 2000US-0249222P.  
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 PR 17-NOV-2000; 2000US-0249226P.  
 PR 17-NOV-2000; 2000US-0249227P.  
 PR 17-NOV-2000; 2000US-0249228P.  
 PR 17-NOV-2000; 2000US-0249229P.  
 PR 17-NOV-2000; 2000US-0249230P.  
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 PR 05-DEC-2000; 2000US-0251030P.  
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 PR 03-DEC-2000; 2000US-0256719P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251858P.  
 PR 08-DEC-2000; 2000US-0251859P.  
 PR 08-DEC-2000; 2000US-0251899P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 05-JAN-2001; 2001US-0259678P.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Rosen CA, Barash SC, Ruben SM;  
 XX WPI; 2001-483426/52.  
 XX  
 XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and metastasis.  
 XX  
 XX Disclosure; SEQ ID NO 19750; 3071pp + Sequence Listing; English.  
 XX  
 XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
 CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting the  
 CC nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/haematopoietic-related diseases, especially  
 CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
 CC represent sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;  
 Query Match 77.9%; Score 14.8; DB 4; Length 19183;  
 Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 GACGGAAGCCCTTCG 18  
 Db 3573 GTACGGAAGCCCTTTG 3590  
 RESULT 95  
 AAL36434  
 ID AAL36434 standard; DNA; 19183 BP.  
 XX

AC AAL36434;  
 XX  
 DT 08-JAN-2002 (first entry)  
 XX  
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 2799.  
 XX  
 KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein;  
 KW musculoskeletal system; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155367-A1.  
 XX  
 XX 02-AUG-2001.  
 XX  
 XX 17-JAN-2001; 2001WO-US001338.  
 XX  
 XX 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180628P.  
 PR 24-FEB-2000; 2000US-0184664P.  
 PR 02-MAR-2000; 2000US-0186350P.  
 PR 16-MAR-2000; 2000US-0189874P.  
 PR 17-MAR-2000; 2000US-0190076P.  
 PR 18-APR-2000; 2000US-0198123P.  
 PR 19-MAY-2000; 2000US-0205515P.  
 PR 07-JUN-2000; 2000US-0209467P.  
 PR 28-JUN-2000; 2000US-0214886P.  
 PR 30-JUN-2000; 2000US-0215135P.  
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 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
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 PR 08-SEP-2000; 2000US-0231443P.  
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 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.

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PR 14-SEP-2000; 2000US-0232397P.
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PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
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PR 13-OCT-2000; 2000US-0239335P.
PR 13-OCT-2000; 2000US-0239337P.
PR 20-OCT-2000; 2000US-0240960P.
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PR 20-OCT-2000; 2000US-0241785P.
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PR 20-OCT-2000; 2000US-0241809P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246526P.
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PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-451937/48.
XX
XX Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the musculoskeletal system including musculoskeletal
PT cancers and also for testing and detection e.g. diagnosis.
XX
XX Example 2; SEQ ID NO 2799; 78lpp + Sequence Listing; English.
XX
XX The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 4; Length 19183;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGGAAAGGCTTTCG 18
Db 3573 GTACGGGAAAGGCTTTTG 3590

RESULT 96
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ID ABX59422 standard; cDNA; 19183 BP.
XX
AC ABX59422;
DT
XX 26-FEB-2003 (first entry)
DE
XX cDNA encoding novel human musculoskeletal system antigen #1766.
KW Gene; ss; musculoskeletal system antigen; cancer; metastasis;
KW re-vascularisation; thrombosis; arteriosclerosis; mineral content;
KW cardiovascular condition; wound; injury; burn; angiogenesis; ulcer;
KW post-operative tissue repair; limb regeneration; neuronal growth;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW AIDS-related complex; chondrocyte growth; bone regeneration;
KW periodontal regeneration; tissue transport; bone graft; skin aging;
KW keratinocyte growth; hair loss; melanocyte growth; cell proliferation;
KW cell growth; organ transplant; cell differentiation; body height; weight;
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 PR 05-JAN-2001; 2000US-0254097P.  
 PR 17-JAN-2001; 2001US-0259678P.  
 PR 17-JAN-2001; 2001US-00764877.

XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Ruben SM, Barash SC;  
 PI WPI; 2004-090458/09.  
 XX New nucleic acid molecule, useful for preparing a medicament for

PT preventing, treating or ameliorating a medical condition e.g., cancer of  
PT musculoskeletal tissues or osteoporosis.

XX Disclosure; SEQ ID NO 2799; 289pp; English.

XX The invention relates to a novel isolated musculoskeletal system-  
CC associated nucleic acid molecule. The nucleic acid of the invention  
CC demonstrates cytostatic and osteopathic activities and may be useful for  
CC preparing a medicament for preventing, treating or ameliorating a medical  
CC condition such as cancer of the musculoskeletal tissues or osteoporosis,  
CC possibly via gene therapy or vaccine production. The current sequence is  
CC that of the human musculoskeletal system-associated genomic DNA of the  
CC invention. The current sequence is not shown within the specification per  
CC se but is available on the USPTO web-site  
CC <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.

SQ Sequence 19183 BP; 5489 A; 3882 C; 4034 G; 5778 T; 0 U; 0 Other;

Query Match 77.9%; Score 14.8; DB 12; Length 19183;  
Best Local Similarity 88.9%; Pred. No. 1.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTCG 18  
Db 3573 GTACGGAAGCCTTTG 3590

RESULT 98

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ID AAK75071 standard; DNA; 30904 BP.

XX AC AAK75071;

XX AC (first entry)

DT 07-NOV-2001

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29883.  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.

XX Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

XX 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

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 (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Barash SC, Ruben SM;  
 XX MPI; 2001-451930/48.  
 DR New cardiovascular system related polynucleotides and polypeptides,  
 XX useful for diagnosing, treating and/or preventing disorders of the  
 PT cardiovascular system.  
 XX  
 XX Claim 1; SEQ ID NO 2314; 674pp; English.  
 PS  
 XX Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode  
 CC the cardiovascular system antigen and their associated polynucleotides are  
 CC Cardiovascular system antigens and their associated polynucleotides are  
 CC useful in the diagnosis, treatment and prevention of various types of  
 CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
 CC chickens or sheep. A pathological condition can be determined by  
 CC detecting the presence or absence of a mutation in a cardiovascular  
 CC system antigen polynucleotide. The treatable disorders include autoimmune  
 CC diseases such as rheumatoid arthritis, hyperproliferative disorders such  
 CC as neoplasms of the breast or liver, cardiovascular disorders such as  
 CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,  
 CC nervous system disorders such as Alzheimer's disease, infections caused  
 CC by bacteria, viruses and fungi, ocular disorders such as corneal  
 CC infection, endocrine disorders such as premature labour and infertility,  
 CC gastrointestinal disorders such as Crohn's disease, renal disorders such  
 CC as glomerulonephritis and respiratory disorders such as asthma and  
 CC pleurisy. The polypeptides can also be used to aid wound healing, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, to regenerate tissues and in chemotaxis. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 77.9%; Score 14.8; DB 4; Length 32249;  
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 Db 13291 AAAGGAAGGCCATTCGG 13274  
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PR 01-DEC-2000; 2000US-0250391P.  
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PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
PR 17-JAN-2001; 2001US-00764869.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Barash SC;  
XX  
XX WPI; 2003-743766/70.  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for preventing, treating, or ameliorating a medical condition,  
PT such as cancer of cardiovascular tissues and cancer metastases.  
XX  
XX Claim 1; SEQ ID NO 2314; 262pp; English.  
XX  
XX The invention relates to human cardiovascular system related polypeptides  
CC and the polynucleotides encoding them. The polypeptides, polynucleotides  
CC and antibodies to the polypeptides are useful for diagnosing a  
CC pathological condition or a susceptibility to a pathological condition,  
CC for preventing, treating, or ameliorating a medical condition, such as  
CC cancer of cardiovascular system tissues, proliferative disorders, foetal  
CC and developmental abnormalities, haematopoietic disorders, diseases of  
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid  
CC arthritis), inflammation, allergies, neurological disorders (e.g.,  
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,  
CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,  
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic  
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-  
CC related disorders, endocrine disorders and infections. The nucleic acids  
CC are also useful for chromosome identification, radiation hybrid mapping  
CC or long-range restriction mapping. The polypeptides and polynucleotides  
CC may also be used as food additives or preservatives to increase or  
CC decrease storage capabilities, fat content or other nutritional  
CC components. This sequence represents human cardiovascular system related  
CC genomic DNA of the invention.  
XX  
SQ Sequence 32249 BP; 8876 A; 6723 C; 7066 G; 9584 T; 0 U; 0 Other;  
  
Query Match 77.9%; Score 14.8; DB 10; Length 32249;  
Best Local Similarity 88.9%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 2 AACGGAAGGCGCTTCGG 19  
Db |||||||||  
13291 AAGGAAGGCGCTTCGG 13274  
  
Search completed: May 19, 2006, 04:19:28  
Job time : 230.994 secs

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GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 02:24:46 ; Search time 1270.71 Seconds  
(without alignments)  
836.120 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19  
Sequence: 1 gaacggaaaggccttcg 19

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 300 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_est7:\*  
7: gb\_est8:\*  
8: gb\_est9:\*  
9: gb\_est10:\*  
10: gb\_est11:\*  
11: gb\_est12:\*  
12: gb\_est13:\*  
13: gb\_est14:\*  
14: gb\_est15:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	17.4	91.6	828	7	BF240426 BF240426
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C 4	16.4	86.3	312	7	BB241896 BB241896
5	16.4	86.3	412	3	BP863510 BP863510
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C 7	16.4	86.3	614	14	LBAP055F03
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9	16.4	86.3	643	3	BU283959 BU283959
10	16.4	86.3	660	11	BH794488 BH794488
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C 16	16.4	86.3	944	8	CO583238 CO583238
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AI225711	uf105.Y
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	97	15.8	83.2	559	4	BX608091	BX608091	C 170	15.8	83.2	750	2	BG916273	BG916273	BG916273	AGENCOURT	
	98	15.8	83.2	560	10	DT902323	DT902323 S25-20976	C 171	15.8	83.2	756	4	CB574053	CB574053	CB574053	AGENCOURT	
	99	15.8	83.2	561	3	BM631920	BM631920 170006875	C 172	15.8	83.2	768	3	BM631278	BM631278	BM631278	AGENCOURT	
	100	15.8	83.2	562	9	DA720663	DA720663	C 173	15.8	83.2	770	3	BP157969	BP157969	BP157969	AGENCOURT	
	101	15.8	83.2	563	3	BQ831564	BQ831564 L161n1226	C 174	15.8	83.2	777	14	DU601889	DU601889	DU601889	AGENCOURT	
	102	15.8	83.2	564	9	DA344775	DA344775	C 175	15.8	83.2	796	3	BG513741	BG513741	BG513741	AGENCOURT	
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	106	15.8	83.2	568	600	12	CC144466	CC144466 XB019C Ba	C 179	15.8	83.2	807	11	BH040811	BH040811	BH040811	RPCI-24-3
	107	15.8	83.2	569	13	CL580164	CL580164 OB_Ba003	C 180	15.8	83.2	814	13	CU562245	CU562245	CU562245	OB_Ba002	
	108	15.8	83.2	570	7	BE375146	BE375146 60125511	C 181	15.8	83.2	824	2	BG520333	BG520333	BG520333	AGENCOURT	
	109	15.8	83.2	571	3	BM651564	BM651564 170006873	C 182	15.8	83.2	826	11	AQ746994	AQ746994	AQ746994	HS 5538 A	
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	112	15.8	83.2	574	11	AQ510446	AQ510446 nbx500950	C 185	15.8	83.2	833	10	DR735212	DR735212	DR735212	FGA508088	
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	114	15.8	83.2	576	3	AA754088	AA754088 97GS0781	C 187	15.8	83.2	845	4	BM979961	BM979961	BM979961	AGENCOURT	
	115	15.8	83.2	577	5	CK627830	CK627830 1p03c11.Y	C 188	15.8	83.2	850	13	CL830926	CL830926	CL830926	OR_CBa005	
	116	15.8	83.2	578	3	BG927981	BG927981 HNC67-1-B	C 189	15.8	83.2	852	8	CR431644	CR431644	CR431644	AGENCOURT	
	117	15.8	83.2	579	3	BM646604	BM646604 170006873	C 190	15.8	83.2	861	2	BI655057	BI655057	BI655057	603282734	
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	126	15.8	83.2	588	12	CE016451	CE016451 tigr-g8s-	C 199	15.8	83.2	900	2	BG175425	BG175425	BG175425	602337780	
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	128	15.8	83.2	590	1	AA652599	AA652599 AL652599	C 201	15.8	83.2	908	2	BG518864	BG518864	BG518864	602578164	
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	130	15.8	83.2	592	5	CJ137946	CJ137946	C 203	15.8	83.2	935	3	BQ950668	BQ950668	BQ950668	AGENCOURT	
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	132	15.8	83.2	594	2	BM633856	BM633856 170006875	C 205	15.8	83.2	939	13	CL844040	CL844040	CL844040	OR_CBa007	
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	149	15.8	83.2	611	6	CNS0FPM	CNS0FPM	C 222	15.8	83.2	1185	9	DN705397	DN705397	DN705397	CLJ759-C02	
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	157	15.8	83.2	619	3	BM641635	BM641635 170006873	C 230	15.8	83.2	1779	6	AK169602	AK169602	AK169602	Mus muscu	
	158	15.8	83.2	620	3	BM635979	BM635979 170006875	C 231	15.8	83.2	1780	6	BC057175	BC057175	BC057175	Mus muscu	
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	DEFINITION	DG11-193n18	DG11-kidney	Canis familiaris	CDNA 3', mRNA sequence.					
FEATURES	Accession	CO684942								
	Version	CO684942.1	GI:50633608							
ORIGIN	Keywords	EST.								
	Source	Canis familiaris (dog)								
ORIGIN	Organism	Canis familiaris								
	Reference	1 (bases 1 to 305)								
ORIGIN	Authors	Schlueter, T., Hermanns, J., Weindel, M., Schuette, D., Kranz, H.,								
	Title	Henrich, J. and Loebbert, R.								
ORIGIN	Journal	Dog arrayTAG CDNA clone collection								
	Comment	Unpublished (2004)								
ORIGIN	Location/Qualifiers	LIION bioscience AG								
	Source	Walhoferstrasse 98, D-69123 Heidelberg, Germany								
ORIGIN	Source	Tel: +49 6221 4038 150								
	Source	Fax: +49 6221 4038 290								
ORIGIN	Source	Email: Thomas.Schlueter@lionbioscience.com.								
	Source	Location/Qualifiers								
ORIGIN	Source	1..305								
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	Source	/note="Organ: kidney; Vector: Dog pBluescript LION"								
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	DEFINITION	BB241896	RIKEN full-length enriched, 3 days neonate	thymus Mus						
ORIGIN	Accession	BB241896								
	Version	BB241896.1	GI:8934642							
ORIGIN	Keywords	EST.								
	Source	Mus musculus (house mouse)								
ORIGIN	Organism	Mus musculus								
	Reference	1 (bases 1 to 312)								
ORIGIN	Authors	Kono, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,								
	Authors	Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,								
ORIGIN	Authors	Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,								
	Authors	Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,								
ORIGIN	Authors	Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,								
	Authors	Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,								



Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamana, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)  
Unpublished (2000)  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S., Sasaki, N., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)  
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

# TITLE JOURNAL COMMENT

Location/Qualifiers  
1. .312  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="A630089H08"  
/tissue\_type="thymus"  
/dev\_stage="3 days neonate"  
/lab\_host="DH10B"  
/clone\_lib="RIKEN full-length enriched, 3 days neonate thymus"  
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'  
GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCTCCCTCC sequence [5' GAGAGAGATTCGAGTTAAATTAATCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

# FEATURES source

Query Match 86.3%; Score 16.4; DB 7; Length 312;  
Best Local Similarity 94.4%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACCGAAGGCTTTCG 19  
|||||  
Db 67 AACCGAAGGCTTTCG 50  
|||||

# ORIGIN

Query Match 86.3%; Score 16.4; DB 7; Length 312;  
Best Local Similarity 94.4%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACCGAAGGCTTTCG 19  
|||||  
Db 67 AACCGAAGGCTTTCG 50  
|||||

# RESULT 5 BP863510

LOCUS BP863510 412 bp mRNA linear EST 17-FEB-2005  
DEFINITION BP863510 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-66-P16 5', mRNA sequence.  
ACCESSION BP863510  
VERSION BP863510.1 GI:59924483  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
1 (bases 1 to 412)  
Seki, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Iida, K., Enju, A., Sakurai, T., Arakawa, T., Carninci, P., Fukuda, S., Iida, J., Kawai, J., Sasaki, D., Shiraki, T., Hayashizaki, Y. and Shinozaki, K.  
Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs Unpublished (2005)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@rtc.riken.go.jp  
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998, 2002). This clone is in a modified pBluescript vector.  
Please visit our web site (http://pfgweb.gsc.riken.jp) and http://range.gsc.riken.jp) for further details.  
Location/Qualifiers  
1. .412  
/organism="Arabidopsis thaliana"  
/mol\_type="mRNA"  
/db\_xref="taxon:3702"  
/clone="RAFL21-66-P16"  
/lab\_host="DH10B"  
/clone\_lib="RAFL21"  
/notes="Site 1: BamHI; Site 2: SalI; Subtraction Library. The sequence was obtained from samples subjected to various stress and plant hormones-treated"

ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 412;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTCG 18  
|||||  
Db 197 GAACGGAAGGCTTTCG 214  
|||||

RESULT 6  
BP863510 603 bp mRNA linear EST 27-NOV-2002  
DEFINITION BP863510 F1 CSRQCHN58 Gallus gallus cDNA clone CHEST492d14 5', mRNA sequence.  
ACCESSION BP863510  
VERSION BP863510.1 GI:25767934  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 603)  
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
A Comprehensive Collection of Chicken cDNAs  
Curr. Biol. 12 (22), 1965-1969 (2002)  
12445392  
Contact: Simon Hubbard  
Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology  
(UMIST)

PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.  
Location/Qualifiers

## FEATURES

source

1. .603  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Compton Line 151"  
/db\_xref="taxon:9031"  
/clone="CHEST492d14"  
/sex="Female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="CSEQCHN58"  
/note="Organ: small intestine; Vector: pBluescript II  
KS(+); Site 1: EcoRI; Site 2: NotI; This normalized  
library was constructed from 1 million independent clones.  
cDNA synthesis was initiated using an oligo(dT) primer,  
using methylated C in the first strand synthesis reaction.  
Following this first strand reaction, double-stranded cDNA  
was blunted, ligated to NotI adapters, digested with  
EcoRI, size-selected, and cloned into the NotI and EcoRI  
compatible sites of a custom modified MCS of the  
pBluescript (KS+) vector. The library was normalized in 2  
rounds using conditions adapted from Soares et al., PNAS  
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6  
(1996): 791, except that a significantly longer  
reannealing hybridization was used."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 603;  
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTTCG 18

Db 273 GAAAGGAAGGCCTTTTCG 290

## RESULT 7

LBAF055F03/c LBAF055F03 614 bp DNA linear GSS 20-JUN-2003  
LOCUS Leishmania braziliensis GSS, clone LBAF055F03, genomic survey  
DEFINITION

sequence.

VERSION BX542565.1 GI:32137791

KEYWORDS GSS; genomic survey sequence.

SOURCE Leishmania braziliensis

ORGANISM Leishmania braziliensis

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Leishmania; Leishmania braziliensis species complex.

## REFERENCE

1 Laurentino,E.C., Ruiz,J.C. and Cruz,A.K.

GSS analysis of the Leishmania braziliensis genome

UNPUBLISHED

2 (bases 1 to 614)

Direct Submission

Cruz,A.K.

Submitted (17-JUN-2003) Cruz A.K., University of Sao Paulo,

Department of Molecular and Cell Biology, FMRP, Avenida

Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL

Clone requests: akcruz@mrp.usp.br.

Location/Qualifiers

1. .614

/organism="Leishmania braziliensis"

/mol\_type="genomic DNA"

/strain="WHOM/BR/75/M2904"

/db\_xref="taxon:5660"

/clone="LBAF055F03"

## . ORIGIN

Query Match 86.3%; Score 16.4; DB 14; Length 614;  
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTTCG 19

Db 31 AACGGAAGGCCTTTAGG 14

## RESULT 8

LOCUS BU306528

DEFINITION BU306528 625 bp mRNA linear EST 27-NOV-2002

sequence. 603739007F1 CSEQCHN56 Gallus gallus cDNA clone CHEST633n2 5', mRNA

ACCESSION BU306528

VERSION BU306528.1 GI:25756262

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 625)

Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,

Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

12445392

COMMENT

Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

source

1. .625 Location/Qualifiers

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Compton line 151"

/db\_xref="taxon:9031"

/clone="CHEST633n2"

/sex="Female"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="CSEQCHN56"

/note="Organ: small intestine; Vector: pBluescript II

KS(+); Site 1: EcoRI; Site 2: NotI; This normalized

library was constructed from 1 million independent clones.

cDNA synthesis was initiated using an oligo(dT) primer,

using methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA

was blunted, ligated to NotI adapters, digested with

EcoRI, size-selected, and cloned into the NotI and EcoRI

compatible sites of a custom modified MCS of the

pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS

(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6

(1996): 791, except that a significantly longer

reannealing hybridization was used."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 3; Length 625;  
Best Local Similarity 94.4%; Pred. NO. 1.8e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTTCG 18

Db 290 GAAAGGAAGGCCTTTTCG 307

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RESULT 9
BU283959
LOCUS
DEFINITION BU283959 643 bp mRNA linear EST 27-NOV-2002
603600041F1 CSEQHN54 Gallus gallus cDNA clone CHEST573a12 5', mRNA
sequence.
ACCESSION BU283959
VERSION BU283959.1 GI:25733402
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 643)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
FEATURES
source
1..643
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST573a12"
/sex="Female"
/tissue_type="not cerebrum or cerebellum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQHN54"
/notes="Organ: brain; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
ORIGIN
Query Match 86.3%; Score 16.4; DB 3; Length 643;
Best Local Similarity 94.4%; Pred. No. 1.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCG 18
||| ||||| ||||| |||||
Db 10 GAAAGGAAGGCGCTTTCG 27

RESULT 10
BH794488
LOCUS
DEFINITION BH794488 660 bp DNA linear GSS 02-APR-2002
ME MBA0002P13f Manihot esculenta Manihot esculenta genomic clone
ME MBA0002P13f, genomic survey sequence.
ACCESSION BH794488
VERSION BH794488.1 GI:19892621
KEYWORDS GSS.
SOURCE Manihot esculenta (cassava)

```

```

ORGANISM
Manihot esculenta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eutrosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
Manihoteae; Manihot.
REFERENCE 1 (bases 1 to 660)
Tomkins,J., Fregene,M., Main,D., Kim,H., Wing,R. and Tohme,J.
Bacterial artificial chromosome (BAC) library resource for
positional cloning of pest and disease resistance genes in cassava
(Manihot esculenta Crantz)
JOURNAL Plant Mol. Biol. 56 (4), 555-561 (2004)
PUBMED 15630619
COMMENT Contact: Tomkins J
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 6419
Fax: 864 656 4293
Email: jtmkns@clemson.edu
Total High Quality bases = 281
Seq primer: TAATAGCACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 658.
FEATURES
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1..660
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/strain="MECW72"
/db_xref="taxon:3983"
/clone="ME MBA0002P13f"
/tissue_type="leaf"
/lab_host="E. coli"
/notes="Vector: pCUGIBAC-1; Site 1: HindIII; Site 2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/cassava/ME_MBA
to order clones from this library see
http://www.genome.clemson.edu/orders "
ORIGIN
Query Match 86.3%; Score 16.4; DB 11; Length 660;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCG 18
||| ||||| ||||| |||||
Db 225 GAAAGGAAGGCGCTTTCG 242

RESULT 11
BU412995
LOCUS
DEFINITION BU412995 709 bp mRNA linear EST 29-NOV-2002
603154843F1 CSQRBL05 Gallus gallus cDNA clone CHEST167e12 5', mRNA
sequence.
ACCESSION BU412995
VERSION BU412995.1 GI:25905666
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 709)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)

```

PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@mist.ac.uk.	
FEATURES	Location/Qualifiers
source	1..709
	/organism="Gallus gallus"
	/mol_type="mRNA"
	/strain="Layer"
	/db_xref="taxon:9031"
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	/sex="Female"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="CSEORBL05"
	/note="Organ: ovary; Vector: pBluescript II KS(+); Site: 1: EcoRI; Site: 2: NotI; Modification of pBluescript II KS(+)
	[Stratagene] vector to accommodate cDNA produced with the
	T-trimmed protocol (Construction of uni-directionally
	cloned cDNA libraries from messenger RNA for improved 3'
	end DNA sequencing by Glenn Fu, et al. U.S. Patent #
	6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
	Ligate in double stranded adaptor containing BsgI and
	BamHI sites [5'ggccgcgtgcagccgcgataccgaaaaaag]
	[5'aattcttttttcggatccgggctgcagc]
ORIGIN	
Query Match	86.3%; Score 16.4; DB 3; Length 709;
Best Local Similarity	94.4%; Pred. No. 1.9e+03;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GAACGGAAAGGCTTTTCG 18
Db	354 GAAAGGAAGGCTTTTCG 371
RESULT 12	
LOCUS	CR077081
DEFINITION	Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP284c21, genomic survey sequence.
ACCESSION	CR077081
VERSION	1
KEYWORDS	GSS; genome survey sequence; MICER.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 835)
AUTHORS	Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
TITLE	Direct Submission
JOURNAL	CB10 1SA, UK. (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. http://www.sanger.ac.uk/MICER
FEATURES	Location/Qualifiers
source	1..835
	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/db_xref="taxon:10090"
	/clone="MHP284c21"
	/clone_lib="MHPP"
ORIGIN	
Query Match	86.3%; Score 16.4; DB 14; Length 835;
Best Local Similarity	94.4%; Pred. No. 1.9e+03;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GAACGGAAAGGCTTTTCG 18
Db	524 GAAAGGAAGGCTTTTCG 541
RESULT 13	
LOCUS	BU409605
DEFINITION	603157733F1 CSEORBL03 Gallus gallus cDNA clone CHEST174b10 5', mRNA sequence.
ACCESSION	BU409605
VERSION	1
KEYWORDS	EST.
SOURCE	Gallus gallus (chicken)
ORGANISM	Gallus gallus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE	1 (bases 1 to 847)
AUTHORS	Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE	A Comprehensive Collection of Chicken cDNAs
JOURNAL	Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED	12445392
COMMENT	Contact: Simon Hubbard Department of Biomolecular Sciences University of Manchester Institute of Science and Technology (UMIST) PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930 Fax: 01612360409 Email: Simon.Hubbard@mist.ac.uk.
FEATURES	Location/Qualifiers
source	1..847
	/organism="Gallus gallus"
	/mol_type="mRNA"
	/strain="Layer and broiler"
	/db_xref="taxon:9031"
	/clone="CHEST174b10"
	/sex="Male and female"
	/tissue_type="Chondrocytes isolated from growth plate cartilage"
	/dev_stage="adult"
	/lab_host="DH10B"
	/clone_lib="CSEORBL03"
	/note="Vector: pBluescript II KS(+); Site: 1: EcoRI; Site: 2: NotI; Modification of pBluescript II KS(+)
	[Stratagene] vector to accommodate cDNA produced with the
	T-trimmed protocol (Construction of uni-directionally
	cloned cDNA libraries from messenger RNA for improved 3'
	end DNA sequencing by Glenn Fu, et al. U.S. Patent #
	6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
	Ligate in double stranded adaptor containing BsgI and
	BamHI sites [5'ggccgcgtgcagccgcgataccgaaaaaag]
	[5'aattcttttttcggatccgggctgcagc]
ORIGIN	
Query Match	86.3%; Score 16.4; DB 3; Length 847;
Best Local Similarity	94.4%; Pred. No. 1.9e+03;
Matches	17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 GAACGGAAAGGCTTTTCG 18
Db	278 GAAAGGAAGGCTTTTCG 295
RESULT 14	
LOCUS	BE881910
DEFINITION	601504886F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906597 5', mRNA sequence.
ACCESSION	BE881910
VERSION	1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 872)
NHI-MGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, MAMMALIAN GENE COLLECTION (MGC)
UNPUBLISHED (1999)
CONTACT: ROBERT STRAUSBERG, PH.D.
EMAIL: c9apbs-i@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9715 row: 1 column: 22
High quality sequence start: 49
High quality sequence stop: 593.
Location/Qualifiers
1. .872
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHI_MGC_71"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "

ORIGIN
Query Match 86.3%; Score 16.4; DB 7; Length 872;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAAGGCCTTCG 19
|||||
Db 762 AACTGAAAGGCCTTCG 779

RESULT 15
DN561788 910 bp mRNA linear EST 14-MAR-2005
LOCUS 92178421 Sea Urchin primary mesenchyme cell cDNA library
DEFINITION Strongylocentrotus purpuratus cDNA clone PMSPR2-102A16 5', mRNA
sequence.
ACCESSION DN561788.1 GI:61120827
VERSION DN561788.1
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 910)
AUTHORS Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
Ertensohn,C.A.
TITLE A large scale analysis of mRNAs expressed by primary mesenchyme
cells of the sea urchin embryo
JOURNAL Development 128 (13), 2615-2627 (2001)
PUBMED 11493577
COMMENT Contact: Erica Sodergren
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-7676
Fax: 713-798-6977
Email: ericas@bcm.tmc.edu
NCBI Trace Archive: 496682679
Insert Length: 1750 Std Error: 0.25
Plate: 102 row: A column: 16.
Location/Qualifiers

FEATURES
source
1. .910
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone_lib="PMSPR2-102A16"
/tissue_type="embryo"
/cell_type="primary mesenchyme cells"
/lab_host="E.coli"
/clone_lib="Sea Urchin primary mesenchyme cell cDNA
library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: MluI; oligo
dT priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match 86.3%; Score 16.4; DB 9; Length 910;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCCTTCG 18
|||||
Db 794 GAACGAAAGGCCTTCG 811

RESULT 16
COS83238/c 944 bp mRNA linear EST 20-JUL-2004
LOCUS ILLUMIGEN MQC 44583 Katze MMLV Macaca mulatta cDNA clone
DEFINITION IBIUW:16736 5' similar to Bases 1 to 944 highly similar to human
ITIH3 (Hs.76716), mRNA sequence.
ACCESSION COS83238
VERSION COS83238.1 GI:50415893
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE 1 (bases 1 to 944)
AUTHORS Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., AgY,M.B.,
Prohl,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
Iadonato,S.P.
TITLE Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL Genome Biol. 6 (7), R60 (2005)
PUBMED 15998449
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.06.18. 633 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:
Illumigen Biosciences Inc. For further information, see
http://www.macaque.org
PCR Primers
FORWARD: CCCTACTAAGGGAACAAAA
BACKWARD: CACTATAGGCGAATTGGTA
Insert Length: 944 Std Error: 0.00
Plate: CL000392 row: H column: 04
Seq primer: CCCTACTAAGGGAACAAAA
POLYA=No.
Location/Qualifiers
1. .944
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUW:16736"
/sex="female"
/dev_stage="adult"
/lab_host="Electromax DH10B"
/clone_lib="Katze_MMLV"

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/notes="Organ: liver; Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I; Created from CloneMiner CDNA\_Library Construction kit (catalog #18249-029)"

## ORIGIN

Query Match 86.3%; Score 16.4; DB 8; Length 944;  
Best Local Similarity 94.4%; Pred. No. 2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCGG 19  
|||||  
Db 837 AACGGAAGGCCTTCGG 820

## RESULT 17

BZ548902/c 1330 bp DNA linear GSS 17-DEC-2002  
LOCUS  
DEFINITION  
pacsl-60\_1548.s1 pacsl-60 Pseudomonas aeruginosa genomic clone  
pacsl-60\_1548, genomic survey sequence.

ACCESSION  
VERSION  
BZ548902.1 GI:27152483  
KEYWORDS  
SOURCE  
Pseudomonas aeruginosa  
ORGANISM

REFERENCE  
1 (bases 1 to 1330)  
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
Pseudomonadaceae; Pseudomonas.

AUTHORS  
Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,  
Burns,J.L., Kaul,R. and Olsen,M.V.

TITLE  
Whole-Genome-Sequence variation among multiple isolates of  
Pseudomonas aeruginosa library

JOURNAL  
COMMENT  
J. Bacteriol. (2002) In press  
Contact: Chris K. Raymond  
Genome Center

University of Washington  
Box 352145, Seattle, WA 98105-2145, USA  
Tel: 2062216954  
Fax: 2066857244  
Email: craymond@u.washington.edu  
Class: shotgun.

## FEATURES

source  
1. .1330  
Location/Qualifiers  
/organism="Pseudomonas aeruginosa"  
/mol\_type="genomic DNA"  
/strain="1-60"  
/db\_xref="taxon:287"  
/clone="pacsl-60\_1548"  
/clone\_lib="pacsl-60"  
/notes="clinical isolate 1-60 Whole genomic shotgun library."

## ORIGIN

Query Match 86.3%; Score 16.4; DB 11; Length 1330;  
Best Local Similarity 94.4%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCGG 19  
|||||  
Db 1240 AACGGAAGGCCTTCGG 1223

## RESULT 18

BF851999 268 bp mRNA linear EST 16-JAN-2001  
LOCUS  
DEFINITION  
MR3-EN0090-111200-003-f09 EN0090 Homo sapiens cDNA, mRNA sequence.

ACCESSION  
VERSION  
BF851999.1 GI:122339161  
KEYWORDS  
SOURCE  
EST.  
Homo sapiens (human)

ORGANISM  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

## REFERENCE

1 (bases 1 to 268)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
10737800

## COMMENT

Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil

Tel: +55-11-2704922  
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR3&t2=MR3-EN0090-  
111200-003-f09&t3=2000-12-11&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 21

High quality sequence stop: 174.

## FEATURES

source  
1. .268  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/dev\_stage="Adult"  
/clone\_lib="EN0090"  
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

## ORIGIN

Query Match 84.2%; Score 16; DB 2; Length 268;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTC 17  
|||||

Db 76 AACGGAAGGCCTTC 91  
|||||

## RESULT 19

CC153371 360 bp DNA linear GSS 25-APR-2003  
LOCUS  
DEFINITION  
CSU-K34.124M19.SP6 CSU-K34 Aedes aegypti genomic clone  
CSU-K34-124M19, genomic survey sequence.

ACCESSION  
VERSION  
CC153371.1 GI:30106667

KEYWORDS  
SOURCE  
GSS.

Aedes aegypti (yellow fever mosquito)  
Aedes aegypti

ORGANISM  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Culicidae; Culicinae; Culicini; Aedes; Stegomyia.

1 (bases 1 to 360)

Loftus,B., Shetty,J., Knudson,D. and Severson,D.

BAC end sequencing of Aedes aegypti

Unpublished (2003)

Other GSSs: CSU-K34.124M19.T7

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

```

Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.
Seq primer: SP6
Class: BAC ends.

FEATURES
    source
        1..360
            Location/Qualifiers
                /organism="Aedes aegypti"
                /mol_type="genomic DNA"
                /db_xref="taxon:7159"
                /clone_lib="CSU-K34"
                /clone="CSU-K34-124M19"
                /note="Vector: pBACE3.6; Site 1: EcoRI; Source DNA: Aedes
                aegypti; strain unknown (derived from freshly hatched
                larvae at the Virus Research Centre, Poona, India.
                Reference: SINGH, K. R. P., 1967 Cell cultures derived
                from larvae of Aedes albopictus (Skuse) and Aedes aegypti
                (L.). Current Science 36: 506-508; ATC-10 cell line ATCC
                CCL-125"

ORIGIN
    Query Match      84.2%; Score 16; DB 12; Length 360;
    Best Local Similarity 100.0%; Pred. No. 2.7e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  CGGAAAGGCCTTTTCGG 19
        |||||
Db      246  CGGAAAGGCCTTTTCGG 261

RESULT 20
AW850543
LOCUS      AW850543              590 bp      mRNA      linear      EST 19-MAY-2000
DEFINITION IL3-CT0219-160200-060-A03 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW850543
VERSION    AW850543.1  GI:7946060
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
    AUTHORS   Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
    Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
    Goldman, G.H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H.,
    Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
    O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
    Simpson, A.J.
    TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
    sequence tags
    JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
    PUBMED   10737800
    COMMENT   Contact: Simpson A.J.G.
    Laboratory of Cancer Genetics
    Ludwig Institute for Cancer Research
    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
    Brazil
    Tel: +55-11-2704922
    Fax: +55-11-2707001
    Email: asimpson@ludwig.org.br
    This sequence was derived from the FAPESP/LICR Human Cancer Genome
    Project. This entry can be seen in the following URL
    (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=IL3-CT0219-160
    200-060-A03&t3=2000-02-16&t4=1)
    Seq primer: puc 18 forward
    High quality sequence stop: 17
    High quality sequence stop: 129.
    Location/Qualifiers
        1..590
            /organism="Homo sapiens"

FEATURES
    source
        1..590
            Location/Qualifiers
                /organism="Homo sapiens"

FEATURES
    source
        1..360
            Location/Qualifiers
                /organism="Aedes aegypti"
                /mol_type="genomic DNA"
                /db_xref="taxon:7159"
                /clone_lib="CSU-K34"
                /clone="CSU-K34-124M19"
                /note="Vector: pBACE3.6; Site 1: EcoRI; Source DNA: Aedes
                aegypti; strain unknown (derived from freshly hatched
                larvae at the Virus Research Centre, Poona, India.
                Reference: SINGH, K. R. P., 1967 Cell cultures derived
                from larvae of Aedes albopictus (Skuse) and Aedes aegypti
                (L.). Current Science 36: 506-508; ATC-10 cell line ATCC
                CCL-125"

ORIGIN
    Query Match      84.2%; Score 16; DB 12; Length 360;
    Best Local Similarity 100.0%; Pred. No. 2.7e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  CGGAAAGGCCTTTTCGG 19
        |||||
Db      246  CGGAAAGGCCTTTTCGG 261

RESULT 21
BZ688362/c
LOCUS      BZ688362              661 bp      DNA      linear      GSS 10-FEB-2003
DEFINITION OGDAD75TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0144N06,
genomic survey sequence.
ACCESSION  BZ688362
VERSION    BZ688362.1  GI:28275551
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays

REFERENCE
    AUTHORS   White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
    Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
    Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
    TITLE     Consortium for Maize Genomics
    JOURNAL   Unpublished (2002)
    COMMENT   Other_GSSs: OGDAD75TM
    Contact: Cathy Whitelaw
    TIGR
    9712 Medical Center Drive, Rockville, MD 20850, USA
    Tel: 301-838-5843
    Fax: 301-838-0208
    Email: whitelaw@tigr.org
    Seq primer: Tf
    Class: methylation filtered.
    Location/Qualifiers
        1..661
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMMBMA0144N06"
            /clone_lib="ZM 0.7 1.5 KB"
            /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
            methylation filtered genomic DNA library"

ORIGIN
    Query Match      84.2%; Score 16; DB 12; Length 661;
    Best Local Similarity 100.0%; Pred. No. 3e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3  ACGAAAGGCCTTTTCG 18
        |||||
Db      227  ACGAAAGGCCTTTTCG 212

RESULT 22
DR891379/c

```

LOCUS	DR891379	JGI_XZT19757.rev NIH_XGC_tropTad5	663 bp	mRNA	linear	EST 01-AUG-2005				
DEFINITION	IMAGE:7596789 3', mRNA sequence.									
ACCESSION	DR891379									
VERSION	DR891379.1	GI:71580631								
KEYWORDS	EST.									
SOURCE	Xenopus tropicalis (western clawed frog)									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.									
REFERENCE	1 (bases 1 to 663)									
AUTHORS	Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.									
TITLE	DOE Joint Genome Institute Xenopus tropicalis EST project									
JOURNAL	Unpublished (2004)									
COMMENT	Other_ESTs: JGI_XZT19757.fwd Contact: Lindquist,E.A., Richardson,P. DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Tel: 925 296 5600 Fax: 925 296 5710 Email: cdna@jgi-psf.org Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <a href="http://tropicalis.berkeley.edu/home">http://tropicalis.berkeley.edu/home</a> cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley DNA Sequencing: DOE Joint Genome Institute: <a href="http://www.jgi.doe.gov">http://www.jgi.doe.gov</a> Clone Distribution: I.M.A.G.E. Consortium/LLNL: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Poly-A: Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting Poly-T sequence has been removed. Plate: XZT 0205 row: j column: 19 High quality sequence stop: 534 POLYA=Yes.									
FEATURES	Location/Qualifiers 1..663 /organism="Xenopus tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="IMAGE:7596789" /tissue_type="whole embryo" /dev_stage="Tadpole (st. 36-41)" /lab_host="E. coli XL1-Blue derivative, Stratagene ElectroTen-Blue" /clone_lib="NIH_XGC_tropTad5" /note="Vector: pCS108; Site_1: SalI; Site_2: NotI; Tadpole library constructed by Russell B. Fletcher in R. Harland's lab using poly A RNA and oligo dt primers (Invitrogen SuperScript Plasmid System for cDNA Synthesis and Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted into vector pCS108 ( <a href="http://mcb.berkeley.edu/labs/harland/pages/plasmids.html">http://mcb.berkeley.edu/labs/harland/pages/plasmids.html</a> )"									
SOURCE	1..663									
ORIGIN	Query Match 84.2%; Score 16; DB 10; Length 663; Best Local Similarity 100.0%; Pred. No. 3e+03; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	2	AACGGAAGGCCTTTC	17							
Db	459	AACGGAAGGCCTTTC	444							
RESULT 23										
CX793255/c										
LOCUS	CX793255	JGI_CAAJ387.rev NIH_XGC_tropBrn2	711 bp	mRNA	linear	EST 31-JAN-2005				
DEFINITION	IMAGE:7640427 3', mRNA sequence.									
ACCESSION	DR891379									
VERSION	DR891379.1	GI:71580631								
KEYWORDS	EST.									
SOURCE	Xenopus tropicalis (western clawed frog)									
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae; Xenopus; Silurana.									
REFERENCE	1 (bases 1 to 711)									
AUTHORS	Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.									
TITLE	DOE Joint Genome Institute Xenopus tropicalis EST project									
JOURNAL	Unpublished (2004)									
COMMENT	Other_ESTs: JGI_CAAJ387.fwd Contact: Lindquist,E.A., Richardson,P. DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Tel: 925 296 5600 Fax: 925 296 5710 Email: cdna@jgi-psf.org Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley: <a href="http://tropicalis.berkeley.edu/home">http://tropicalis.berkeley.edu/home</a> ) cDNA Library Preparation: DOE Joint Genome Institute: <a href="http://www.jgi.doe.gov">http://www.jgi.doe.gov</a> DNA Sequencing: DOE Joint Genome Institute: <a href="http://www.jgi.doe.gov">http://www.jgi.doe.gov</a> Clone Distribution: I.M.A.G.E. Consortium/LLNL: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Plate: CAAJ 0005 row: e column: 1 High quality sequence stop: 645.									
FEATURES	Location/Qualifiers 1..711 /organism="Xenopus tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="IMAGE:7640427" /tissue_type="Brain" /dev_stage="Adult" /lab_host="ElectroMAX_DH10B" /clone_lib="NIH_XGC_tropBrn2" /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI; This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCCTAGATCGGAG CGGCGCCCTTTTCTTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCCAGCGTCCG and 5'CGGACGCGTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."									
SOURCE	1..711									
ORIGIN	Query Match 84.2%; Score 16; DB 9; Length 711; Best Local Similarity 100.0%; Pred. No. 3e+03; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	2	AACGGAAGGCCTTTC	17							
Db	515	AACGGAAGGCCTTTC	500							
RESULT 24										
CX798411/c										
LOCUS	CX798411	JGI_CAAJ13264.rev NIH_XGC_tropBrn2	736 bp	mRNA	linear	EST 28-JUL-2005				
DEFINITION	IMAGE:7643358 3', mRNA sequence.									
ACCESSION	CX798411									
VERSION	CX798411.2	GI:71459585								



```

KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 763)
REFERENCE Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
AUTHORS Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSSs: OGWED19TH
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
FEATURES Location/Qualifiers
source 1..763
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBMA0557D14"
/notes="Vector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
ORIGIN
Query Match 84.2%; Score 16; DB 12; Length 763;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACGGAAGGCTTTCG 18
Db 328 ACGGAAGGCTTTCG 343

RESULT 26
LOCUS CX797048/c 803 bp mRNA linear EST 28-JUL-2005
DEFINITION JGI_CAAJ12493.rev NIH XGC tropBrn2 Xenopus tropicalis cDNA clone
IMAGE:7642446 3', mRNA sequence.
ACCESSION CX797048
VERSION CX797048.2 GI:71459157
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 803)
REFERENCE Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C.,
AUTHORS Brokstein,P. and Lindquist,E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT On Jan 31, 2005 this sequence version replaced gi:58351677.
Other_ESTs: JGI_CAAJ12493.fwd
Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
Clone Sequencing: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CAAJ 0137 row: 0 column: 4
High quality sequence stop: 730
POLYA=Yes.
FEATURES Location/Qualifiers
source 1..736
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7643358"
/tissue_type="Brain"
/dev_stage="Adult"
/lab_host="ElectroMAX DH10B"
/clone_lib="NIH XGC tropBrn2"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
Invitrogen pCMVSPORT6 vector. The work was done at DOE
Joint Genome Institute. Poly A RNA were primed with 5'
GACTAGTCTAGATCGGAG CGCGCGCCCTTTTCTTTT 3'. cDNA
were ligated to SalI adapter (5' TCGACCCACGCGTCG and
5'CGGACGCGTGGG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested pCMVSPORT6 vector."
ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 736;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCTTTC 17
Db 509 AACGGAAGGCTTTC 494

RESULT 25
CC684169 763 bp DNA linear GSS 19-JUN-2003
LOCUS OGWED19TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0557D14,
DEFINITION genomic survey sequence.
ACCESSION CC684169
VERSION CC684169.1 GI:32088945
KEYWORDS GSS.
SOURCE Zea mays

```

http://image.llnl.gov  
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: CAAJ 0129 row: i column: 4  
High quality sequence stop: 760  
POLYA=Yes.

FEATURES  
source Location/Qualifiers  
1. .803  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7642446"  
/tissue\_type="Brain"  
/dev\_stage="Adult"  
/lab\_host="ElectroMAX DH10B"  
/clone\_lib="NIH XGC tropBn2"  
/notes="Vector: pCMVspport6; Site.1: Sali; Site.2: NotI;  
This library was made from dt primed cDNA and cloned into Invitrogen pCMVspport6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCTAGATCGCGAG CGCGCGCCTTTTITTTT 3'. CDNA were ligated to Sali adapter (5' TCGACCCAGCGTCCG and 5'CGGACGGCTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and Sali digested pCMVspport6 vector."

ORIGIN  
Query Match 84.2%; Score 16; DB 9; Length 803;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTC 17  
Db 391 AACGGAAGGCCTTTC 376  
|||||

RESULT 27  
CX815303  
LOCUS  
DEFINITION  
JGI CAAK1288.fwd NIH XGC tropBn3 Xenopus tropicalis cDNA clone  
IMAGE:7652603 5', mRNA sequence.  
CX815303  
CX815303.1 GI:58369930  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 829)  
Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
Other ESTs: JGI CAAK1288.rev  
Contact: Lindquist,E.A., Richardson,P.  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley:  
http://tropicalis.berkeley.edu/home)  
cDNA Library Preparation: DOE Joint Genome Institute:  
http://www.jgi.doe.gov  
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.

indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: CAAK 0013 row: p column: 9  
High quality sequence stop: 817.

FEATURES  
source Location/Qualifiers  
1. .829  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7652603"  
/tissue\_type="Brain"  
/dev\_stage="Adult"  
/lab\_host="ElectroMAX DH10B"  
/clone\_lib="NIH XGC tropBn3"  
/notes="Vector: pCMVspport6; Site.1: Sali; Site.2: NotI;  
This library was made from dt primed cDNA and cloned into Invitrogen pCMVspport6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTAGTTCTAGATCGCGAG CGCGCGCCTTTTITTTT 3'. CDNA were ligated to Sali adapter (5' TCGACCCAGCGTCCG and 5'CGGACGGCTGGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and Sali digested pCMVspport6 vector."

ORIGIN  
Query Match 84.2%; Score 16; DB 9; Length 829;  
Best Local Similarity 100.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTC 17  
Db 636 AACGGAAGGCCTTTC 651  
|||||

RESULT 28  
CX815302/c  
LOCUS  
DEFINITION  
JGI CAAK1288.rev NIH XGC tropBn3 Xenopus tropicalis cDNA clone  
IMAGE:7652603 3', mRNA sequence.  
CX815302  
CX815302.2 GI:71464988  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Xenopus tropicalis (western clawed frog)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 853)  
Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
On Jan 31, 2005 this sequence version replaced gi:58369929.  
Other ESTs: JGI CAAK1288.fwd  
Contact: Lindquist,E.A., Richardson,P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley:  
http://tropicalis.berkeley.edu/home)  
cDNA Library Preparation: DOE Joint Genome Institute:  
http://www.jgi.doe.gov  
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
Clone Distribution: I.M.A.G.E. Consortium/LLNL:  
http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
Plate: CAAK 0013 row: p column: 9

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High quality sequence stop: 793
POLYA=Yes.
FEATURES
    source
        Location/Qualifiers
            1..853
                /organism="Xenopus tropicalis"
                /mol_type="mRNA"
                /db_xref="taxon:8364"
                /clone="IMAGE:7652603"
                /tissue_type="Brain"
                /dev_stage="Adult"
                /lab_host="ElectroMAX DH10B"
                /clone_lib="NIH_XGC_tropBrn3"
                /notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
                This library was made from dt primed cDNA and cloned into
                Invitrogen pCMVSPORT6 vector. The work was done at DOE
                Joint Genome Institute. Poly A RNA were primed with 5'
                GACTAGTCTPAGATCCGAG CGCGCGCCCTTTTTTT 3'. CDNA
                were ligated to SalI adapter (5' TCGACCCACGCGCCG and
                5'CGGACGCGTGGG), digested with NotI, size fractionated in
                1.1% agarose gel electrophoresis and ligated into NotI and
                SalI digested pCMVSPORT6 vector."
ORIGIN
    Query Match      84.2%; Score 16; DB 9; Length 853;
    Best Local Similarity 100.0%; Pred. No. 3.1e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACCGAAAGGCGCTTC 17
    |||||
Db 392 AACCGAAAGGCGCTTC 377

RESULT 29
CNS02922/c
LOCUS
DEFINITION
    Tetraodon nigroviridis genome survey sequence PUC-ORI end of clone
    245N04 of library G from Tetraodon nigroviridis, genomic survey
    sequence.
VERSION
    AL186707.1 GI:7824811
KEYWORDS
    GSS; genome survey sequence.
SOURCE
    Tetraodon nigroviridis
    ORGANISM
        Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
    1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
        Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
        Saurin,W. and Weissenbach,J.
        Estimate of human gene number provided by genome-wide analysis
        using Tetraodon nigroviridis DNA sequence
        Nat. Genet. 25 (2), 235-238 (2000)
        10835645
2
REFERENCE
    2 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
        Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
        Saurin,W., Bernot,A. and Weissenbach,J.
        Characterization and repeat analysis of the compact genome of the
        freshwater pufferfish Tetraodon nigroviridis
        Genome Res. 10 (7), 939-949 (2000)
        10899143
3 (bases 1 to 883)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

```

```

FEATURES
    source
        Location/Qualifiers
            1..883
                /organism="Tetraodon nigroviridis"
                /mol_type="genomic DNA"
                /db_xref="taxon:99883"
                /clone="245N04"
                /clone_lib="G"
                /notes="Genoscope sequence ID : COAG245DG02SP1
                end : PUC-ORI"
ORIGIN
    Query Match      84.2%; Score 16; DB 14; Length 883;
    Best Local Similarity 100.0%; Pred. No. 3.1e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTT 16
    |||||
Db 366 GAACGGAAGGCGCTTT 351

RESULT 30
CC712360/c
LOCUS
DEFINITION
    OGULG58TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0467119,
    genomic survey sequence.
VERSION
    CC712360
CC712360.1 GI:32117136
KEYWORDS
    GSS.
SOURCE
    Zea mays
    ORGANISM
        Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
    1 (bases 1 to 945)
    AUTHORS
        Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
        Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
        Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
        Consortium for Maize Genomics
        Unpublished (2002)
        Other GSSs: OGULG58TV
        Contact: Cathy Whitelaw
        TIGR
        9712 Medical Center Drive, Rockville, MD 20850, USA
        Tel: 301-838-5943
        Fax: 301-838-0208
        Email: whitelaw@tigr.org
        Seq primer: TR
        Class: methylation filtered.
        Location/Qualifiers
            1..945
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone_lib="ZMMBMA0467119"
                /clone_lib="ZM_0.7_1.5_KB"
                /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"
ORIGIN
    Query Match      84.2%; Score 16; DB 12; Length 945;
    Best Local Similarity 100.0%; Pred. No. 3.2e+03;
    Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAGGCGCTTCG 18
    |||||
Db 703 ACGGAAGGCGCTTCG 688

RESULT 31
CC78267/c
LOCUS
DEFINITION
    CC78267
    OGULH26TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0460F04,

```

```

genomic survey sequence.
CC678267
VERSION CC678267.1 GI:32083043
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 949)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGUHJ26TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Classes: methylation filtered.
Location/Qualifiers
1..949
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM.0.7.1.5.KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 84.2%; Score 16; DB 12; Length 949;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCGTTTCG 18
Db 555 ACGGAAAGGCGTTTCG 570

RESULT 33
DN695496
LOCUS
DEFINITION DN695496 1136 bp mRNA linear EST 30-MAR-2005
CLJ01-D08.51d-s SHGC-CLJ Gasterosteus aculeatus cDNA clone
CLJ01-D08 5', mRNA sequence.
ACCESSION DN695496
VERSION DN695496.1 GI:62053862
KEYWORDS EST.
SOURCE Gasterosteus aculeatus (three spined stickleback)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1136)
Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
Schmutz,J. and Myers,R.M.
Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2003)
Contact: Grimwood, Jane
Stanford Human Genome Center
Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 01
High quality sequence stop: 812.

FEATURES
source
1..1136
/organism="Gasterosteus aculeatus"
/mol_type="mRNA"
/strain="Bitrufjordur marine sticklebacks, Iceland"
/db_xref="taxon:69293"
/clone="CLJ01-D08"
/sex="mixed male and female"
/tissue_type="whole larva"
/development="21 day old larvae collected at Swarup Stage 30
(J. Embryol. Exp. Morphol 6: 373-383,1958)"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CLJ"
/notes="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTTCTAGTCGAGCGCGCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed

```

in the blunt end cloning, leaving a junction of the form 'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:  
[http://www.openbiosystems.com/cdna\\_library\\_construction\\_fa\\_q.php#8](http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8) The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:  
<http://www.openbiosystems.com/stickleback>"

## ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 1136;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCGCTTTC 17  
 |||||  
 Db 947 AACGGAAGGCGCTTTC 962

## RESULT 34

DT995972 1390 bp mRNA linear EST 22-SEP-2005  
 LOCUS CNB181-G02.yld-s SHGC-CNB Gasterosteus aculeatus cDNA clone  
 DEFINITION

ACCESSION DT995972  
 VERSION DT995972  
 KEYWORDS EST.

SOURCE Gasterosteus aculeatus (three spined stickleback)

ORGANISM Gasterosteus aculeatus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes; Gasterosteidae; Gasterosteus.

## REFERENCE

1 (bases 1 to 1390)  
 Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.

Expressed sequence tags from *Gasterosteus aculeatus*

## TITLE

Unpublished (2003)

## JOURNAL

Comment: Grimwood, Jane

Stanford Human Genome Center

Stanford University School of Medicine

975 S California Ave, Palo Alto, CA 94304, USA

Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@hgc.stanford.edu

Plate: 181

High quality sequence start: 26

High quality sequence stop: 835.

## FEATURES

1..1390 Location/Qualifiers

/organism="Gasterosteus aculeatus"

/mol\_type="mRNA"

/strain="Conner Creek sticklebacks, WA USA"

/db\_xref="taxon:69293"

/clone="CNB181-G02"

/sex="mixed male and female"

/tissue\_type="brain"

/dev\_stage="adult"

/lab\_hosts="DH10B (T1 phage resistant)"

/clone\_lib="SHGC-CNB"

/note="Vector: Express 1; Total and poly A+ RNA was isolated from the indicated stickleback tissue, and a cDNA library was constructed in the Express 1 plasmid vector by Open Biosystems. First strand cDNA synthesis was primed with an 54 bp linker primer containing an oligodT sequence preceded by a synthetic NotI site (first strand primer: 5'-GACTAGTCTAGATCGGAGCGGCC(T)25-3'). Following

second strand synthesis, cDNAs were made blunt at the end corresponding to the original 5 prime end of mRNA, and cloned directionally into the NotI and EcoRV sites of Express 1. Note that the EcoRV site is typically destroyed in the blunt end cloning, leaving a junction of the form

'xxxATC' (where is ATC is the second half of the EcoRV site, and xxx is derived from the cDNA sequence). A map of the Express 1 vector is available at:  
[http://www.openbiosystems.com/cdna\\_library\\_construction\\_fa\\_q.php#8](http://www.openbiosystems.com/cdna_library_construction_fa_q.php#8) The primary library was transformed and amplified in DH10B (T1 phage resistant) bacteria. Clones available from Open Biosystems:  
<http://www.openbiosystems.com/stickleback>"

## ORIGIN

Query Match 84.2%; Score 16; DB 10; Length 1390;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCGCTTTC 17  
 |||||  
 Db 1273 AACGGAAGGCGCTTTC 1288

## RESULT 35

BM633199 169 bp mRNA linear EST 26-FEB-2002  
 LOCUS 17000687506761 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION

ACCESSION BM633199  
 VERSION BM633199  
 KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae; Anophelinae; Anopheles.

## REFERENCE

1 (bases 1 to 169)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,

Charlab,R., Collins,E.H., Venter,J.C. and Hoffman,S.L.

Celera Anopheles gambiae EST project

Unpublished (2002)

## TITLE

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004AY7 row: H column: 16

Seq primer: M13 Reverse.

## FEATURES

1..169 Location/Qualifiers

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std.

chromosome)"

/db\_xref="taxon:7165"

/clone="19600449642370"

/dev\_stage="Adult"

/lab\_host="DH10B"

/clone\_lib="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: Sali; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 169;  
 Best Local Similarity 89.8%; Pred. No. 3.1e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCGCTTTCGG 19  
 |||||  
 Db 52 GAACGGAAAGGCGCTTTCGG 70

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RESULT 36
DT929107      225 bp      mRNA      linear      EST 20-SEP-2005
LOCUS      PCRS10047 Hematopoietic stem cells Mus musculus cDNA, mRNA
DEFINITION      sequence.
ACCESSION      DT929107
VERSION      DT929107.1 GI:75959729
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 225)
AUTHORS      Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and
              Lemischka,I.R.
TITLE      Identification of Stem Cell Molecular Repertoire by Alternative
              Splicing
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT      Contact: Pritsker M
              Lab of Ihor Lemischka, Department of Molecular Biology
              Princeton University
              Princeton, NJ 08544, USA
              Tel: 609 258 5657
              Fax: 609 258 1704
              Email: pritsker@molbio.princeton.edu.
FEATURES             source
     1..225
     /organism="Mus musculus"
     /mol_type="mRNA"
     /db_xref="taxon:10090"
     /tissue_type="Hematopoietic stem cells"
     /cell_type="Hematopoietic stem cells"
     /clone_lib="Hematopoietic stem cells"
     /notes="cDNA library was made from FACS-purified
             hematopoietic stem cells"
ORIGIN
Query Match      83.2%; Score 15.8; DB 10; Length 225;
Best Local Similarity 89.5%; Pred. No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GAACGGAAGGCGCTTCGG 19
      ||||| ||||| |||||
Db      122 GAACGGAAGGCGCTTCGG 140
      ||||| ||||| |||||
RESULT 37
CV341801/c
LOCUS      CV341801
DEFINITION      MRO-HT0559-160500-019-b11 HT0559 Homo sapiens cDNA, mRNA sequence.
ACCESSION      CV341801
VERSION      CV341801.1 GI:52665015
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 255)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. http://www.ludwig.org.br.
FEATURES             source
     1..255
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /dev_stage="Adult"
     /clone_lib="HT0559"
     /note="Organ: head_neck; Vector: puc18; Site:1: SmaI;
             Site:2: SmaI; A mini-library was made by cloning products
             derived from ORESTES PCR (U.S. Letters Patent application
             No. 196,716 - Ludwig Institute for Cancer Research)
             profiles into the pUC 18 vector. Reverse transcription of
             tissue mRNA and cDNA amplification were performed under
             low stringency conditions."
ORIGIN
Query Match      83.2%; Score 15.8; DB 8; Length 255;
Best Local Similarity 89.5%; Pred. No. 3.3e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      1 GAACGGAAGGCGCTTCGG 19
      ||||| ||||| |||||
Db      250 GAATGGAAGGCTTCGG 232
      ||||| ||||| |||||
RESULT 38
CV341780/c
LOCUS      CV341780
DEFINITION      MRO-HT0559-060600-030-b12 HT0559 Homo sapiens cDNA, mRNA sequence.
ACCESSION      CV341780
VERSION      CV341780.1 GI:52664994
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 256)
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
              Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
              Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
              Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
              O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
              Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED      10737800
COMMENT      Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. http://www.ludwig.org.br.
FEATURES             source
     1..256
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /dev_stage="Adult"
     /clone_lib="HT0559"
     /note="Organ: head_neck; Vector: puc18; Site:1: SmaI;
```

Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 8; Length 256;  
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTCGG 19  
 |||||  
 Db 250 GAATGGAAGGCTTTCGG 232

## RESULT 39

BB276884/c

## LOCUS

BB276884 RIKEN full-length enriched, 10 days neonate cortex Mus  
 musculus cDNA clone A830099J18 3' similar to AF040965 Homo sapiens  
 unknown protein IT12 mRNA, mRNA sequence.

## ACCESSION

BB276884.1 GI:8973905

## VERSION

EST.

## KEYWORDS

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 263)

## REFERENCE

## AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,  
 Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,  
 Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,  
 Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,  
 Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,  
 Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,  
 Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,  
 Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Sugihara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,  
 Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watanishi, A.,  
 Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,  
 Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and  
 Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al.)

## TITLE

## JOURNAL

## COMMENT

Unpublished (2000)  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,  
 Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Thermostabilization and thermoactivation of thermolabile enzymes by  
 trehalose and its application for the synthesis of full length  
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)  
 Itoh, M., Ktsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,  
 Okazaki, Y. and Hayashizaki, Y.  
 Automated filtration-based high-throughput plasmid preparation  
 system. Genome Res. 9 (5), 463-470 (1999)  
 Carninci, P. and Hayashizaki, Y.  
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
 19-44 (1999)

Please visit our web site (http://genome.rtc.riken.go.jp) for

further details.

## FEATURES

## source

1. .263

/organism="Mus musculus"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 5; Length 267;

Best Local Similarity 89.5%; Pred. No. 3.3e+03;

/mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="A830099J18"  
 /tissue\_type="cortex"  
 /dev\_stage="10 days neonate"  
 /lab\_host="DH10B"  
 /clone\_lib="RIKEN full-length enriched, 10 days neonate  
 cortex"  
 /notes="Site 1: Sali; Site 2: BamHI; cDNA library was  
 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 20.0 and subtraction to Rot = 459.0. Second  
 strand cDNA was prepared with the primer adapter of  
 sequence [5' GAGAGAGATTCTCGAGTTAAATTAATATCCCCCCCCC  
 3']. cDNA was cleaved with XhoI and BamHI. Vector: a  
 modified pBluescript KS(+) after bulk excision from Lambda  
 FLC I."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 263;  
 Best Local Similarity 89.5%; Pred. No. 3.3e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTTCGG 19

|||||

Db 112 GAATGGAAGGCTTTCGG 94

## RESULT 40

CF045077

LOCUS

CF045077 QJZ Zea mays cDNA clone QJZ8a11, mRNA sequence.

DEFINITION

CF045077

ACCESSION

CF045077.1 GI:32940258

VERSION

EST.

KEYWORDS

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 267)

AUTHORS

Genoplante.

TITLE

Unpublished (2003)

JOURNAL

COMMENT

Contact: Genoplante

Genoplante

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (http://www.genoplante.com

and http://genoplante-info.infobiogen.fr).

FEATURES

Location/Qualifiers

1. .267

/organism="Zea mays"

/mol\_type="mRNA"

/cultivar="F2"

/db\_xref="taxon:4577"

/clone="QJZ8a11"

/tissue\_type="cell lignification part of the 6th leaf"

/clone\_lib="QJZ"





Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

```
FEATURES
source
1. .279
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="D930045D23"
/sex="mixed"
/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 15 days embryo
head"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTTTTTCCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCAGTGAATTAATATCCGCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"
```

ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 279;  
Best Local Similarity 89.5%; Pred. No. 3.3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
|||||  
Db 231 GAACGGAATGCCTTCAG 213

RESULT 43

LOCUS CF044432 288 bp mRNA linear EST 17-JUL-2003

DEFINITION QJ29g07.yg QJ29g07, mRNA sequence.

ACCESSION CF044432

VERSION CF044432.1 GI:32939613

KEYWORDS EST.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 288)

TITLE Genoplante, a major partnership french program in plant genomics

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES source

1. .288  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="F2"  
/db\_xref="taxon:4577"  
/clone="QJ29g07"

ORIGIN

Query Match 83.2%; Score 15.8; DB 5; Length 288;  
Best Local Similarity 89.5%; Pred. No. 3.3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
|||||  
Db 209 GAACGGAAGGCTTCGG 227

RESULT 44

LOCUS CB710003 292 bp mRNA linear EST 10-APR-2003

DEFINITION AMGNNUC.NRDG1-00123-A7-A nrdg1 (10855) Rattus norvegicus cDNA clone  
nrdg1-00123-a7 5', mRNA sequence.

ACCESSION CB710003

VERSION CB710003.1 GI:29767151

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Rattus.

AUTHORS 1 (bases 1 to 292)

TITLE Angen EST Program.

JOURNAL Angen Rat EST Program

COMMENT Unpublished (2003)  
Contact: Dan Fitzpatrick  
Angen, Inc  
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00123 row: a column: 7.

FEATURES source

1. .292  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="nrdg1-00123-a7"  
/tissue\_type="Dorsal Root Ganglia"  
/notes="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; rat  
dorsal root ganglia"

ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 292;  
Best Local Similarity 89.5%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19  
|||||  
Db 137 GAACGGAAGGCTTCGG 155

RESULT 45

LOCUS CC939630/c 299 bp DNA linear GSS 13-AUG-2003

DEFINITION ZMMBBb0239D20.r ZMMBBb Zea mays genomic clone ZMMBBb0239D20 3',  
genomic survey sequence.

ACCESSION CC939630

VERSION CC939630.1 GI:33625477

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

AUTHORS 1 (bases 1 to 299)

TITLE Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.  
and Wing, R.  
Sequencing of the maize genome

[illegible]



was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (G14732114[gb|AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 83.2%; Score 15.8; DB 11; Length 325;  
Best Local Similarity 89.5%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19

Db 262 GAACGGAAGGCGCTTCGG 280

RESULT 50

BY343361/c

LOCUS

DEFINITION BY343361 RIKEN full-length enriched, whole joints Mus musculus cDNA

clone L230045E11 5', mRNA sequence.

ACCESSION

VERSION BY343361.1 GI:26572849

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 331)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perle, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

JOURNAL

PUBMED 1246851

COMMENT

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers

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/clone="L230045E11"  
/tissue\_type="whole joints"  
/clone\_lib="RIKEN full-length enriched, whole joints"

ORIGIN

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19

Db 55 GAATGGAGAGGCGCTTCGG 37

RESULT 51

BY335795/c

LOCUS

DEFINITION BY335795 RIKEN full-length enriched, synovial fibroblasts Mus

musculus cDNA clone L130045J21 5', mRNA sequence.

ACCESSION BY335795

VERSION BY335795.1 GI:26530055

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 335)

REFERENCE

AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V.,



Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akaira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al. 2001)  
 Unpublished (2001)  
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 Email: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
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 wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Itoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
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 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
 e mouse tissues.  
 Location/Qualifiers  
 1. 337  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="F530005B04"  
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 /dev\_stage="adult"  
 /lab\_host="SOLP"  
 /clone\_lib="RIKEN full-length enriched, adult male kidney"  
 /notes="Site\_1: XhoI; Site\_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'  
 GAGAGAGAGCGCGCGCAACTCGAGTTTTTTTTTTTNN 3', cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence 5'  
 GAGAGAGAGATCCAGAGCTCAATTAAATTAATTAACCCCCCCCC 3'.  
 cDNA was cleaved with XhoI and SstI."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 337;  
 Best Local Similarity 89.5%; Pred.No. 3.4e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCGCTTCGG 19

Db 38 GAATGAGAGGCGCTTCGG 20

RESULT 54

BY103528/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

BY103528 338 bp mRNA linear EST 07-DEC-2002  
 BY103528 RIKEN full-length enriched, pooled tissues, adult spleen,  
 etc. Mus musculus cDNA clone K630151F09 5', mRNA sequence.  
 BY103528  
 BY103528.1 GI:26214145  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 338)

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Otsu,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schombach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,W., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlstedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wyszynski,B., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Iishi,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 12456851

## TITLE

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prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES  
source  
1. .338  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone="K630151F09"  
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adult spleen, etc."  
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## ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 338;  
Best Local Similarity 89.5%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

Db 55 GAATGGAGAGCCCTTCGG 37

## RESULT 55

BY193164/c

LOCUS  
DEFINITION  
BY193164 RIKEN full-length enriched, B6-derived CD11 +ve dendritic  
cells Mus musculus cDNA clone F730001D03 5', mRNA sequence.

ACCESSION  
BY193164

VERSION  
BY193164.1 GI:26370122

KEYWORDS  
EST.

SOURCE  
Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

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## AUTHORS

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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
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Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,  
Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs

## TITLE

JOURNAL

PUBMED

COMMENT

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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with  
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Normalization and subtraction of cap-trapper-selected cDNAs to  
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RIKEN integrated sequence analysis (RISA) system--384-format  
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cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

## FEATURES

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## ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 342;  
Best Local Similarity 89.5%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCCTTCGG 19

Db 57 GAATGGAGAGCCCTTCGG 39

## RESULT 56

BY202264

LOCUS

DEFINITION  
BY202264 RIKEN full-length enriched, B6-derived CD11 +ve dendritic  
cells Mus musculus cDNA clone F730112B18 5', mRNA sequence.

assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

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ORIGIN

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Db 84 GAACGGAAAGGCGCTTTCGG 102  
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RESULT 57

BY212596/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBLISHED

COMMENT

BY202264

BY202264.1

GI:26381895

EST.

Mus musculus

Mus musculus (house mouse)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
1 (bases 1 to 363)  
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.  
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12466851  
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

Location/Qualifiers  
1. .363  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="F730112B18"  
/cell\_type="B6-derived CD11 +ve dendritic cells"  
/clone\_lib="RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells"

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Best Local Similarity 89.5%; Pred. No. 3.5e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGGCGCTTTCGG 19  
|||||  
Db 84 GAACGGAAAGGCGCTTTCGG 102  
|||||

RESULT 57  
LOCUS BY212596/c  
DEFINITION BY212596 RIKEN full-length enriched, activated spleen Mus musculus cDNA clone F830017B06 5', mRNA sequence.  
ACCESSION BY212596  
VERSION BY212596.1 GI:26393243  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 369)  
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gough,J., Grimmond,S., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Ramachandran,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Perteau,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reid,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Inotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBLISHED 12466851  
COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)



1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
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 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
 Trust/MRC building Addenbrookes Hospital Cambridge) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.

# FEATURES

source

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1. 369
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F830017B06"
/tissue_type="activated spleen"
/clone_lib="RIKEN full-length enriched, activated spleen"
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# ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 369;  
 Best Local Similarity 89.5%; Pred. No. 3.5e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19

Db 55 GAATGGAGAGCCCTTCGG 37

# RESULT 58

BY222901/c

LOCUS BY222901 RIKEN full-length enriched, activated spleen Mus musculus  
 DEFINITION cDNA clone F830230123 5', mRNA sequence.  
 ACCESSION BY222901  
 VERSION BY222901.1 GI:26404004  
 KEYWORDS EST.

SOURCE Mus musculus (house mouse)

# ORGANISM

Mus musculus  
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 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.  
 1 (bases 1 to 370)

# REFERENCE

# AUTHORS

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaado, I., Otsu, N., Saito, R., Suzuki, H., Yananaka, I.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,  
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawai, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A.,  
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 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tonit, M.,  
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 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation  
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 Nature 420, 563-573 (2002)

12468551

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 Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

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Normalization and subtraction of cap-trapper-selected cDNAs to

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10 (11), 1757-1771 (2000)

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encyclopedia: real-time sequence clustering for construction of a

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Genomic Sciences Center and Genome Science Laboratory in RIKEN

Division of Experimental Animal Research in Riken contributed to

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further details.

Location/Qualifiers

1. 370

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="NOD"

/db\_xref="taxon:10090"

/clone="F830230123"

/tissue\_type="activated spleen"

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# ORIGIN

Query Match 83.2%; Score 15.8; DB 4; Length 370;  
 Best Local Similarity 89.5%; Pred. No. 3.5e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCCTTTCGG 19  
|||||  
Db 55 GAATGGAGAGCCTTTCGG 37

RESULT 59  
BY216278/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BY216278 378 bp mRNA linear EST 10-DEC-2002  
BY216278 RIKEN full-length enriched, activated spleen Mus musculus  
cDNA clone F830042M04 5', mRNA sequence.

BY216278  
BY216278.1 GI:26397025  
EST.  
Mus musculus (house mouse)

Mus musculus  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muroidae; Murinae; Mus.

1 (bases 1 to 378)

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I.,  
Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A.,  
Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C.,  
Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H.,  
Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V.,  
Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A.,  
Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T.,  
Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S.,  
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Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A.,  
Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R.,  
Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T.,  
Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J.J., Ring B.Z., Ringwald M.,  
Sandalin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y.,  
Wells C., Wilming L.G., Wyszynski B., Yanagisawa M., Yang I.,  
Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P.,  
Hayashizaki N., Hirozane-Kishikawa T., Konno H., Nakamura M.,  
Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K.,  
Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y.,  
Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K.,  
Shingawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S.,  
Rogers J., Birney E. and Hayashizaki Y.

Analysis of the mouse transcriptome based on functional annotation  
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Nature 420, 563-573 (2002)

12466851

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S.,  
Hirozane T., Imotani K., Ishii Y., Itoh M., Kawai J., Konno H.,  
Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R.,  
Ohno M., Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K.,  
Shiraki T., Tagami M., Waki K., Warahiki A., Muramatsu M. and  
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
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Trust/MRC Building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

Location/Qualifiers  
1. .378  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="NOD"  
/db\_xref="taxon:10090"  
/clone="F830042M04"  
/tissue\_type="activated spleen"  
/clone\_lib="RIKEN full-length enriched, activated spleen"

ORIGIN  
Query Match 83.2%; Score 15.8; DB 4; Length 378;  
Best Local Similarity 89.5%; Pred. No. 3 5e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGCCTTTCGG 19  
|||||  
Db 55 GAATGGAGAGCCTTTCGG 37

RESULT 60  
AA652906  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AA652906 379 bp mRNA linear EST 25-NOV-1997  
ns68a07.s1 NCI CGAP Pr2 Homo sapiens cDNA clone IMAGE:1189756  
similar to gb:U01124 40S RIBOSOMAL PROTEIN S13 (HUMAN);, mRNA  
sequence.  
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AA652906.1 GI:2594558  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.

1 (bases 1 to 379)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabps@mail.nih.gov  
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,  
M.D., Michael Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: David B. Krizman, Ph.D.  
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
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Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .379  
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/clone_lib="NCI_CGAP_Pr2"
/notes="vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 379;
Best Local Similarity 89.5%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTCGG 19
Db 354 GAAAGGAAGCCCTTCGG 372

RESULT 61
LOCUS      AW762692
DEFINITION ur58d11.y1 NCI_CGAP Mam3 Mus musculus cDNA clone IMAGE:3154485 5'
similar to TR:Q26422 Q26422 FACTOR C. [1] ;, mRNA sequence.
ACCESSION  AW762692
VERSION     AW762692.1 GI:7694623
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 379)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1057241
Seq primer: -40RP from Gibco
High quality sequence stop: 378.
Location/Qualifiers
1. 379
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
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/clone="IMAGE:3154485"
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/dev stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Mam3"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.

Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
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## ORIGIN

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Query Match      83.2%; Score 15.8; DB 7; Length 379;
Best Local Similarity 89.5%; Pred. No. 3.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 257 GAAAGGAAGCCCTTCGG 275
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## RESULT 62

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LOCUS      BY280232/c
DEFINITION BY280232 RIKEN full-length enriched, visual cortex Mus musculus
cDNA clone K430345N21 5', mRNA sequence.
ACCESSION  BY280232
VERSION     BY280232.1 GI:26470569
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
```

## REFERENCE

```

1 (bases 1 to 384)
Okazaki, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
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Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
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Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
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Itoh, M., Kigawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
```

## TITLE

```

JOURNAL     Nature 420, 563-573 (2002)
PUBMED      12468851
COMMENT     Contact: Yoshihide Hayashizaki
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Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ono, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
```

## FEATURES

## source

Hayashizaki,Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hiroawa,Wako-shi,Saitama 351-0198 Japan ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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VERSION  
KEYWORDS  
SOURCE  
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1 (bases 1 to 385)  
The FANTOM Consortium and RIKEN Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group). The transcriptional landscape of the mammalian genome Science 309 (5740), 1559-1563 (2005)  
16141072  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-resgsc.riken.jp, URL:http://genome.gsc.riken.jp/  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Michelle Brinkmeier and Sally Camper ( Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor,MI 48109-0638 USA ) whose assistance we gratefully acknowledge. Please visit our web site for further details.  
URL:http://genome.gsc.riken.jp/.

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VERSION  
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1 (bases 1 to 385)  
Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and Lemischka,I.R.  
Diversification of Stem Cell Molecular Repertoire by Alternative Splicing  
Proc. Natl. Acad. Sci. U.S.A. (2005) In press  
Contact: Pritsker M  
Lab of Ihor Lemischka, Department of Molecular Biology Princeton University  
Princeton, NJ 08544, USA  
Tel: 609 258 5657  
Fax: 609 258 1704  
Email: pritsker@molbio.princeton.edu.

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 1 (bases 1 to 388)  
 REFERENCE  
 AUTHORS  
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaado, I., Otsu, N., Sato, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aikawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Tasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
 TITLE  
 Nature 420, 563-573 (2002)  
 JOURNAL  
 PUBMED  
 COMMENT  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
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 Fax: 81-45-503-9216  
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
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 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (Laboratory for Neuronal Circuit Development Brain Science Institute RIKEN 2-1 Hirosewa, Wako-shi, Saitama 351-0198 Japan) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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 1 (bases 1 to 388)  
 REFERENCE  
 AUTHORS  
 Pritsker, M., Doniger, T. T., Kramer, L. C., Westcot, S. E. and Lemischka, I. R.  
 Diversification of Stem Cell Molecular Repertoire by Alternative Splicing  
 Proc. Natl. Acad. Sci. U.S.A. (2005) In press  
 Contact: Pritsker M  
 Lab of Thor Lemischka, Department of Molecular Biology  
 Princeton University  
 Princeton, NJ 08544, USA  
 Tel: 609 258 5657  
 Fax: 609 258 1704  
 Email: pritsker@molbio.princeton.edu.

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ACCESSION
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  1 (bases 1 to 411)
REFERENCE
  Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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  Nature 420, 563-573 (2002)
  12466851
  Contact: Yoshihide Hayashizaki
  Laboratory for Genome Exploration Research Group, RIKEN Genomic
  Sciences Center (GSC), Yokohama Institute
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  1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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  Fax: 81-45-503-9216
  Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
  Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
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  Hayashizaki, Y. Direct Submission
  Computational Analysis of Full-length Mouse cDNAs Compared with
  Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
  Normalization and subtraction of cap-trapper-selected cDNAs to
  prepare full-length cDNA libraries for rapid discovery of new
  genes. Genome Res. 10 (10), 1617-1630 (2000)
  RIKEN integrated sequence analysis (RISA) system--384-format
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  10 (11), 1757-1771 (2000)
  Computer-based methods for the mouse full-length cDNA
  encyclopedia: real-time sequence clustering for construction of a
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  cDNA library was prepared and sequenced in Mouse Genome
  Encyclopedia Project of Genome Exploration Research Group in Riken

```

Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Michela Pagiolini and Takao K. Hensch (  
Laboratory for Neuronal Circuit Development Brain Science Institute  
RIKEN 2-1 Hirose, Wako-shi, Saitama 351-0198 Japan ) whose  
assistance we gratefully acknowledge. Please visit our web site  
(http://genome.gsc.riken.go.jp) for further details.

## FEATURES

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Query Match 83.2%; Score 15.8; DB 4; Length 411;  
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QY 1 GAACGGAAGGCTTTTCGG 19

DB 58 GAATGGAGAGGCTTTTCGG 40

## RESULT 70

BM654471

LOCUS

DEFINITION

17000687383524 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

19600449670164 5', mRNA sequence.

ACCESSION

BM654471

VERSION

BM654471.1 GI:18953982

KEYWORDS

EST.

SOURCE

ORGANISM

Anopheles gambiae (African malaria mosquito)

Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

Culicidae; Anophelinae; Anopheles.

1 (bases 1 to 417)

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,

Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

Celera Genomics

Unpublished (2002)

CELERA ANOPHELES GAMBIAE EST PROJECT

CONTACT: Holt R.A.

CELERA GENOMICS

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

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Seq primer: M13 Reverse.

Location/Qualifiers

source

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Not 1 site is 3'. Clones available through the Malaria

Research and Reference Reagent Resource Center

(www.malaria.mr4.org)."

## ORIGIN

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Matches	17; Conservative	0; Mismatches	2; Indels			
0; Gaps						
QY	1	GAACGGAAGGCGCTTTCCG 19				
DB	300	GAACGGAAGTACTTTCCG 318				
RESULT 71						
AI509463/c						
LOCUS						
DEFINITION	vxi2all.y1 Soares_thymus_2NDMT Mus musculus CDNA clone					
IMAGE	IMAGE:1264220 5', mRNA sequence.					
AI509463						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
COMMENT						
<p>Unpublished (1997)</p> <p>Contact: Robert Strausberg, Ph.D.</p> <p>Email: cgaabs@mail.nih.gov</p> <p>This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information.</p> <p>MGI:666772</p> <p>This read is a RESEQUENCE of a previously sequenced mouse clone correct orientation)</p> <p>Seq primer: -40RP from Gibco</p> <p>High quality sequence stop: 420.</p>						
FEATURES	Location/Qualifiers					
	<p>1..429</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="IMAGE:1264220"</p> <p>/sex="male"</p> <p>/tissue_type="thymus"</p> <p>/dev_stage="4 weeks"</p> <p>/lab_host="DH10B"</p> <p>/clone_lib="Soares thymus_2NDMT"</p> <p>/note="Vector: pT73D-PacI; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',</p> <p>TGTTACCAATCTGAATGGAGCGCCCGTGTATTTTTTTTTTTTTTTTTTTTTT</p> <p>3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."</p>					
ORIGIN						
Query Match	83.2%; Score 15.8; DB 1; Length 429;					
Best Local Similarity	89.5%; Pred. No. 3.6e+03;					
Matches	17; Conservative	0; Mismatches	2; Indels			
0; Gaps						
QY	1	GAACGGAAGGCGCTTTCCG 19				
DB	39	GAATGGAGGCGCTTTCCG 21				
RESULT 72						
BB848488/c						
LOCUS						
DEFINITION	vxi2all.y1 Soares_thymus_2NDMT Mus musculus CDNA clone					
IMAGE	IMAGE:1264220 5', mRNA sequence.					
AI509463						
VERSION						
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
COMMENT						
<p>Unpublished (2001)</p> <p>Contact: Yoshihide Hayashizaki</p> <p>Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute</p> <p>The Institute of Physical and Chemical Research (RIKEN)</p> <p>1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan</p> <p>Tel: 81-45-503-9222</p> <p>Fax: 81-45-503-9216</p> <p>Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/</p> <p>Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.</p> <p>Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)</p> <p>wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.</p> <p>RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)</p> <p>Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.</p> <p>Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)</p> <p>Please visit our web site (http://genome.gsc.riken.go.jp) for further details.</p> <p>e mouse tissues.</p> <p>Location/Qualifiers</p> <p>1..431</p> <p>/organism="Mus musculus"</p> <p>/mol_type="mRNA"</p> <p>/strain="C57BL/6J"</p> <p>/db_xref="taxon:10090"</p> <p>/clone="F930002H15"</p> <p>/tissue_type="inner ear"</p> <p>/dev_stage="adult"</p> <p>/clone_lib="RIKEN full-length enriched, adult inner ear"</p>						
ORIGIN						
Query Match	83.2%; Score 15.8; DB 7; Length 431;					
Best Local Similarity	89.5%; Pred. No. 3.6e+03;					
Matches	17; Conservative	0; Mismatches	2; Indels			
0; Gaps						
QY	1	GAACGGAAGGCGCTTTCCG 19				
DB	52	GAATGGAGGCGCTTTCCG 34				
RESULT 73						
BB848488/c						
LOCUS						
DEFINITION	vxi2all.y1 Soares_thymus_2NDMT Mus musculus CDNA clone					
IMAGE	IMAGE:1264220 5', mRNA sequence.					
AI509463						



```

CB758843
LOCUS          CB758843          434 bp      mRNA      linear      EST 16-MAY-2003
DEFINITION    AMGNNUC:NRW3-00049-A9-A white adipose tiss (10469) Rattus
               norvegicus cDNA clone nrwa3-00049-a9 5', mRNA sequence.
ACCESSION     CB758843
VERSION       CB758843.1  GI:29847234
KEYWORDS      EST.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE     1 (bases 1 to 434)
AUTHORS       Angen EST Program.
TITLE         Angen Rat EST Program
JOURNAL       Unpublished (2003)
COMMENT       Contact: Dan Fitzpatrick
               Angen, Inc
               One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
               Tel: 805 447-4881
               Plate: 00049 row: a column: 9.
FEATURES             Location/Qualifiers
     source          1..434
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="nrwa3-00049-a9"
                     /tissue_type="adipose tiss"
                     /clone_lib="white adipose tiss (10469)"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; white
                     adipose tiss adult female Wistar rats, >250 grams"
ORIGIN
Query Match      83.2%; Score 15.8; DB 4; Length 434;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTCGG 19
|||||
Db 117 GAACGGAAAGCCTTCGG 135

RESULT 74
CO651130
LOCUS          CO651130          441 bp      mRNA      linear      EST 01-MAY-2005
DEFINITION    ccp23_D04 08 Chondrus crispus protoplasts Zap Express Library
               Chondrus crispus cDNA clone ccp23 D04 08 5' similar to orf [Ricin
               communis] with an e-value of 5,00E-23, mRNA sequence.
ACCESSION     CO651130
VERSION       CO651130.1  GI:62994086
KEYWORDS      EST.
SOURCE        Chondrus crispus (carrageen)
ORGANISM      Chondrus crispus
               Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
               Gigartiniaceae; Chondrus.
REFERENCE     1 (bases 1 to 441)
AUTHORS       Collen,J., Roeder,V., Rousvoal,S., Collin,O., Kloareg,B. and
               Boyen,C.
TITLE         An expressed sequence tag analysis of thallus and regenerating
               protoplasts of Chondrus crispus (Gigartinales, Rhodophyceae)
JOURNAL       Unpublished (2004)
COMMENT       Contact: Collen J.
               CNRS UMR 7139 Vegetaux marins et biomolécules
               Station Biologique de Roscoff
               Place Georges Teissier, 29680 ROSCOFF, FRANCE
               Tel: 33 2 98 29 23 23
               Fax: 33 2 98 29 23 24
               Email: collen-roscoff.fr
               http://www.sb-roscoff.fr/chondrus.html
               PCR Primers
               FORWARD: Universal T3
               BACKWARD: Universal T7
               Seq primer: AATTAAACCCCTCACTAAAGG (T3)

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FEATURES             Location/Qualifiers
     source          1..441
                     /organism="Chondrus crispus"
                     /mol_type="mRNA"
                     /db_xref="taxon:2769"
                     /clone="ccp23_D04_08"
                     /cell_type="protoplasts"
                     /clone_lib="Chondrus crispus protoplasts Zap Express
                     Library"
                     /note="Vector: pbK-CMV; Site_1: Eco RI; Site_2: XhoI"
ORIGIN
Query Match      83.2%; Score 15.8; DB 8; Length 441;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAAGCCTTCGG 19
|||||
Db 372 GAACGGAAAGGCCATTCCG 390

RESULT 75
AI225711/c
LOCUS          AI225711          449 bp      mRNA      linear      EST 29-OCT-1998
DEFINITION    uf10f05.y1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
               IMAGE:1510977 5', mRNA sequence.
ACCESSION     AI225711
VERSION       AI225711.1  GI:3808764
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 449)
AUTHORS       Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
               Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
               Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
               Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
               Waterston,R.
TITLE         The WashU-HMI Mouse EST Project
JOURNAL       Unpublished (1996)
COMMENT       Contact: Marra M/Mouse EST Project
               WashU-HMI Mouse EST Project
               Washington University School of MedicineP
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: mouseest@watson.wustl.edu
               This clone is available royalty-free through LLNL ; contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               MGI:937829
               Seq primer: -40RP from Gibco
               High quality sequence stop: 441.
FEATURES             Location/Qualifiers
     source          1..449
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1510977"
                     /sex="female (lactating)"
                     /tissue_type="mammary gland"
                     /lab_host="DH10B"
                     /clone_lib="Soares_mammary_gland_NMLMG"
                     /note="Vector: pT73D-FacI; 1st strand cDNA was prepared
                     from mammary gland tissue from a lactating female, and was
                     then primed with a Not I - oligo(dT) primer.
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized. Library was constructed by Bento Soares
                     and M. Fatima Bonaldo."

```



Waterston, R.  
The WashU-HMI Mouse EST Project  
Unpublished (1996)  
Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:923651  
Seq primer: custom primer used  
High quality sequence stop: 475.

FEATURES  
source  
1..487  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1450335"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Sugano mouse liver mlia"  
/note="Organ: liver; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTGGCCTACTGG], digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTTCTGCTCTAAAGCTGGC and 3' end  
primer CGACCTGCAGCTCGAGCACA."

ORIGIN  
Query Match 83.2%; Score 15.8; DB 1; Length 487;  
Best Local Similarity 89.5%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTTCGG 19  
|||||  
Db 25 GAATGGAGAGCCCTTTCGG 7

ORIGIN  
Query Match 83.2%; Score 15.8; DB 1; Length 487;  
Best Local Similarity 89.5%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTTCGG 19  
|||||  
Db 25 GAATGGAGAGCCCTTTCGG 7

RESULT 79  
BM649929  
LOCUS  
DEFINITION 17000687370141 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449640353 5', mRNA sequence.  
ACCESSION BM649929  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Anopheles gambiae (African malaria mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Culicidae; Anophelinae; Anopheles.  
1 (bases 1 to 489)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Genomics  
Contact: Holt R.A.  
45 w. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580

FEATURES  
source  
1..492  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449655267"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center

Email: Holtra@celera.com  
Plate: NU01004A9Q row: D column: 15  
Seq primer: M13 Reverse.

FEATURES  
source  
1..489  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449640353"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center  
(www.malaria.mr4.org)."

ORIGIN  
Query Match 83.2%; Score 15.8; DB 3; Length 489;  
Best Local Similarity 89.5%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCCCTTTCGG 19  
|||||  
Db 36 GAACGGAAGTACTTTCGG 54

RESULT 80  
BM623849  
LOCUS  
DEFINITION 17000687489874 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
19600449655267 5', mRNA sequence.  
ACCESSION BM623849  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Anopheles gambiae (African malaria mosquito)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
Culicidae; Anophelinae; Anopheles.  
1 (bases 1 to 492)  
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
Celera Genomics  
Contact: Holt R.A.  
45 w. Gude Dr., Rockville, MD 20850, USA  
Tel: 2404533151  
Fax: 2404534580  
Email: Holtra@celera.com  
Plate: NU01004A9Q row: B column: 01  
Seq primer: M13 Reverse.

FEATURES  
source  
1..492  
/organism="Anopheles gambiae"  
/mol\_type="mRNA"  
/strain="RSP-ST (Reduced susc. to Permethrin - std.  
chromosome)"  
/db\_xref="taxon:7165"  
/clone="19600449655267"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/clone\_lib="A.Gam.ad.cDNA1"  
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole  
adult mosquitoes (mixed sex) frozen on liquid nitrogen.  
cDNA inserts >500 bp cloned directionally into pSport 1.  
Not 1 site is 3'. Clones available through the Malaria  
Research and Reference Reagent Resource Center

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(www.malaria.mr4.org).
ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 492;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 285 GAACGGAAGTACTTTTCGG 303
|||||

RESULT 81
AW090720/c
LOCUS
DEFINITION xc95e03.x1 NCI_CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592028 3',
mRNA sequence.
ACCESSION AW090720
VERSION AW090720.1 GI:6048064
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 495)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 426.
FEATURES
source
1..495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2592028"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Brn35"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dn.
Average insert size 1.33 Kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog # 11544-012"

ORIGIN
Query Match      83.2%; Score 15.8; DB 7; Length 495;
Best Local Similarity 89.5%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 249 GAACGGAAGGCGCTTTTCGG 231
|||||

RESULT 82
BF362878/c
LOCUS
DEFINITION MR0-NN0087-260600-017-f09 NN0087 Homo sapiens cDNA, mRNA sequence.

(www.malaria.mr4.org).
ACCESSION BF362878
VERSION BF362878.1 GI:11325007
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 517)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.S.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-NN0087-
260600-017-f09&t3=2000-06-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 33.
FEATURES
source
1..517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NN0087"
/notes="Organ: nervous normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Query Match      83.2%; Score 15.8; DB 7; Length 517;
Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTTTTCGG 19
|||||
Db 394 GAACGGAAGGCGCTTACGG 376
|||||

RESULT 83
CO651195
LOCUS
DEFINITION ccp24_E05_09 Chondrus crispus protoplasts Zap Express Library
Chondrus Crispus cDNA clone ccp24_E05_09 5', similar to orf [Ricin
communis] with an e-value of 5,00E-23, mRNA sequence.
CO651195
VERSION CO651195.1 GI:62994151
KEYWORDS EST.
SOURCE Chondrus crispus (carrageen)
ORGANISM Chondrus crispus
Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
Gigartinales; Chondrus.
1 (bases 1 to 517)

```

**AUTHORS** Collen,J., Roeder,V., Rousvoal,S., Collin,O., Kloareg,B. and Boyen,C.  
**TITLE** An expressed sequence tag analysis of thallus and regenerating protoplasts of *Chondrus crispus* (Gigartinales, Rhodophyceae)  
**JOURNAL** Unpublished (2004)  
**COMMENT** Contact: Collen J  
 CNRS UMR 7139 Vegetaux marins et biomolécules  
 Station Biologique de Roscoff  
 Place Georges Teissier, 29680 ROSCOFF, FRANCE  
 Tel: 33 2 98 29 23 23  
 Fax: 33 2 98 29 23 24  
 Email: collen-roscoff.fr  
 http://www.sb-roscoff.fr/chondrus.html  
**PCR Primers**  
 FORWARD: Universal T3  
 BACKWARD: Universal T7  
 Seq primer: AATTAACCTCACTAAAGG (T3)  
 High quality sequence stop: 517.  
**FEATURES**  
 Location/Qualifiers  
 1..517  
 /organism="Chondrus crispus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:2769"  
 /clone="ccp24\_E05\_09"  
 /cell\_type="protoplasts"  
 /clone\_lib="Chondrus crispus protoplasts Zap Express Library"  
 /note="Vector: pbK-CMV; Site\_1: Eco RI; Site\_2: Xho1"  
**ORIGIN**  
 Query Match 83.2%; Score 15.8; DB 8; Length 517;  
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 365 GAACGGAAGGCTTTCGG 383  
**RESULT 84**  
 AI226747/c  
 LOCUS AI226747 519 bp mRNA linear EST 29-OCT-1998  
 DEFINITION uJ15D10.Y1 Sugano mouse kidney mKia Mus musculus cDNA clone  
 IMAGE:1908091 5', mRNA sequence.  
 ACCESSION AI226747.1 GI:3809800  
 VERSION AI226747  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 519)  
 REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 The WashU-HMMI Mouse EST Project  
 Unpublished (1996)  
 CONTACT: Marra M/Mouse EST Project  
 WashU-HMMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:376287  
 Seq primer: custom primer used  
 High quality sequence stop: 516.  
 Location/Qualifiers  
 1..522  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**RESULT 85**  
 AA510135/c  
 LOCUS AA510135 522 bp mRNA linear EST 08-JUL-1999  
 DEFINITION vH57e02.r1 Soares mammary\_gland\_NBMGM Mus musculus cDNA clone  
 IMAGE:891098 5', mRNA sequence.  
 ACCESSION AA510135.1 GI:2247989  
 VERSION AA510135  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
 1 (bases 1 to 522)  
 REFERENCE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.  
 The WashU-HMMI Mouse EST Project  
 Unpublished (1996)  
 CONTACT: Marra M/Mouse EST Project  
 WashU-HMMI Mouse EST Project  
 Washington University School of MedicineP  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:519058  
 Seq primer: -28m13 rev2 ET from Amersham  
 High quality sequence stop: 494.  
 Location/Qualifiers  
 1..522  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**FEATURES**  
 Location/Qualifiers  
 1..522  
 /organism="Mus musculus"  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
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 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**FEATURES**  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**FEATURES**  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**FEATURES**  
 Location/Qualifiers  
 1..522  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /note="Sugano mouse kidney mKia"  
 /clone\_lib="Sugano mouse kidney mKia"  
 /note="Organ: kidney; Vector: pME18S-FL3; Site\_1: DraIII (CACTGTGTG); Site\_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer  
 (ATGTGGCTTTTCTTTTCTTTT); double-stranded cDNA was ligated to a DraIII adaptor (TGTTCGCTACTGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTCTAAAGCTGG and 3' end primer CGACTGCAGCTCGAGACA."  
 Qy 1 GAACGGAAGGCTTTCGG 19  
 Db 162 GAATGAGAGGCTTTCGG 144  
**FEATURES**  
 Location/Qualifiers  
 1..522  
 /organism="Mus musculus



**AUTHORS** Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,  
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
**TITLE** Celera Anopheles gambiae EST project  
**JOURNAL** Unpublished (2002)  
**COMMENT** Contact: Holt R.A.

Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01003CY0 row: B column: 20  
 Seq primer: M13 Reverse.

**FEATURES**  
 source Location/Qualifiers

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1. 526
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449640310"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
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**ORIGIN**

Query Match 83.2%; Score 15.8; DB 3; Length 526;  
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19  
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 Db 101 GAACGGAAGTACTTTTCGG 119

RESULT 89

DB281202  
 LOCUS DB281202 UTERU3 Homo sapiens cDNA clone UTERU3008097 5', mRNA  
 DEFINITION

ACCESSION DB281202  
 VERSION DB281202.1 GI:83211312  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 537)

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,  
 Yamashita,R., Yamamoto,J., Sekine,M., Tsutitani,K., Wakaguri,H.,  
 Iehi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,  
 Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,  
 Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,  
 Tanabe,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.  
 Diversification of Transcriptional Modulation: Large-scale  
 Identification and Characterization of Putative Alternative  
 Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai  
 FLJ Project (HRI Team)  
 Helix Research Institute  
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: flj-cdna@nifty.com  
 NEDO human cDNA project (New Energy and Industrial Technology

**FEATURES**  
 source Location/Qualifiers

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1. 537
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UTERU3008097"
/tissue_type="uterus"
/clone_lib="UTERU3"
/note="Vector: pME18SFL3".
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**ORIGIN**

Query Match 83.2%; Score 15.8; DB 9; Length 537;  
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19  
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 Db 519 GAATGGAAGTCTTTTCGG 537

RESULT 90

DB642702

LOCUS

DEFINITION

BX642702 540 bp mRNA linear EST 04-SEP-2003

DKFZp781D1916 r1 781 (synonym: hlcc4) Homo sapiens cDNA clone

DKFZp781D1916 5', mRNA sequence.

ACCESSION

VERSION BX642702.1 GI:34477035

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE 1 (bases 1 to 540)

AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,

Fobo,G., Han,M. and Wiemann,S.

EST (Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., et al.)

Unpublished (2003)

CONTACT: MIPS

INGOLSTAEDTER Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by BMFZ (Biomedical Research Center at the Heinrich-

Heine-University, Dueseldorf/Germany) within the cDNA sequencing

consortium of the German Genome Project. No sl sequence available.

This clone (DKFZp781D1916) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

**FEATURES**

source Location/Qualifiers

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1. 540
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp781D1916"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiA; Site_2: SfiIB;
cDNA-collection"
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**ORIGIN**

Query Match 83.2%; Score 15.8; DB 4; Length 540;  
 Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCCTTTTCGG 19





Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mousees@watson.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMGE Consortium (info@image.llnl.gov) for further information.  
MGI: 977379

Seq primer: custom primer used  
High quality sequence stop: 519.

#### FEATURES

source  
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/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:1921087"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGTGG); Site 2: DraIII (CACTATGG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTGGCCTTTTCTTTTCTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [TGTGGCTACTGG], digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end  
primer CGACCTGCAGCTGACACA."

ORIGIN  
Query Match 83.2%; Score 15.8; DB 1; Length 554;  
Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGNAAGCGCTTTTCGG 19  
Db 163 GAATGGAGAGCGCTTTTCGG 145

#### ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 554;  
Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGNAAGCGCTTTTCGG 19  
Db 163 GAATGGAGAGCGCTTTTCGG 145

QY 1 GAACGGNAAGCGCTTTTCGG 19  
Db 163 GAATGGAGAGCGCTTTTCGG 145

#### RESULT 94

DA532796  
LOCUS DA532796 FEBRA2 Homo sapiens cDNA clone FEBRA2026540 5', mRNA  
DEFINITION DA532796 556 bp mRNA linear EST 07-NOV-2005  
sequence.

ACCESSION DA532796.1 GI:81127099

VERSION DA532796

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homniidae; Homo.  
1 (bases 1 to 556)

#### REFERENCE

AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,  
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,  
Ihii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,  
Yonekawa,T., Otsuka,K., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,  
Murakawa,K., Iehida,S., Ishibashi,T., Takahashi-Fujii,A.,  
Tanase,I., Nagai,K., Kikuchi,H., Nakai,K., Isogai,I. and Sugano,S.  
Diversification of Transcriptional Modulation: Large-scale  
Identification and Characterization of Putative Alternative  
Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)

#### JOURNAL

PUBMED 16344560

CONTACT: Takao Isogai

FLJ Project (HRI Team)

Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology  
Developmental Organization, Japan); cDNA library construction:  
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
pass sequencing: RAB.

#### FEATURES

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1. .556  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="FEBRA2026540"  
/tissue\_type="brain"  
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/clone\_lib="FEBRA2"  
/note="Vector: pME18SFL3"

#### ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 556;  
Best Local Similarity 89.5%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGAAAGCGCTTTTCGG 19  
Db 518 GAATGGAAAGCGCTTTTCGG 536

#### RESULT 95

DT916410  
LOCUS DT916410 557 bp mRNA linear EST 19-SEP-2005  
DEFINITION DT916410 557 bp mRNA linear EST 19-SEP-2005  
sequence.  
ACCESSION DT916410  
VERSION DT916410.1 GI:75896891  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 557)

Pritsker,M., Doniger,T.T., Kramer,L.C., Westcot,S.E. and  
Lemischka,I.R.

Diversification of Stem Cell Molecular Repertoire by Alternative  
Splicing

Proc. Natl. Acad. Sci. U.S.A. (2005) In press

Contact: Pritsker M

Lab of Ihor Lemischka, Department of Molecular Biology

Princeton University

Princeton, NJ 08544, USA

Tel: 609 258 5657

Fax: 609 258 1704

Email: pritsker@molbio.princeton.edu.

Location/Qualifiers

1. .557  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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hematopoietic stem cells"

hematopoietic stem cells"

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hematopoietic stem cells"

hematopoietic stem cells"

QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 96	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
DEFINITION	LOCUS	CD3111444	Strongylocentrotus purpuratus cDNA clone	567 bp	mRNA	linear	EST 19-SEP-2005
ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
KEYWORDS	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19-SEP-2005
TITLE	JOURNAL	Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.	Integration of 20,000 unique sea urchin EST clusters	567 bp	mRNA	linear	EST 19-SEP-2005
COMMENT	FEATURES	Contact: Poustka AJ	Laboraty 145, dept.Lehrach	567 bp	mRNA	linear	EST 19-SEP-2005
QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 97	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
DEFINITION	LOCUS	CD3111444	Strongylocentrotus purpuratus cDNA clone	567 bp	mRNA	linear	EST 19-SEP-2005
ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
KEYWORDS	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19-SEP-2005
TITLE	JOURNAL	Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.	Integration of 20,000 unique sea urchin EST clusters	567 bp	mRNA	linear	EST 19-SEP-2005
COMMENT	FEATURES	Contact: Poustka AJ	Laboraty 145, dept.Lehrach	567 bp	mRNA	linear	EST 19-SEP-2005
QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 98	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
DEFINITION	LOCUS	CD3111444	Strongylocentrotus purpuratus cDNA clone	567 bp	mRNA	linear	EST 19-SEP-2005
ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
KEYWORDS	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19-SEP-2005
TITLE	JOURNAL	Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.	Integration of 20,000 unique sea urchin EST clusters	567 bp	mRNA	linear	EST 19-SEP-2005
COMMENT	FEATURES	Contact: Poustka AJ	Laboraty 145, dept.Lehrach	567 bp	mRNA	linear	EST 19-SEP-2005
QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 99	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
DEFINITION	LOCUS	CD3111444	Strongylocentrotus purpuratus cDNA clone	567 bp	mRNA	linear	EST 19-SEP-2005
ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
KEYWORDS	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19-SEP-2005
TITLE	JOURNAL	Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.	Integration of 20,000 unique sea urchin EST clusters	567 bp	mRNA	linear	EST 19-SEP-2005
COMMENT	FEATURES	Contact: Poustka AJ	Laboraty 145, dept.Lehrach	567 bp	mRNA	linear	EST 19-SEP-2005
QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 100	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
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ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
KEYWORDS	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19-SEP-2005
TITLE	JOURNAL	Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A., Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.	Integration of 20,000 unique sea urchin EST clusters	567 bp	mRNA	linear	EST 19-SEP-2005
COMMENT	FEATURES	Contact: Poustka AJ	Laboraty 145, dept.Lehrach	567 bp	mRNA	linear	EST 19-SEP-2005
QY	Db	1	GAACGGAAAGCCTTCGG 19 	558 bp	mRNA	linear	EST 16-SEP-2003
RESULT 101	LOCUS	CD3111444	StrP691.004808 Sea urchin larva cDNA library MPMPg691	567 bp	mRNA	linear	EST 07-AUG-2003
DEFINITION	LOCUS	CD3111444	Strongylocentrotus purpuratus cDNA clone	567 bp	mRNA	linear	EST 19-SEP-2005
ACCESSION	VERSION	CD3111444	MPMPg691I0995;MPI_SURUDI_9519 5', mRNA sequence.	567 bp	mRNA	linear	EST 19-SEP-2005
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ORGANISM	SOURCE	EST.	Strongylocentrotus purpuratus	567 bp	mRNA	linear	EST 19-SEP-2005
REFERENCE	AUTHORS	1	(bases 1 to 558)	567 bp	mRNA	linear	EST 19

TITLE	Lemischka, I.R. Diversification of Stem Cell Molecular Repertoire by Alternative Splicing
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. (2005) In press
COMMENT	Contact: Pritsker M Lab of Ihor Lemischka, Department of Molecular Biology Princeton University Princeton, NJ 08544, USA Tel: 609 258 5657 Fax: 609 258 1704 Email: pritsker@molbio.princeton.edu.

## FEATURES

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ORIGIN
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Best Local Similarity 89.5%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19
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Db 115 GAACGGAAAGCGCTTTCGG 133

RESULT 99
BM631920
LOCUS BM631920 568 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687503458 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
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**RESULT 99**

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	Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;		
	Culicidae; Anophelinae; Anopheles.		
REFERENCE	1 (bases 1 to 568)		
AUTHORS	Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,		
	Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.		
TITLE	Celera Anopheles gambiae EST project		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Holt, R.A.		

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**source**

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/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria

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Research and Reference Reagent Resource Center  
([www.malaria.mr4.org](http://www.malaria.mr4.org)).

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ORIGIN
      83.2%;   Score 15.8;  DB 3;   Length 568;
Query Match      Best Local Similarity 89.5%;   Pred. NO. 3.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  GAACGGAAAGGCCTTTTCGG 19
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DEFINITION	DA720663	NT2RI3	Homo sapiens	CDNA clone	575 bp	mRNA	linear	EST 13-NOV-2005
ACCESSION	DA720663	NT2RI3	Homo sapiens	CDNA clone	575 bp	mRNA	linear	EST 13-NOV-2005
VERSION	DA720663.1	NT2RI3	Homo sapiens	CDNA clone	575 bp	mRNA	linear	EST 13-NOV-2005
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SOURCE	DA720663	NT2RI3	Homo sapiens	CDNA clone	575 bp	mRNA	linear	EST 13-NOV-2005
ORGANISM	DA720663	NT2RI3	Homo sapiens	CDNA clone	575 bp	mRNA	linear	EST 13-NOV-2005

REFERENC  
AUTHOR

**ADDITIONAL AUTHORS**  
 Yamura, K., Wakamatsu, J., Suda, T., Oka, T., Mishioka, I., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kuhlida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibaashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.

**TITLE**  
 Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

**JOURNAL**  
 Genome Res. 16 (1), 55-65 (2006)

**PMID**  
 16344560

**COMMENT**  
 Contract: Takao, Isogai

## COMMENT

PLJ Project (HRI Team)  
Helix Research Institute  
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction:  
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,  
Research Association for Biotechnology (RAB) and Biotechnology  
Center, National Institute of Technology and Evaluation; 3'-end one  
pass sequencing: RAB.

## FEATURES source

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## ORIGIN

Query Match	83.2%;	Score 15.8;	DB 9;	Length 575;
Best Local Similarity	89.5%;	Pred. No. 3.7e+03;		
Matches 17;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	GAACGGAAAGGCTTTTCGG	19	
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Job time : 1282.71 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:46:33 ; Search time 762.175 Seconds  
(without alignments)  
306.314 Million cell updates/sec

Title: US-10-665-708-24

Perfect score: 19

Sequence: 1 gaacggaaagccttcg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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7	18	94.7	25	3	US-09-738-274-21
8	18	94.7	25	10	US-10-665-708-21
9	17.4	91.6	25	8	US-10-220-212A-31
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11	17.4	91.6	454	7	US-10-438-774-15
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1453	8	US-10-296-115-424	Sequence 424, App
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96	14.8	77.9	7564	13	US-11-097-143-13213	Sequence 19213, A	169	14.4	75.8	623	12	US-10-301-480-516849	Sequence 516849,
97	14.8	77.9	19183	3	US-09-764-877-2799	Sequence 2799, Ap	170	14.4	75.8	623	12	US-10-301-480-1130258	Sequence 1130258,
98	14.8	77.9	19183	7	US-10-242-515-2799	Sequence 2799, Ap	171	14.4	75.8	635	4	US-09-925-065A-459500	Sequence 459500,
99	14.8	77.9	32249	3	US-09-764-869-2314	Sequence 2314, Ap	172	14.4	75.8	635	5	US-09-925-065A-459500	Sequence 459500,
100	14.8	77.9	32249	6	US-10-091-504-2314	Sequence 2314, Ap	173	14.4	75.8	635	5	US-09-925-065A-459500	Sequence 459500,
101	14.8	77.9	32249	7	US-10-227-577-2314	Sequence 2314, Ap	174	14.4	75.8	635	5	US-09-925-065A-459500	Sequence 459500,
102	14.8	77.9	42104	6	US-10-087-192-1138	Sequence 1138, Ap	175	14.4	75.8	836	7	US-10-027-632-125589	Sequence 125589,
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104	14.8	77.9	89328	3	US-09-873-367C-332	Sequence 332, App	177	14.4	75.8	1158	13	US-11-097-143-33038	Sequence 99, Appl
105	14.8	77.9	89328	10	US-10-843-641A-332	Sequence 332, App	178	14.4	75.8	1158	13	US-11-097-143-33038	Sequence 33038, A
106	14.8	77.9	173115	15	US-11-112-908-65	Sequence 65, Appl	179	14.4	75.8	1284	9	US-10-425-115-30454	Sequence 30454, A
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ALIGNMENTS

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US-09-738-274-24
; Sequence 24, Application US/09738274
; Publication No. US20030165824A1

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; GENERAL INFORMATION:
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/09/738,274
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
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; SOFTWARE: PatentIn Ver. 2.0
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; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: oligonucleotide
US-09-738-274-24

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; APPLICANT: BRENTANO, Steven T.
; APPLICANT: JUCKER, Markus T.
; APPLICANT: DELGADO, Francisco D.
; APPLICANT: CLEUZIAT, Philippe
; APPLICANT: RODRIGUE, Marc
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF
; FILE REFERENCE: GP107-02.UT
; CURRENT APPLICATION NUMBER: US/10/665,708
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: US/09/738,274
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 60/172,190
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 42
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US-10-665-708-24

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; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
; PRIOR APPLICATION NUMBER: 60/172,190  
; PRIOR FILING DATE: 1999-12-17  
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; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; PRIOR FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
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; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/09/738,274  
; CURRENT FILING DATE: 2000-12-15  
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; PRIOR FILING DATE: 1999-12-17  
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US-09-738-274-22

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; GENERAL INFORMATION:  
; APPLICANT: BRENTANO, Steven T.  
; APPLICANT: JUCKER, Markus T.  
; APPLICANT: DELGADO, Francisco D.  
; APPLICANT: CLEUZAT, Philippe  
; APPLICANT: RODRIGUE, Marc  
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
; FILE REFERENCE: GP107-02.UT  
; CURRENT APPLICATION NUMBER: US/10/665,708  
; CURRENT FILING DATE: 2003-09-18  
; PRIOR APPLICATION NUMBER: US/09/738,274  
; PRIOR FILING DATE: 2000-12-15  
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US-10-665-708-22

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RESULT 7

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 ; GENERAL INFORMATION:  
 ; APPLICANT: BRENTANO, Steven T.  
 ; APPLICANT: JUCKER, Markus T.  
 ; APPLICANT: DELGADO, Francisco D.  
 ; APPLICANT: CLEUZAT, Philippe  
 ; APPLICANT: RODRIGUE, Marc  
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: GP107-02.UT  
 ; CURRENT APPLICATION NUMBER: US/09/738,274  
 ; PRIOR FILING DATE: 2000-12-15  
 ; PRIOR FILING DATE: 1999-12-17  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 21  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; OTHER INFORMATION: oligonucleotide  
 US-09-738-274-21

Query Match 94.7%; Score 18; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTCG 18  
 Db 8 GAACGGAAGGCCTTTCG 25

RESULT 8

US-10-665-708-21  
 ; Sequence 21, Application US/10665708  
 ; Publication No. US20050100915A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BRENTANO, Steven T.  
 ; APPLICANT: JUCKER, Markus T.  
 ; APPLICANT: DELGADO, Francisco D.  
 ; APPLICANT: CLEUZAT, Philippe  
 ; APPLICANT: RODRIGUE, Marc  
 ; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION AND DETECTION OF  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: GP107-02.UT  
 ; CURRENT APPLICATION NUMBER: US/10/665,708  
 ; PRIOR FILING DATE: 2003-09-18  
 ; PRIOR APPLICATION NUMBER: US/09/738,274  
 ; PRIOR FILING DATE: 2000-12-15  
 ; PRIOR FILING DATE: 1999-12-17  
 ; NUMBER OF SEQ ID NOS: 42  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 21  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: primer  
 ; OTHER INFORMATION: oligonucleotide  
 US-10-665-708-21

Query Match 94.7%; Score 18; DB 10; Length 25;

Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAACGGAAGGCCTTTCG 18  
 Db 8 GAACGGAAGGCCTTTCG 25

RESULT 9

US-10-220-212A-31  
 ; Sequence 31, Application US/10220212A  
 ; Publication No. US20040110129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Government of the United States of America as represented by the  
 ; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes  
 ; APPLICANT: Health  
 ; APPLICANT: Beckman Coulter, Inc.  
 ; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: 4239-58135  
 ; CURRENT APPLICATION NUMBER: US/10/220,212A  
 ; CURRENT FILING DATE: 2002-08-27  
 ; PRIOR APPLICATION NUMBER: 60/186,840  
 ; PRIOR FILING DATE: 2000-03-03  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 31  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Mycobacterium-specific oligonucleotide  
 US-10-220-212A-31

Query Match 91.6%; Score 17.4; DB 8; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 69;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTCG 19  
 Db 1 GAACGGAAGGCCTTTCG 19

RESULT 10

US-10-220-212A-33  
 ; Sequence 33, Application US/10220212A  
 ; Publication No. US20040110129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Government of the United States of America as represented by the  
 ; APPLICANT: Secretary, Department of Health & Human Services, the National Institutes  
 ; APPLICANT: Health  
 ; APPLICANT: Beckman Coulter, Inc.  
 ; TITLE OF INVENTION: Multiplex Hybridization System for the Identification of Pathogen  
 ; MYCOBACTERIUM SPECIES  
 ; FILE REFERENCE: 4239-58135  
 ; CURRENT APPLICATION NUMBER: US/10/220,212A  
 ; CURRENT FILING DATE: 2002-08-27  
 ; PRIOR APPLICATION NUMBER: 60/186,840  
 ; PRIOR FILING DATE: 2000-03-03  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 33  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Mycobacterium-specific oligonucleotide  
 US-10-220-212A-33

Query Match 91.6%; Score 17.4; DB 8; Length 25;  
 Best Local Similarity 94.7%; Pred. No. 69;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 1 GAACGGAAGGCGCTTCGG 19

RESULT 11  
US-10-438-774-15  
; Sequence 15, Application US/10438774  
; Publication No. US20040010504A1  
; GENERAL INFORMATION:  
; APPLICANT: Hinrichs, Steven  
; APPLICANT: Mohammed, Amr  
; APPLICANT: Ali, Hesham  
; APPLICANT: Kuyper, Dan  
; TITLE OF INVENTION: Custom Sequence Databases and Methods of  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: UNMC.63174-US  
; CURRENT APPLICATION NUMBER: US/10/438,774  
; PRIOR FILING DATE: 2003-05-14  
; PRIOR APPLICATION NUMBER: 60/381,015  
; PRIOR FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 454  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic sequence  
US-10-438-774-15

Query Match 91.6%; Score 17.4; DB 7; Length 454;  
Best Local Similarity 94.7%; Pred. No. 72;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 4 GAACGGAAGGCGCTTCGG 22

RESULT 12  
US-10-697-802A-6  
; Sequence 6, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 6  
; LENGTH: 1449  
; TYPE: DNA  
; ORGANISM: Mycobacterium fortuitum  
US-10-697-802A-6

Query Match 91.6%; Score 17.4; DB 10; Length 1449;  
Best Local Similarity 94.7%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 27 GAACGGAAGGCGCTTCGG 45

RESULT 13  
US-10-697-802A-13  
; Sequence 13, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG

; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 13  
; LENGTH: 1455  
; TYPE: DNA  
; ORGANISM: Mycobacterium mucogenicum  
US-10-697-802A-13

Query Match 91.6%; Score 17.4; DB 10; Length 1455;  
Best Local Similarity 94.7%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 37 GAACGGAAGGCGCTTCGG 55

RESULT 14  
US-10-697-802A-5  
; Sequence 5, Application US/10697802A  
; Publication No. US20050130168A1  
; GENERAL INFORMATION:  
; APPLICANT: HAN, XIANG-YANG  
; APPLICANT: PHAM, AUDREY S.  
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM  
; FILE REFERENCE: 01-001  
; CURRENT APPLICATION NUMBER: US/10/697,802A  
; CURRENT FILING DATE: 2003-10-31  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 5  
; LENGTH: 1482  
; TYPE: DNA  
; ORGANISM: Mycobacterium farcinogenes  
US-10-697-802A-5

Query Match 91.6%; Score 17.4; DB 10; Length 1482;  
Best Local Similarity 94.7%; Pred. No. 74;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 35 GAACGGAAGGCGCTTCGG 53

RESULT 15  
US-10-779-543-8365  
; Sequence 8365, Application US/10779543  
; Publication No. US20050227917A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams et al  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II  
; FILE REFERENCE: 2300-21302  
; CURRENT APPLICATION NUMBER: US/10/779,543  
; CURRENT FILING DATE: 2004-02-12  
; PRIOR APPLICATION NUMBER: 10/076,555  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: 09/217,471  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/068,755  
; PRIOR FILING DATE: 1997-12-23  
; PRIOR APPLICATION NUMBER: 60/080,664  
; PRIOR FILING DATE: 1998-04-03  
; PRIOR APPLICATION NUMBER: 60/105,234  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 09/297,648  
; PRIOR FILING DATE: 2000-04-10  
; PRIOR APPLICATION NUMBER: PCT/US99/01619  
; PRIOR FILING DATE: 1999-01-28



; Sequence 544396, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 544396  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-544396

Query Match 83.2%; Score 15.8; DB 4; Length 513;  
Best Local Similarity 89.5%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 226 GAAGGAAAGGCCATTCGG 244

RESULT 20  
US-09-925-065A-544397  
; Sequence 544397, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 544397  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-544397

Query Match 83.2%; Score 15.8; DB 4; Length 513;  
Best Local Similarity 89.5%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 226 GAAGGAAAGGCCATTCGG 244

RESULT 21  
US-09-925-065A-544396  
; Sequence 544396, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 544396  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-544396

Query Match 83.2%; Score 15.8; DB 5; Length 513;  
Best Local Similarity 89.5%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 226 GAAGGAAAGGCCATTCGG 244

RESULT 22  
US-09-925-065A-544397  
; Sequence 544397, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 544397  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-544397

Query Match 83.2%; Score 15.8; DB 5; Length 513;  
Best Local Similarity 89.5%; Pred. No. 5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19

```
Db      226 GAAGGGAAGGCCATTTCGG 244
||||| ||||| ||||| ||||| |||||
Query Match      83.2%; Score 15.8; DB 8; Length 620;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 23
US-10-450-763-3105
; Sequence 3105, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 3105
; LENGTH: 576
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (419)..(3)
; OTHER INFORMATION: 32% homologous to Santalum album proline rich
; OTHER INFORMATION: protein, accession number AF020261, Smith-Waterman Score=109.
US-10-450-763-3105

Query Match      83.2%; Score 15.8; DB 10; Length 576;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| ||||| |||||
Db      512 GAATGGAAGGCTTTCGG 530

RESULT 24
US-10-437-963-34505
; Sequence 34505, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 34505
; LENGTH: 620
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(620)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_38514C.1
US-10-437-963-34505

Db      226 GAAGGGAAGGCCATTTCGG 244
||||| ||||| ||||| ||||| |||||
Query Match      83.2%; Score 15.8; DB 8; Length 620;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 25
US-10-425-115-59269
; Sequence 59269, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 59269
; LENGTH: 635
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_15404C.1
US-10-425-115-59269

Query Match      83.2%; Score 15.8; DB 9; Length 635;
Best Local Similarity 89.5%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAAGCCTTTCGG 19
||||| ||||| ||||| ||||| |||||
Db      454 GAGCGGAAGGCTGTTCGG 472

RESULT 26
US-10-027-632-292604
; Sequence 292604, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292604
; LENGTH: 638
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292604
```

Query Match 83.2%; Score 15.8; DB 6; Length 638;  
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
||| ||||| |||||  
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 27  
US-10-027-632-292605  
; Sequence 292605, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 292605  
; LENGTH: 638  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-292605

Query Match 83.2%; Score 15.8; DB 6; Length 638;  
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
||| ||||| |||||  
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 28  
US-10-027-632-292604  
; Sequence 292604, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 292604  
; LENGTH: 638  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-292604

Query Match 83.2%; Score 15.8; DB 7; Length 638;  
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
||| ||||| |||||  
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 29  
US-10-027-632-292605  
; Sequence 292605, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 292605  
; LENGTH: 638  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-292605

Query Match 83.2%; Score 15.8; DB 7; Length 638;  
Best Local Similarity 89.5%; Pred. No. 5e+02; 2; Indels 0; Gaps 0;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTCGG 19  
||| ||||| |||||  
Db 228 GAAGGGAAGGCCATTCGG 246

RESULT 30  
US-10-522-454-1  
; Sequence 1, Application US/10522454  
; Publication No. US20050244938A1  
; GENERAL INFORMATION:  
; APPLICANT: Hill, Russell T.  
; APPLICANT: Hamann, Mark T.  
; APPLICANT: Peraud, Olivier  
; APPLICANT: Kasanah, Noer  
; TITLE OF INVENTION: MANZAMINE-PRODUCING ACTINOMYCETES

; FILE REFERENCE: 4115-180  
; CURRENT APPLICATION NUMBER: US/10/522,454  
; PRIOR FILING DATE: 2005-01-20  
; PRIOR APPLICATION NUMBER: PCT/USO3/24238  
; PRIOR FILING DATE: 2003-08-01  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 1403  
; TYPE: DNA  
; ORGANISM: Actinomyces sp.  
US-10-522-454-1

Query Match 83.2%; Score 15.8; DB 10; Length 1403;  
Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 32 GAGCGGAAGGCTTTTCGG 50

RESULT 31  
US-10-230-026-6  
; Sequence 6, Application US/10230026  
; Publication No. US20030124695A1  
; GENERAL INFORMATION:  
; APPLICANT: MICHAEL G. BRAMUCCI  
; APPLICANT: PATRICIA C. BRZOSTOWICZ  
; APPLICANT: KRISTY N. KOSTICHKA  
; APPLICANT: VASANTHA NAGARAJAN  
; APPLICANT: PIERRE E. ROUVIERE  
; APPLICANT: STUART M. THOMAS  
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES  
; FILE REFERENCE: CL1789 US NA  
; CURRENT APPLICATION NUMBER: US/10/230,026  
; CURRENT FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: 60/315,546  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 6  
; LENGTH: 1439  
; TYPE: DNA  
; ORGANISM: Rhodococcus erythropolis AN12  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1417)..(1417)  
; OTHER INFORMATION: N = G or A or T or C  
US-10-230-026-6

Query Match 83.2%; Score 15.8; DB 7; Length 1439;  
Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 38 GAGCGGTAAGGCTTTTCGG 56

RESULT 32  
US-10-486-307-6  
; Sequence 6, Application US/10486307  
; Publication No. US20040267001A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. duPont de Nemours, Inc.  
; TITLE OF INVENTION: GENES ENCODING BAEYER-VILLIGER MONOOXYGENASES  
; FILE REFERENCE: CL1789 PCT  
; CURRENT APPLICATION NUMBER: US/10/486,307  
; CURRENT FILING DATE: 2004-02-05  
; PRIOR APPLICATION NUMBER: 60/315,546  
; PRIOR FILING DATE: 2001-08-29  
; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 6  
; LENGTH: 1439  
; TYPE: DNA  
; ORGANISM: Rhodococcus erythropolis AN12  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1417)..(1417)  
; OTHER INFORMATION: N = G or A or T or C  
US-10-486-307-6

Query Match 83.2%; Score 15.8; DB 9; Length 1439;  
Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 38 GAGCGGTAAGGCTTTTCGG 56

RESULT 33  
US-11-035-296-1  
; Sequence 1, Application US/11035296  
; Publication No. US20050203005A1  
; GENERAL INFORMATION:  
; APPLICANT: VICURON PHARMACEUTICALS INC.  
; APPLICANT: LAZZARINI, Ameriga  
; APPLICANT: GASTALDO, Luciano  
; APPLICANT: CANDIANI, Gianpaolo  
; APPLICANT: CICILIATO, Ismaela  
; APPLICANT: LOSI, Daniele  
; APPLICANT: MARINELLI, Flavia  
; APPLICANT: SELVA, Enrico  
; APPLICANT: PARENTI, Franco  
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY  
; FILE REFERENCE: 892,280-195  
; CURRENT APPLICATION NUMBER: US/11/035,296  
; CURRENT FILING DATE: 2005-01-12  
; PRIOR APPLICATION NUMBER: US 10/521,336  
; PRIOR FILING DATE: 2005-01-11  
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658  
; PRIOR FILING DATE: 2004-07-12  
; PRIOR APPLICATION NUMBER: EP 03016306.7  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1  
; LENGTH: 1443  
; TYPE: DNA  
; ORGANISM: Microbispora sp. ATCC PTA-5024  
US-11-035-296-1

Query Match 83.2%; Score 15.8; DB 13; Length 1443;  
Best Local Similarity 89.5%; Pred. No. 5.1e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTTCGG 19  
||| ||||| ||||| |||||  
Db 37 GAGCGGAAGGCTTTTCGG 55

RESULT 34  
US-11-045-628-1  
; Sequence 1, Application US/11045628  
; Publication No. US20050233952A1  
; GENERAL INFORMATION:  
; APPLICANT: VICURON PHARMACEUTICALS INC.  
; APPLICANT: LAZZARINI, Ameriga  
; APPLICANT: GASTALDO, Luciano  
; APPLICANT: CANDIANI, Gianpaolo  
; APPLICANT: CICILIATO, Ismaela  
; APPLICANT: LOSI, Daniele

```

; APPLICANT: MARINELLI, Flavia
; APPLICANT: SELVA, Enrico
; APPLICANT: PARENTI, Franco
; TITLE OF INVENTION: ANTIBIOTIC 107891, ITS FACTORS A1 AND A2, PHARMACEUTICALLY
; TITLE OF INVENTION: ACCEPTABLE SALTS AND COMPOSITIONS, AND USE THEREOF
; FILE REFERENCE: 892,280-500
; CURRENT APPLICATION NUMBER: US/11/045,628
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 11/035,296
; PRIOR FILING DATE: 2005-01-12
; PRIOR APPLICATION NUMBER: US 10/521,336
; PRIOR FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: PCT/EP2004/007658
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: EP 03016306.7
; PRIOR FILING DATE: 2003-07-18
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Microbispora sp. ATCC PTA-5024
US-11-045-628-1

```

```

Query Match      83.2%; Score 15.8; DB 13; Length 1443;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GAACGGAAGGCGCTTCGG 19
   |||||
Db 37 GAGCGGAAGGCGCTTCGG 55

```

```

RESULT 35
US-10-697-802A-7
; Sequence 7, Application US/10697802A
; Publication No. US20050130168A1
; GENERAL INFORMATION:
; APPLICANT: HAN, XIANG-YANG
; APPLICANT: PHAM, AUDREY S.
; TITLE OF INVENTION: METHOD OF DETERMINING A SPECIES OF A BACTERIUM
; FILE REFERENCE: 01-001
; CURRENT APPLICATION NUMBER: US/10/697,802A
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 7
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Mycobacterium goodsonae
US-10-697-802A-7

```

```

Query Match      83.2%; Score 15.8; DB 10; Length 1461;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

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QY 1 GAACGGAAGGCGCTTCGG 19
   |||||
Db 27 GAACGGAAGGCGCTTCGG 45

```

```

RESULT 36
US-11-228-416-5
; Sequence 5, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINGER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSd1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15

```

```

; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH898 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-5

```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1480;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GAACGGAAGGCGCTTCGG 19
   |||||
Db 57 GAGCGGAAGGCGCTTCGG 75

```

```

RESULT 37
US-11-228-416-6
; Sequence 6, Application US/11228416
; Publication No. US2006000852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINGER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSd1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospira sp. CNH440 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:

```



```
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-6

Query Match      83.2%; Score 15.8; DB 16; Length 1480;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
Db 57 GAGCGGAAGGCCCTTCGG 75

RESULT 38
US-11-228-416-8
; Sequence 8, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: PENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH725 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide t at position 1456 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-8

Query Match      83.2%; Score 15.8; DB 16; Length 1480;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTCGG 19
```

```
Db 57 GAGCGGAAGGCCCTTCGG 75

RESULT 39
US-11-228-416-9
; Sequence 9, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: PENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1480
; TYPE: DNA
; ORGANISM: Salinospora sp. CNH964 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1423)..(1423)
; OTHER INFORMATION: n is signature nucleotide g position 1456 of 16S rDNA
US-11-228-416-9

Query Match      83.2%; Score 15.8; DB 16; Length 1480;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCCTTCGG 19
Db 57 GAGCGGAAGGCCCTTCGG 75

RESULT 40
US-11-228-416-3
; Sequence 3, Application US/11228416
; Publication No. US2006008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: PENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT APPLICATION NUMBER: US/11/228,416
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
```

```

; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1481
; TYPE: DNA
; ORGANISM: Salinispora sp. CNH643 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (352)..(352)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1424)..(1424)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-3

```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1481;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75

```

```

RESULT 41
US-11-228-416-4
; Sequence 4, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Salinispora sp. CNH646 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (442)..(442)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA

```

```

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1425)..(1425)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-4

```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1482;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75

```

```

RESULT 42
US-11-228-416-7
; Sequence 7, Application US/11228416
; Publication No. US20060008852A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF CALIFORNIA, SAN DIEGO
; APPLICANT: FENICAL, William
; APPLICANT: JENSEN, Paul R.
; APPLICANT: MINCER, Tracy J.
; TITLE OF INVENTION: MARINE ACTINOMYCETE TAXON FOR DRUG AND FERMENTATION PRODUCT DISCO
; FILE REFERENCE: UCSD1630-1
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/991,518B
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 60/249,356
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1483
; TYPE: DNA
; ORGANISM: Salinispora sp. CNH536 16S ribosomal RNA gene, partial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (198)..(198)
; OTHER INFORMATION: n is signature nucleotide a at position 207 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (351)..(351)
; OTHER INFORMATION: n is signature nucleotide c at position 306 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (443)..(443)
; OTHER INFORMATION: n is signature nucleotide t at position 467 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (444)..(444)
; OTHER INFORMATION: n is signature nucleotide t at position 468 of 16S rDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1426)..(1426)
; OTHER INFORMATION: n is signature nucleotide g at position 1456 of 16S rDNA
US-11-228-416-7

```

```

Query Match      83.2%; Score 15.8; DB 16; Length 1483;
Best Local Similarity 89.5%; Pred. No. 5.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GAACGGAAGGCGCTTCGG 19
Db 57 GAGCGGAAGGCGCTTCGG 75

```

```
RESULT 43
US-10-488-528-3
; Sequence 3, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2896
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(1525)
US-10-488-528-3
Query Match      83.2%; Score 15.8; DB 10; Length 2896;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGCCCTTCGG 19
Db      1486 GAACGGAAGCCCTTCGG 1504

RESULT 44
US-10-488-528-1
; Sequence 1, Application US/10488528
; Publication No. US20050119459A1
; GENERAL INFORMATION:
; APPLICANT: Kaplan, Feige
; APPLICANT: Swezey, Neil B.
; TITLE OF INVENTION: Late Gestation Lung Genes, Fragments and Uses Thereof
; FILE REFERENCE: 457-110pct
; CURRENT APPLICATION NUMBER: US/10/488,528
; CURRENT FILING DATE: 2004-03-03
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3054
; TYPE: DNA
; ORGANISM: rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)...(1576)
US-10-488-528-1
Query Match      83.2%; Score 15.8; DB 10; Length 3054;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGCCCTTCGG 19
Db      1540 GAACGGAAGCCCTTCGG 1558

RESULT 45
US-09-764-877-3363
; Sequence 3363, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper

; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363
Query Match      83.2%; Score 15.8; DB 3; Length 6883;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGCCCTTCGG 19
Db      478 GAATGGAAGGTCCTTCGG 496

RESULT 46
US-10-242-515-3363
; Sequence 3363, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3363
; LENGTH: 6883
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-3363
Query Match      83.2%; Score 15.8; DB 7; Length 6883;
Best Local Similarity 89.5%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGCCCTTCGG 19
Db      478 GAATGGAAGGTCCTTCGG 496

RESULT 47
US-10-856-499-60
; Sequence 60, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
```

```
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-60
```

```
Query Match      81.1%; Score 15.4; DB 9; Length 455;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GAACGGAAGGCCTTTC 17
Db 27 GACCGGAAGGCCTTTC 43
```

```
RESULT 48
US-10-856-499-1958
; Sequence 1958, Application US/10856499
; Publication No. US20040259145A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C2
; CURRENT APPLICATION NUMBER: US/10/856,499
; CURRENT FILING DATE: 2004-05-28
; NUMBER OF SEQ ID NOS: 2370
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1958
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-10-856-499-1958
```

```
Query Match      81.1%; Score 15.4; DB 9; Length 455;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GAACGGAAGGCCTTTC 17
Db 27 GACCGGAAGGCCTTTC 43
```

```
RESULT 49
US-10-767-701-30317/c
; Sequence 30317, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 30317
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
```

```
; OTHER INFORMATION: Clone ID: 9853201
US-10-767-701-30317
```

```
Query Match      81.1%; Score 15.4; DB 8; Length 530;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ACGGAAGGCCTTTCG 19
Db 305 ACTGAAGGCCTTTCG 289
```

```
RESULT 50
US-10-301-480-442948
; Sequence 442948, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 442948
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-442948
```

```
Query Match      81.1%; Score 15.4; DB 12; Length 625;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GAACGGAAGGCCTTTC 17
Db 277 GAACGGAAGGCCTTTC 293
```

```
RESULT 51
US-10-301-480-1056357
; Sequence 1056357, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1056357
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1056357
```

```
Query Match      81.1%; Score 15.4; DB 12; Length 625;
Best Local Similarity 94.1%; Pred. No. 8.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 GAACGGAAGGCCTTTC 17
```

Db 277 GAACGGAAGGCTCTTC 293

## RESULT 52

US-09-925-065A-373045  
; Sequence 373045, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 373045  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-373045

Query Match 81.1%; Score 15.4; DB 4; Length 634;  
Best Local Similarity 94.1%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 286 GAACGGAAGGCTCTTC 302

## RESULT 53

US-09-925-065A-373045  
; Sequence 373045, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 373045  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-373045

Query Match 81.1%; Score 15.4; DB 5; Length 634;  
Best Local Similarity 94.1%; Pred. No. 8.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 286 GAACGGAAGGCTCTTC 302

## RESULT 54

US-10-750-185-42960  
; Sequence 42960, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42960  
; LENGTH: 1187  
; TYPE: DNA  
; ORGANISM: Bovine 19866881327789  
US-10-750-185-42960

Query Match 81.1%; Score 15.4; DB 10; Length 1187;  
Best Local Similarity 94.1%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 224 GAACGGAAGGCTCTTC 240

## RESULT 55

US-10-750-623-42960  
; Sequence 42960, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 42960  
; LENGTH: 1187  
; TYPE: DNA  
; ORGANISM: Bovine 19866881327789  
US-10-750-623-42960

Query Match 81.1%; Score 15.4; DB 10; Length 1187;  
Best Local Similarity 94.1%; Pred. No. 8.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTCTTC 17

Db 224 GAACGGAAGGCTCTTC 240

Db 224 GAACGAAAGGCCTTTC 240

RESULT 56

US-10-750-185-34543

; Sequence 34543, Application US/10750185

; Publication No. US20050260603A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-2

; CURRENT APPLICATION NUMBER: US/10/750,185

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 34543

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Bovine 19866880465649

US-10-750-185-34543

Query Match 81.1%; Score 15.4; DB 10; Length 2665;

Best Local Similarity 94.1%; Pred. No. 8.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGAAAGGCCTTTC 17

Db 916 GAACAGAAAGGCCTTTC 932

RESULT 57

US-10-750-623-34543

; Sequence 34543, Application US/10750623

; Publication No. US20050287531A1

; GENERAL INFORMATION:

; APPLICANT: MMI GENOMICS, INC.

; APPLICANT: DENISE, Sue K.

; APPLICANT: KERR, Richard

; APPLICANT: ROSENFELD, David

; APPLICANT: HOLM, Tom

; APPLICANT: BATES, Stephen

; APPLICANT: FANTIN, Dennis

; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS

; FILE REFERENCE: MM1100-1

; CURRENT APPLICATION NUMBER: US/10/750,623

; CURRENT FILING DATE: 2003-12-31

; PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 34543

; LENGTH: 2665

; TYPE: DNA

; ORGANISM: Bovine 19866880465649

US-10-750-623-34543

Query Match 81.1%; Score 15.4; DB 10; Length 2665;

Best Local Similarity 94.1%; Pred. No. 8.3e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAACGAAAGGCCTTTC 17

Db 916 GAACAGAAAGGCCTTTC 932

RESULT 58

US-11-097-143-3737

; Sequence 3737, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: 60/191,637

; PRIOR FILING DATE: 2000-03-23

; NUMBER OF SEQ ID NOS: 43008

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3737

; LENGTH: 5433

; TYPE: DNA

; ORGANISM: DROSOPHILA

US-11-097-143-3737

Query Match 81.1%; Score 15.4; DB 13; Length 5433;

Best Local Similarity 94.1%; Pred. No. 8.5e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCCTTTCG 18

Db 1687 AACGTAAGGCCTTTCG 1703

RESULT 59

US-11-097-143-3736/c

; Sequence 3736, Application US/11097143

; Publication No. US20050208558A1

; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig

; APPLICANT: et al.

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; FILE REFERENCE: CL000728

; CURRENT APPLICATION NUMBER: US/11/097,143

; CURRENT FILING DATE: 2005-04-04

; PRIOR APPLICATION NUMBER: 60/157,832

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: 60/160,191

; PRIOR FILING DATE: 1999-10-19

; PRIOR APPLICATION NUMBER: 60/161,932

; PRIOR FILING DATE: 1999-10-28

; PRIOR APPLICATION NUMBER: 60/164,769

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: 60/173,383

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: 60/175,693

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: 60/184,831

; PRIOR FILING DATE: 2000-02-24

Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
Query Match	Best Local Similarity	Score	DB	Length	Mismatches	Indels	Gaps
81.1%	94.1%	15.4	13	7162	0	0	0
15	16	Conservative	0	0	0	0	0
Qy	2	AACGAAAGCCTTTTCG	18				
Db	4182	AACGTAAGGCCTTTTCG	4166				
RESULT 60							
US-10-012-697-422/c							
Sequence 422, Application US/10012697							
Publication No. US20030215803A1							
GENERAL INFORMATION:							
APPLICANT: Escobedo, Jaime							
APPLICANT: Garcia, Pablo Dominguez							
APPLICANT: Kassam, Altaf							
APPLICANT: Lamson, George							
APPLICANT: Scott, Beth							
APPLICANT: Dmanac, Radoje							
APPLICANT: Crkvenjakov, Radomir							
APPLICANT: Dickson, Mark							
APPLICANT: Dmanac, Snezana							
APPLICANT: Labat, Ivan							
APPLICANT: Leshkowitz, Dena							
APPLICANT: Kita, David							
APPLICANT: Garcia, Veronica							
APPLICANT: Jones, Lee William							
APPLICANT: Stache-Crain, Birgit							
TITLE OF INVENTION: HUMAN GENES AND GENE EXPRESSION PRODUCTS							
TITLE OF INVENTION: ISOLATED FROM HUMAN PROSTATE							
FILE REFERENCE: 2300-16252							
CURRENT APPLICATION NUMBER: US/10/012,697							
CURRENT FILING DATE: 2003-01-21							
PRIOR APPLICATION NUMBER: 60/254,648							
PRIOR FILING DATE: 2000-12-07							
PRIOR APPLICATION NUMBER: 60/275,668							
PRIOR FILING DATE: 2001-03-13							
NUMBER OF SEQ ID NOS: 1568							
SOFTWARE: FastSeq for Windows Version 4.0							
SEQ ID NO 422							
LENGTH: 297							
TYPE: DNA							
ORGANISM: Homo sapiens							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,							
LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297							
OTHER INFORMATION: n = A,T,C or G							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,							
LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297							
OTHER INFORMATION: n = A,T,C or G							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,							
LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297							
OTHER INFORMATION: n = A,T,C or G							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: 124, 150, 151, 180, 193, 218, 221, 229, 236, 237, 239, 241,							
LOCATION: 243, 250, 252, 260, 278, 281, 285, 286, 297							
OTHER INFORMATION: n = A,T,C or G							
FEATURE:							
NAME/KEY: misc feature							
LOCATION: 124, 150, 151, 180, 193, 218, 221, 229							

```
; Sequence 24598, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 24598
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_122440C.1
US-10-425-115-24598

Query Match 78.9%; Score 15; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCCTTT 16
Db 94 AACGGAAGGCCCTTT 80

RESULT 63
US-10-029-386-13162
; Sequence 13162, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13162
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.97
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: g114758021, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q14585, EVALUE 1.00e-48
; OTHER INFORMATION: EST_HUMAN HIT: BE742835.1, EVALUE 0.00e+00
US-10-029-386-13162

Query Match 78.9%; Score 15; DB 7; Length 592;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAAGGCCCTTTCGG 19
Db 532 GGAAAGGCCCTTTCGG 546

RESULT 64
US-10-641-643-689
; Sequence 689, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; TITLE OF INVENTION: GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 689:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1429 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: TLYMNOT02
; CLONE: 450088
; SEQUENCE DESCRIPTION: SEQ ID NO: 689 :
US-10-641-643-689

Query Match 78.9%; Score 15; DB 8; Length 1429;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGAAAGGCCCTTTCGG 19
Db 264 GGAAAGGCCCTTTCGG 278

RESULT 65
US-10-296-115-424/c
; Sequence 424, Application US/10296115
; Publication No. US20040053248A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: No. US20040053248A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 784PCT
; CURRENT APPLICATION NUMBER: US/10/296,115
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 1478
; SEQ ID NO 424
; LENGTH: 1453
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-296-115-424
```



```
;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2196)
; OTHER INFORMATION: zinc finger protein 463(ZNF463) gene.
US-11-000-688-253

Query Match      78.9%; Score 15; DB 15; Length 2196;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTTCGG 19
    |||||
Db 1173 GGAAGGCGCTTTCGG 1159

RESULT 66
US-10-221-625-108
; Sequence 108, Application US/10221625
; Publication No. US20040033942A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: AZIMZAI, Valda
; APPLICANT: BANDMAN, Olga
; APPLICANT: TANG, Y. Tom
; APPLICANT: MATHUR, Preete
; APPLICANT: SHAH, Purvi
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: REDDY, Roopa
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; FILE REFERENCE: PF-0761 PCT
; CURRENT APPLICATION NUMBER: US/10/221.625
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: PERL Program
; SEQ ID NO 108
; LENGTH: 2173
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040033942A1 095210CB1
US-10-221-625-108

Query Match      78.9%; Score 15; DB 8; Length 2173;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTTCGG 19
    |||||
Db 989 GGAAGGCGCTTTCGG 1003

RESULT 67
US-11-000-688-253
; Sequence 253, Application US/11000688
; Publication No. US20050287544A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, Francois
; APPLICANT: HOULGATTE, Remi
; APPLICANT: BIRNBAUM, Daniel
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF COLON CANCER WITH DNA ARRAYS
; FILE REFERENCE: 1423-R-03
; CURRENT APPLICATION NUMBER: US/11/000.688
; CURRENT FILING DATE: 2004-12-01
; PRIOR APPLICATION NUMBER: US 60/525,987
; PRIOR FILING DATE: 2003-12-01
; NUMBER OF SEQ ID NOS: 1596
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 253
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Artificial Sequence

;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial sequences:primer
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(2196)
; OTHER INFORMATION: zinc finger protein 463(ZNF463) gene.
US-11-000-688-253

Query Match      78.9%; Score 15; DB 15; Length 2196;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGAAGGCGCTTTCGG 19
    |||||
Db 1320 GGAAGGCGCTTTCGG 1334

RESULT 68
US-11-097-143-7973
; Sequence 7973, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097.143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7973
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-7973

Query Match      78.9%; Score 15; DB 13; Length 3003;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCGCTT 15
    |||||
Db 2424 GAACGGAAGGCGCTT 2438

RESULT 69
US-09-764-864-123
; Sequence 123, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ23
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
```

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; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 123
;   LENGTH: 3293
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-864-123

Query Match      78.9%; Score 15; DB 3; Length 3293;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5  GGAAAGGCGCTTTCGG 19
Db      892  GGAAAGGCGCTTTCGG 906

RESULT 70
US-10-437-963-66272
; Sequence 66272, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 66272
; LENGTH: 5913
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_67239C.1
US-10-437-963-66272

Query Match      78.9%; Score 15; DB 8; Length 5913;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4  CGGAAAGGCGCTTTCG 18
Db      4911  CGGAAAGGCGCTTTCG 4925

RESULT 71
US-11-097-143-7972
; Sequence 7972, Application US/11097143
; Publication No. US20050208556A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
;

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; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7972
; LENGTH: 8544
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-7972

Query Match      78.9%; Score 15; DB 13; Length 8544;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  GAACGGAAGGCGCTT 15
Db      6899  GAACGGAAGGCGCTT 6913

RESULT 72
US-10-831-286A-38180
; Sequence 38180, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38180
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Corynebacterium jeikeium
US-10-831-286A-38180

Query Match      77.9%; Score 14.8; DB 11; Length 20;
Best Local Similarity 88.9%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  GAACGGAAGGCGCTTTCG 18
Db      1  GAACGGAAGGCGCTTTCG 18

RESULT 73
US-10-437-963-91974
; Sequence 91974, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
;

```

```
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 91974
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90498C.1
US-10-437-963-91974

Query Match          77.9%; Score 14.8; DB 8; Length 275;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTCGG 19
Db 222 AACGGAAGGCCTTTCGG 239

RESULT 74
US-10-424-599-79317
; Sequence 79317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 79317
; LENGTH: 362
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_42639C.1
US-10-424-599-79317

Query Match          77.9%; Score 14.8; DB 8; Length 362;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTCGG 19
Db 59 AAAGGAAGGCCTTTCGG 76

RESULT 75
US-10-717-897-63/c
; Sequence 63, Application US/10717897
; Publication No. US20040163146A1
; GENERAL INFORMATION:
; APPLICANT: PHILLIPS, JONATHAN
; APPLICANT: PUTHIGAE, SATHISH
; APPLICANT: YAO, JIALONG
; APPLICANT: FLINN, BARRY
; APPLICANT: FORSTER, RICHARD S.
; APPLICANT: EAGLETON, CLARE
; TITLE OF INVENTION: VASCULAR-PREFERRED PROMOTERS
; FILE REFERENCE: 044463-0264
; CURRENT APPLICATION NUMBER: US/10/717,897
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: 60/428,287
; PRIOR FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 86
```

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; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 63
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-717-897-63

Query Match          77.9%; Score 14.8; DB 8; Length 365;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTCGG 19
Db 158 AACGGAAGGCCTTTCGG 141

RESULT 76
US-10-437-963-65283/c
; Sequence 65283, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 65283
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_66346C.1
US-10-437-963-65283

Query Match          77.9%; Score 14.8; DB 8; Length 369;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTTCGG 19
Db 210 AACGGAAGGCCTTTCGG 193

RESULT 77
US-10-424-599-36941/c
; Sequence 36941, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 36941
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13335C.1
```

```
US-10-424-599-36941

Query Match      77.9%; Score 14.8; DB 8; Length 414;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACCGAAGGCTTTTCG 19
  |||||
Db 127 AACCGAAGGCTTGTCTG 110

RESULT 78
US-09-925-065A-187308/c
; Sequence 187308, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187308
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187308

Query Match      77.9%; Score 14.8; DB 4; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 79
US-09-925-065A-187308/c
; Sequence 187308, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187308
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-187308

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 81
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 82
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 83
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 84
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 85
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 86
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890761
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-890761

Query Match      77.9%; Score 14.8; DB 12; Length 529;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCG 18
  |||||
Db 126 GAGTGAAGGCTTTTCG 109

RESULT 87
US-10-301-480-890761/c
; Sequence 890761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER
```

Qy 1 GAACGGAAGGCCCTTTCG 18  
Db 126 GAGTGGAAAGGCCCTTTCG 109

```

RESULT 82
US-09-925-065A-632445
; Sequence 632445, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of
;       Nucleotide Polymorphisms in the
;       Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 632445
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-632445

```

Query Match	Score	DB	Length
Best Local Similarity	77.9%	14.8	541
Matches	88.9%		
Conservative	0		
Mismatches	0		
Indels	0		
Gaps	0		

Qy 2 AACGGAAGGCCTTTCGG 19  
Dy 354 AACAGAAAGGCCTTTCGG 371

```

RESULT 83
US-09-925-065A-632445
; Sequence 632445, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 632445
; LENGTH: 541
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-632445

```

Query Match	77.9%	Score 14.8	DB 5	Length 541
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Best Local Similarity 88.9%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGGCGCTTCGG 19  
||| ||||| |||  
Db 354 AACAGAAAGCGCTTTGGG 371

```

RESULT 84
US-09-864-761-16483/c
; Sequence 16483, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/532,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/006666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006655
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/006670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16483
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013568.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
US-09-864-761-16483

```

Query Match	77.9%	Score 14.8;	DB 3;	Length 591;
Best Local Similarity	88.9%	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
Gaps	0;			

10, COMBUSTIBLES 2, 2100000

QY 1 GAACGGAAGGCCTTCG 18  
Db 266 GATGGGAAGGCCTTCG 249

```

RESULT 85
US-09-925-065A-848570/c
; Sequence 848570, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848570
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848570

```

Query Match	77.9%	Score 14.8;	DB 4;	Length 597;
Best Local Similarity	88.9%	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

QY 2 AACGAAAGGCCTTTTCGG 19  
Db 240 AAAGGAAAGGACTTTTCGG 223

```

RESULT 86
US-09-925-065A-848570/c
; Sequence 848570, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of
; TITLE OF INVENTION: Nucleotide Polymorphisms
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 848570
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-848570

```

Query Match 77.9%; Score 14.8; DB 5; Length 597;

Best Local Similarity 88.9%; Pred. No. 1.7e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AACGGAAGCCTTCGG 19  
||| ||||| |||||  
Db 240 AAAGGAAGGACTTCGG 223

```

RESULT 87
US-09-925-065A-692790
; Sequence 692790, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692790
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 64
; OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-692790

```

Query Match	77.9%	Score 14.8;	DB 4;	Length 633;
Best Local Similarity	88.9%	Pred. No. 1.7e+03;		
Matches 16;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Qy 1 GAACGGAAGGCCCTTCG 18  
Db 178 GAATGGAAAGGTCCTTCG 195

```

RESULT 88
US-09-925-065A-692790
; Sequence 692790, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0

```

```

; NUMBER OF SEQ ID NOS: 337088
; SOFTWARE: FastSEQ for Windows Version 4.0

```

```

; NUMBER OF SEQ ID NOS: 337088
; SOFTWARE: FastSEQ for Windows Version 4.0

```

```

; NUMBER OF SEQ ID NOS: 337088
; SOFTWARE: FastSEQ for Windows Version 4.0

```



```

; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 220788
; LENGTH: 658
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-220788

Query Match      77.9%; Score 14.8; DB 5; Length 658;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AACGGAAGGCTTTTCG 19
        |||||
Db      621 AACGGAAGGCATTTCG 638

RESULT 93
US-10-282-122A-15227
; Sequence 15227, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Onisen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15227
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Bordetella pertussis

```

```

US-10-282-122A-15227

Query Match      77.9%; Score 14.8; DB 8; Length 981;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCTTTTCG 18
        |||||
Db      169 GAACGGAAGGCATCG 186

RESULT 94
US-11-136-527-2075/c
; Sequence 2075, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2075
; LENGTH: 4591
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-2075

Query Match      77.9%; Score 14.8; DB 16; Length 4591;
Best Local Similarity 88.9%; Pred. No. 1.7e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCTTTTCG 18
        |||||
Db      1046 GACTGGAAGGCTTTTCG 1029

RESULT 95
US-10-270-333-106
; Sequence 106, Application US/10270333
; Publication No. US20030092124A1
; GENERAL INFORMATION:
; APPLICANT: Cravchik, Anibal
; TITLE OF INVENTION: ISOLATED G-PROTEIN COUPLED RECEPTORS,
; FILE REFERENCE: NUCLEIC ACID MOLECULES ENCODING GPCR PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF AS INSECTICIDAL TARGETS
; FILE REFERENCE: CL000733CON
; CURRENT APPLICATION NUMBER: US/10/270,333
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/168,677
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/175,691
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/191,638
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 7564
; TYPE: DNA
; ORGANISM: Drosophila
; US-10-270-333-106

Query Match      77.9%; Score 14.8; DB 6; Length 7564;
Best Local Similarity 88.9%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 AACGGAAGGCTTTTCG 19
        |||||

```



Db 4458 AACGAAATGCTTTCG 4475

## RESULT 96

US-11-097-143-19213  
; Sequence 19213, Application US/11097143  
; Publication No. US2005020858A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; TITLE OF INVENTION: DROSOPHILA GENES.  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19213  
; LENGTH: 7564  
; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-19213

Query Match 77.9%; Score 14.8; DB 13; Length 7564;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4458 AACGAAATGCTTTCG 4475

## RESULT 97

US-09-764-877-2799  
; Sequence 2799, Application US/09764877  
; Patent No. US20020147140A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005  
; CURRENT APPLICATION NUMBER: US/09/764,877  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2799  
; LENGTH: 19183  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-877-2799

Query Match 77.9%; Score 14.8; DB 3; Length 19183;  
Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 3573 GTACGGAAGGCCTTTG 3590

## RESULT 98

US-10-242-515-2799  
; Sequence 2799, Application US/10242515  
; Publication No. US20040009488A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC005C1  
; CURRENT APPLICATION NUMBER: US/10/242,515  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,877  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 4031  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2799  
; LENGTH: 19183  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-515-2799

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Best Local Similarity 88.9%; Pred. No. 1.8e+03;  
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Db 3573 GTACGGAAGGCCTTTG 3590

## RESULT 99

US-09-764-869-2314/c  
; Sequence 2314, Application US/09764869  
; Patent No. US20020061521A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007  
; CURRENT APPLICATION NUMBER: US/09/764,869  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 2442  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2314  
; LENGTH: 32249  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-764-869-2314

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Job time : 774.175 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2006, 03:57:04 ; Search time 11.7892 Seconds  
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Title: US-10-665-708-24
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Searched: 224314 seqs, 35277956 residues

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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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C 4	13.4	70.5	814	6	US-10-525-126-124	Sequence 124, App	
5	13.4	70.5	11611	6	US-10-541-993-4	Sequence 4, Appli	
6	13.2	69.5	471	7	US-11-217-529-77805	Sequence 77805, A	
7	13.2	69.5	492	7	US-11-217-529-173378	Sequence 173378, A	
C 8	13.2	69.5	498	7	US-11-217-529-76021	Sequence 76021, A	
C 9	13.2	69.5	1269	7	US-11-217-529-75	Sequence 75, Appl	
10	13.2	69.5	3102	7	US-11-217-529-82302	Sequence 82302, A	
11	13	68.4	25	7	US-11-217-529-91576	Sequence 91576, A	
12	13	68.4	25	7	US-11-217-529-152160	Sequence 152160, A	
C 13	13	68.4	404	6	US-10-488-619-347	Sequence 347, App	
14	13	68.4	702	7	US-11-217-529-81537	Sequence 81537, A	
15	13	68.4	2853	7	US-11-217-529-76130	Sequence 76130, A	
C 16	12.8	67.4	25	7	US-11-217-529-115745	Sequence 115745, A	
C 17	12.8	67.4	25	7	US-11-217-529-152423	Sequence 152423, A	
C 18	12.8	67.4	617	6	US-10-488-619-1859	Sequence 1859, Ap	
19	12.8	67.4	711	6	US-10-488-619-1860	Sequence 1860, Ap	
C 20	12.8	67.4	806	6	US-10-488-619-2939	Sequence 2939, Ap	
C 21	12.8	67.4	1098	7	US-11-217-529-5765	Sequence 5765, Ap	
22	12.8	67.4	1242	7	US-11-217-529-75628	Sequence 75628, A	
C 23	12.8	67.4	1260	7	US-11-217-529-5375	Sequence 5375, Ap	
C 24	12.8	67.4	1653	6	US-10-468-193-25	Sequence 25, Appl	
25	12.8	67.4	1695	7	US-11-217-529-4098	Sequence 4098, Ap	

C 99	12.2	64.2	410	6	US-10-488-619-466	Sequence 466, App	172	11.8	62.1	150	7	US-11-139-257-9	Sequence 9, Appli
100	12.2	64.2	462	6	US-10-488-619-319	Sequence 319, App	173	11.8	62.1	210	7	US-11-139-257-14	Sequence 14, Appl
101	12.2	64.2	573	7	US-11-217-529-81230	Sequence 81230, A	174	11.8	62.1	213	7	US-11-139-257-12	Sequence 12, Appl
102	12.2	64.2	636	7	US-11-217-529-79746	Sequence 79746, A	175	11.8	62.1	279	7	US-11-217-529-1024	Sequence 1024, Ap
C 103	12.2	64.2	858	7	US-11-217-529-1257	Sequence 1257, App	176	11.8	62.1	362	6	US-10-488-619-1084	Sequence 1084, Ap
C 104	12.2	64.2	888	7	US-11-217-529-77141	Sequence 77141, A	177	11.8	62.1	378	7	US-11-301-554-889	Sequence 889, App
C 105	12.2	64.2	893	6	US-10-488-619-2064	Sequence 2064, Ap	c 178	11.8	62.1	443	7	US-11-301-554-162	Sequence 162, App
C 106	12.2	64.2	906	7	US-11-217-529-2768	Sequence 2768, Ap	c 178	11.8	62.1	447	6	US-10-473-173-139	Sequence 139, App
C 107	12.2	64.2	918	7	US-11-217-529-5478	Sequence 5478, Ap	180	11.8	62.1	501	7	US-11-217-529-17344	Sequence 17344, A
C 108	12.2	64.2	933	7	US-11-217-529-4222	Sequence 4222, Ap	c 181	11.8	62.1	505	6	US-10-488-619-96	Sequence 96, Appl
C 109	12.2	64.2	1029	7	US-11-217-529-81270	Sequence 81270, A	182	11.8	62.1	523	6	US-10-488-619-2036	Sequence 2026, Ap
C 110	12.2	64.2	1082	6	US-10-511-937-2916	Sequence 2916, Ap	183	11.8	62.1	581	6	US-10-488-619-2947	Sequence 2947, Ap
C 111	12.2	64.2	1089	7	US-11-217-529-4005	Sequence 4005, Ap	c 184	11.8	62.1	619	6	US-10-488-619-2110	Sequence 2110, Ap
C 112	12.2	64.2	1143	7	US-11-217-529-3940	Sequence 3940, Ap	c 185	11.8	62.1	627	7	US-11-217-529-79008	Sequence 79008, A
C 113	12.2	64.2	1155	7	US-11-217-529-999	Sequence 999, App	c 186	11.8	62.1	630	6	US-10-488-619-1455	Sequence 1455, Ap
C 114	12.2	64.2	1197	7	US-11-217-529-5027	Sequence 5027, Ap	187	11.8	62.1	658	6	US-10-488-619-2511	Sequence 2511, Ap
C 115	12.2	64.2	1326	7	US-11-217-529-80747	Sequence 80747, A	188	11.8	62.1	669	7	US-11-257-062-37	Sequence 37, Appl
C 116	12.2	64.2	1344	7	US-11-217-529-4610	Sequence 4610, Ap	189	11.8	62.1	733	6	US-10-488-619-2084	Sequence 2084, Ap
C 117	12.2	64.2	1410	6	US-10-511-937-447	Sequence 447, App	c 190	11.8	62.1	744	7	US-11-217-529-4512	Sequence 4512, Ap
C 118	12.2	64.2	1422	7	US-11-136-524-69	Sequence 69, Appl	c 191	11.8	62.1	791	6	US-10-488-619-2086	Sequence 2086, Ap
C 119	12.2	64.2	1473	6	US-10-528-032-6	Sequence 6, Appli	c 192	11.8	62.1	792	6	US-10-488-619-2510	Sequence 2510, Ap
C 120	12.2	64.2	1565	6	US-10-505-928-93	Sequence 93, Appl	c 193	11.8	62.1	819	7	US-11-217-529-1255	Sequence 1255, Ap
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C 122	12.2	64.2	1687	6	US-10-528-032-7	Sequence 7, Appli	c 195	11.8	62.1	921	6	US-10-488-619-948	Sequence 948, App
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C 124	12.2	64.2	1816	6	US-10-528-032-3	Sequence 3, Appli	c 197	11.8	62.1	948	7	US-11-249-111-60	Sequence 60, Appl
C 125	12.2	64.2	1847	6	US-10-528-032-3	Sequence 3, Appli	c 198	11.8	62.1	975	7	US-11-217-529-82684	Sequence 82684, A
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C 127	12.2	64.2	1893	7	US-11-217-529-77547	Sequence 77547, A	c 200	11.8	62.1	996	7	US-11-217-529-490	Sequence 490, App
C 128	12.2	64.2	1950	6	US-10-528-032-4	Sequence 4, Appli	c 201	11.8	62.1	1003	7	US-11-226-605-56	Sequence 56, Appl
C 129	12.2	64.2	1959	7	US-11-217-529-75971	Sequence 75971, A	c 202	11.8	62.1	1006	6	US-10-525-126-108	Sequence 108, App
C 130	12.2	64.2	1968	7	US-11-312-958-13	Sequence 13, Appl	c 203	11.8	62.1	1032	7	US-11-217-529-80676	Sequence 80676, A
C 131	12.2	64.2	1980	7	US-11-217-529-76411	Sequence 76411, A	c 204	11.8	62.1	1074	7	US-11-217-529-76912	Sequence 76912, A
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C 133	12.2	64.2	2010	7	US-11-217-529-3479	Sequence 3479, Ap	c 206	11.8	62.1	1134	7	US-11-217-529-81013	Sequence 81013, A
C 134	12.2	64.2	2020	6	US-10-528-032-2	Sequence 2, Appli	c 207	11.8	62.1	1158	7	US-11-217-529-2819	Sequence 2819, Ap
C 135	12.2	64.2	2079	7	US-11-217-529-76446	Sequence 76446, A	c 208	11.8	62.1	1197	7	US-11-217-529-1881	Sequence 1881, Ap
C 136	12.2	64.2	2175	7	US-11-217-529-76502	Sequence 76502, A	c 209	11.8	62.1	1212	7	US-11-217-529-4487	Sequence 4487, Ap
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C 138	12.2	64.2	2545	6	US-10-511-937-440	Sequence 440, App	c 211	11.8	62.1	1281	7	US-11-217-529-76563	Sequence 76563, A
C 139	12.2	64.2	2545	7	US-11-301-554-1900	Sequence 1900, Ap	c 212	11.8	62.1	1395	7	US-11-183-218-63	Sequence 63, Appl
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C 141	12.2	64.2	3054	7	US-11-217-529-76540	Sequence 76540, A	c 214	11.8	62.1	1446	7	US-11-217-529-76007	Sequence 76007, A
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C 143	12.2	64.2	3408	6	US-10-505-928-184	Sequence 184, App	c 216	11.8	62.1	1512	7	US-11-217-529-76633	Sequence 76633, A
C 144	12.2	64.2	3408	6	US-10-511-937-337	Sequence 337, App	c 217	11.8	62.1	1551	7	US-11-217-529-78642	Sequence 78642, A
C 145	12.2	64.2	3552	7	US-11-217-529-173640	Sequence 173640, A	c 221	11.8	62.1	1790	7	US-11-242-505A-1	Sequence 1, Appli
C 146	12.2	64.2	3588	6	US-10-505-928-84	Sequence 84, Appl	c 222	11.8	62.1	1809	7	US-11-217-529-174100	Sequence 174100, A
C 147	12.2	64.2	3655	6	US-10-511-937-346	Sequence 346, App	c 224	11.8	62.1	1830	7	US-11-136-524-33	Sequence 33, Appl
C 148	12.2	64.2	4329	7	US-11-217-529-1487	Sequence 1487, Ap	c 225	11.8	62.1	1899	7	US-11-217-529-613	Sequence 613, App
C 149	12.2	64.2	4773	6	US-10-511-455-1	Sequence 1, Appli	c 226	11.8	62.1	1931	1	US-09-949-925-78	Sequence 78, Appl
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C 151	12.2	64.2	70665	6	US-10-505-928-596	Sequence 596, App	c 228	11.8	62.1	2049	7	US-11-217-529-2347	Sequence 2347, Ap
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C 158	12	63.2	1632	7	US-11-217-529-2539	Sequence 2539, Ap	c 235	11.8	62.1	2436	7	US-11-217-529-82283	Sequence 82283, A
C 159	12	63.2	2145	7	US-11-217-529-77295	Sequence 77295, A	c 236	11.8	62.1	2529	7	US-11-217-529-81730	Sequence 81730, A
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C 161	12	63.2	3394	7	US-11-217-529-195593	Sequence 195593, A	c 238	11.8	62.1	2823	7	US-11-217-529-4032	Sequence 4032, Ap
C 162	12	63.2	3394	7	US-11-217-529-195594	Sequence 195594, A	c 239	11.8	62.1	2823	7	US-11-217-529-78134	Sequence 78134, A
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C 164	12	63.2	3394	7	US-11-217-529-195596	Sequence 195596, A	c 241	11.8	62.1	3003	7	US-11-217-529-774	Sequence 774, App
C 165	12	63.2	3394	7	US-11-217-529-195597	Sequence 195597, A	c 242	11.8	62.1	3117	7	US-11-217-529-1461	Sequence 1461, Ap
C 166	11.8	62.1	25	7	US-11-217-529-17209	Sequence 17209, A	c 243	11.8	62.1	3273	7	US-11-217-529-4879	Sequence 4879, Ap
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C 170	11.8	62.1	25	7	US-11-217-529-146321	Sequence 146321, A							
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c 248	11.8	62.1	7268	6	US-10-559-415-189	Sequence 189, App
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c 254	11.6	61.1	25	7	US-11-217-529-150193	Sequence 150193, A
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c 256	11.6	61.1	64	7	US-11-267-871-397	Sequence 397, App
c 257	11.6	61.1	64	7	US-11-267-871-397	Sequence 397, App
c 258	11.6	61.1	64	7	US-11-267-871-398	Sequence 398, App
c 259	11.6	61.1	64	7	US-11-267-871-398	Sequence 398, App
c 260	11.6	61.1	223	7	US-11-301-554-390	Sequence 390, App
c 261	11.6	61.1	381	7	US-11-217-529-687	Sequence 687, App
c 262	11.6	61.1	381	7	US-11-217-529-76242	Sequence 76242, A
c 263	11.6	61.1	492	6	US-10-488-619-1313	Sequence 1313, App
c 264	11.6	61.1	525	7	US-11-217-529-76870	Sequence 76870, A
c 265	11.6	61.1	582	7	US-11-217-529-81363	Sequence 81363, A
c 266	11.6	61.1	602	6	US-10-946-650-47	Sequence 47, Appl
c 267	11.6	61.1	618	6	US-10-488-619-2949	Sequence 2949, App
c 268	11.6	61.1	687	7	US-11-217-529-76986	Sequence 76986, A
c 269	11.6	61.1	696	7	US-11-217-529-76990	Sequence 76990, A
c 270	11.6	61.1	705	6	US-10-488-619-1292	Sequence 1292, App
c 271	11.6	61.1	732	6	US-10-488-619-1763	Sequence 1763, App
c 272	11.6	61.1	762	7	US-11-217-529-77142	Sequence 77142, A
c 273	11.6	61.1	795	7	US-11-217-529-2988	Sequence 2988, App
c 274	11.6	61.1	804	7	US-11-226-605-46	Sequence 46, Appl
c 275	11.6	61.1	804	7	US-11-217-529-76245	Sequence 76245, A
c 276	11.6	61.1	837	7	US-11-217-529-173884	Sequence 173884, A
c 277	11.6	61.1	879	7	US-11-217-529-76737	Sequence 76737, A
c 278	11.6	61.1	903	7	US-11-217-529-4440	Sequence 4440, App
c 279	11.6	61.1	906	6	US-10-196-749-541	Sequence 541, App
c 280	11.6	61.1	1003	7	US-11-226-605-62	Sequence 62, Appl
c 281	11.6	61.1	1038	7	US-11-217-529-77058	Sequence 77058, A
c 282	11.6	61.1	1041	7	US-11-217-529-3938	Sequence 3938, App
c 283	11.6	61.1	1050	7	US-11-217-529-1275	Sequence 1275, App
c 284	11.6	61.1	1092	7	US-11-217-529-190860	Sequence 190860, A
c 285	11.6	61.1	1158	7	US-11-217-529-190921	Sequence 190921, A
c 286	11.6	61.1	1191	7	US-11-217-529-81390	Sequence 81390, A
c 287	11.6	61.1	1248	7	US-11-217-529-3809	Sequence 3809, App
c 288	11.6	61.1	1275	7	US-11-217-529-79354	Sequence 79354, A
c 289	11.6	61.1	1350	7	US-11-217-529-2929	Sequence 2929, App
c 290	11.6	61.1	1400	7	US-11-284-877-14	Sequence 14, Appl
c 291	11.6	61.1	1434	7	US-11-284-877-13	Sequence 13, Appl
c 292	11.6	61.1	1473	7	US-11-217-529-3098	Sequence 3098, App
c 293	11.6	61.1	1554	7	US-11-217-529-6019	Sequence 6019, App
c 294	11.6	61.1	1612	7	US-11-217-529-195610	Sequence 195610, A
c 295	11.6	61.1	1612	7	US-11-217-529-195611	Sequence 195611, A
c 296	11.6	61.1	1612	7	US-11-217-529-195612	Sequence 195612, A
c 297	11.6	61.1	1612	7	US-11-217-529-195634	Sequence 195634, A
c 298	11.6	61.1	1612	7	US-11-217-529-195635	Sequence 195635, A
c 299	11.6	61.1	1612	7	US-11-217-529-195636	Sequence 195636, A
c 300	11.6	61.1	1614	7	US-11-217-529-6108	Sequence 6108, App

ALIGNMENTS

RESULT 1						
US-11-217-529-6038						
Sequence 6038, Application US/11217529						
Publication No. US20060099612A1						
GENERAL INFORMATION:						
APPLICANT: SUNTORY LIMITED						
APPLICANT: NAKAO, YOSHIHIRO						
APPLICANT: NAKAMURA, NORIHISA						
APPLICANT: KODAMA, YUKIKO						
APPLICANT: FUJIMURA, TOMOKO						
APPLICANT: ASHIKARI, TOSHIHIKO						
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS						
Query Match	75.8%	Score 14.4;	DB 7;	Length 2454;		
Best Local Similarity	93.8%	Pred. No. 20;				
Matches	15;	Conservative	0;	Mismatches	1;	Indels
Gaps	0;					
QY	2	AACGGAAGGCCTTTC	17			
DB	1022	AATGGAAGGCCTTTC	1037			
RESULT 2						
US-11-217-529-77876						
Sequence 77876, Application US/11217529						
Publication No. US20060099612A1						
GENERAL INFORMATION:						
APPLICANT: SUNTORY LIMITED						
APPLICANT: NAKAO, YOSHIHIRO						
APPLICANT: NAKAMURA, NORIHISA						
APPLICANT: KODAMA, YUKIKO						
APPLICANT: FUJIMURA, TOMOKO						
APPLICANT: ASHIKARI, TOSHIHIKO						
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS						
Query Match	74.7%	Score 14.2;	DB 7;	Length 1950;		
Best Local Similarity	84.2%	Pred. No. 25;				
Matches	16;	Conservative	0;	Mismatches	3;	Indels
Gaps	0;					
QY	1	GAACGGAAGGCCTTTCGG	19			
DB	1234	GAACGGAAGGCCTTTCGG	1252			
RESULT 3						
US-11-217-529-5130/c						
Sequence 5130, Application US/11217529						
Publication No. US20060099612A1						
GENERAL INFORMATION:						
APPLICANT: SUNTORY LIMITED						
APPLICANT: NAKAO, YOSHIHIRO						
APPLICANT: NAKAMURA, NORIHISA						
APPLICANT: KODAMA, YUKIKO						
APPLICANT: FUJIMURA, TOMOKO						
APPLICANT: ASHIKARI, TOSHIHIKO						
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS						
Query Match	74.7%	Score 14.2;	DB 7;	Length 1950;		
Best Local Similarity	84.2%	Pred. No. 25;				
Matches	16;	Conservative	0;	Mismatches	3;	Indels
Gaps	0;					
QY	1	GAACGGAAGGCCTTTCGG	19			
DB	1234	GAACGGAAGGCCTTTCGG	1252			

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; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5130
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5130

Query Match          70.5%; Score 13.4; DB 7; Length 762;
Best Local Similarity 93.3%; Pred. No. 59;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACGGAAGGCCTTT 16
      ||||||| |||||
Db      539 AACGGAAGGCCTTT 525

RESULT 4
US-10-525-126-124/c
; Sequence 124, Application US/10525126
; Publication No. US20060093596A1
; GENERAL INFORMATION:
; APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
; TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
; FILE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
; FILE REFERENCE: 6899-6/PAR
; CURRENT APPLICATION NUMBER: US/10/525,126
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: PCT/CA03/01323
; PRIOR FILING DATE: 2003-08-22
; PRIOR APPLICATION NUMBER: 60/404,922
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 124
; LENGTH: 814
; TYPE: DNA
; ORGANISM: Platichthys stellatus
US-10-525-126-124

Query Match          70.5%; Score 13.4; DB 6; Length 814;
Best Local Similarity 93.3%; Pred. No. 60;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACGGAAGGCCTTT 16
      ||||||| |||||
Db      254 AACGGAAGGCCTTT 240

RESULT 5
US-10-541-993-4
; Sequence 4, Application US/10541993
; Publication No. US20060099670A1
; GENERAL INFORMATION:
; APPLICANT: Matsushek, Markus
; APPLICANT: Heinekamp, Thorsten
; APPLICANT: Schmidt, Andre
; APPLICANT: Brakhage, Axel
; TITLE OF INVENTION: Method for the genetic modification of organisms of the genus
; FILE OF INVENTION: Blakeslea, corresponding organisms, and the use of the same
; FILE REFERENCE: 13311-00010-US
; CURRENT APPLICATION NUMBER: US/10/541,993
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: PCT/EP2004/000100
; PRIOR FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: DE 103 00 549.4
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: DE 103 41 272.7
; PRIOR FILING DATE: 2003-09-08

; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
; NAME/KEY: misc feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (318)..(318)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (526)..(526)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8946)..(8946)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10028)..(10028)
; OTHER INFORMATION: n is a, c, g, or t
US-10-541-993-4

Query Match          70.5%; Score 13.4; DB 6; Length 11611;
Best Local Similarity 93.3%; Pred. No. 83;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCCTT 15
      ||||||| |||||
Db      8484 GAACGGAAGGCCTT 8498

RESULT 6
US-11-217-529-77805
; Sequence 77805, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77805
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77805

Query Match          69.5%; Score 13.2; DB 7; Length 471;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 AACGGAAGGCCTTT 19
      ||||||| |||||
Db      156 AACGGAAGGCCTTT 173
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RESULT 7
US-11-217-529-173378
; Sequence 173378, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 173378
; LENGTH: 492
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-173378

Query Match      69.5%; Score 13.2; DB 7; Length 492;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCCTTTTCG 18
DB 439 GAGCGGAAAGGCCTATTG 456

RESULT 8
US-11-217-529-76021/c
; Sequence 76021, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76021
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76021

Query Match      69.5%; Score 13.2; DB 7; Length 498;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAAGGCCTTTTCG 19
DB 145 AACGGAAAGGCCTTTTCG 128

RESULT 9
US-11-217-529-75/c
; Sequence 75, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

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; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-75

Query Match      69.5%; Score 13.2; DB 7; Length 1269;
Best Local Similarity 83.3%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAAGGCCTTTTCG 19
DB 507 AAGGGAAGGCCTGTAGG 490

RESULT 10
US-11-217-529-82302
; Sequence 82302, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82302
; LENGTH: 3102
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82302

Query Match      69.5%; Score 13.2; DB 7; Length 3102;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAAGGCCTTTTCG 19
DB 1395 AATGGAAATGCCATTTCG 1412

RESULT 11
US-11-217-529-91576
; Sequence 91576, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91576
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-91576

Query Match      68.4%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGAAAGGCCTTT 16
Db 9 CGGAAAGGCCTTT 21

RESULT 12
US-11-217-529-152160
; Sequence 152160, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 152160
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-152160

Query Match      68.4%; Score 13; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTT 15
Db 10 ACGGAAAGGCCTT 22

RESULT 13
US-10-488-619-347/c
; Sequence 347, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 347
; LENGTH: 404
; TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(404)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-347

Query Match      68.4%; Score 13; DB 6; Length 404;
Best Local Similarity 92.9%; Pred. No. 90;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGAAAGGCCTTCG 18
Db 235 GGAAAGGCCTTCG 222

RESULT 14
US-11-217-529-81537
; Sequence 81537, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81537
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-81537

Query Match      68.4%; Score 13; DB 7; Length 702;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTT 15
Db 332 ACGGAAAGGCCTT 344

RESULT 15
US-11-217-529-76130
; Sequence 76130, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76130
; LENGTH: 2853
; TYPE: DNA
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; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-76130

Query Match 68.4%; Score 13; DB 7; Length 2853;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGGAAGGCTTTT 16  
| | | | | | | | | | | | | | | | | |  
Db 2501 CGGAAGGCTTTT 2513

RESULT 16  
US-11-217-529-115745/c  
; Sequence 115745, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIRO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 115745  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-115745

Query Match 67.4%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 81;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ACGGAAGGCTTTTCG 18  
| | | | | | | | | | | | | | | | | |  
Db 16 ACGGAAGGCTTTTCG 1

RESULT 17  
US-11-217-529-152423/c  
; Sequence 152423, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIRO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR FILING DATE: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 152423  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-152423

Query Match 67.4%; Score 12.8; DB 7; Length 25;  
Best Local Similarity 87.5%; Pred. No. 81;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 GAACGGAAGGCTTTT 16  
| | | | | | | | | | | | | | | | | |  
Db 18 GAATGCAAGGCTTTT 3

RESULT 18  
US-10-488-619-1860/c  
; Sequence 1860, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1860  
; LENGTH: 617  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-1860

Query Match 67.4%; Score 12.8; DB 6; Length 617;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTT 16  
| | | | | | | | | | | | | | | | | |  
Db 582 GAAAAGAAAGGCTTTT 567

RESULT 19  
US-10-488-619-1859  
; Sequence 1859, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1859  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-1859

Query Match 67.4%; Score 12.8; DB 6; Length 711;  
Best Local Similarity 87.5%; Pred. No. 1.2e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GAACGGAAGGCTTTT 16  
| | | | | | | | | | | | | | | | | |  
Db 647 GAAAAGAAAGGCTTTT 662

RESULT 20  
US-10-488-619-2939/c  
; Sequence 2939, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619



Query Match 67.4%; Score 12.8; DB 6; Length 1653;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 4 CGGAAGGCGCTTCGG 19  
| | | | | | | | | |  
Db 1582 CGTAAGACCTTCGG 1567

RESULT 25  
US-11-217-529-4098  
; Sequence 4098, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4098  
; LENGTH: 1695  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; FEATURE:  
; NAME/KEY: modified base  
; LOCATION: (794)..(862)  
; OTHER INFORMATION: a, c, g, t, unknown, or other  
US-11-217-529-4098

Query Match 67.4%; Score 12.8; DB 7; Length 1695;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTT 16  
| | | | | | | | | |  
Db 939 GAACGGAAGGCGCTTT 954  
RESULT 26  
US-11-217-529-81561/c  
; Sequence 81561, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 81561  
; LENGTH: 1785  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-81561

Query Match 67.4%; Score 12.8; DB 7; Length 1785;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 GAACGGAAGGCGCTTT 16  
| | | | | | | | | |  
Db 1369 GAATGCAAGGCGCTTT 1354

RESULT 27  
US-11-217-529-76599/c  
; Sequence 76599, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 76599  
; LENGTH: 2178  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-76599

Query Match 67.4%; Score 12.8; DB 7; Length 2178;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCGCTTTCG 18  
| | | | | | | | | |  
Db 249 ACTGAAAGGCGCTGTCG 234

RESULT 28  
US-11-217-529-78291/c  
; Sequence 78291, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 78291  
; LENGTH: 2223  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-78291

Query Match 67.4%; Score 12.8; DB 7; Length 2223;  
Best Local Similarity 87.5%; Pred. No. 1.4e+02;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCGCTTTCG 18  
| | | | | | | | | |

Db 1838 ACGAAAGCTTTTCG 1823

RESULT 29

US-11-226-605-50/c

; Sequence 50, Application US/11226605

; Publication No. US2006008859A1

; GENERAL INFORMATION:

; APPLICANT: Hosted, Thomas

; APPLICANT: Walker, Scott

; APPLICANT: Bayne, Marvin

; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE

; FILE REFERENCE: IN06198US01

; CURRENT APPLICATION NUMBER: US/11/226,605

; CURRENT FILING DATE: 2005-09-14

; PRIOR APPLICATION NUMBER: 60/609940

; PRIOR FILING DATE: 2004-09-15

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 50

; LENGTH: 2387

; TYPE: DNA

; ORGANISM: Photinus pyralis

US-11-226-605-50

Query Match 67.4%; Score 12.8; DB 7; Length 2387;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CGGAAAGGCTTTTCG 19

|||||

Db 2180 CGGTAAGACCTTTTCG 2165

RESULT 30

US-11-217-529-6038/c

; Sequence 6038, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6038

; LENGTH: 2454

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

; FEATURE:

; NAME/KEY: modified base

; LOCATION: (2284)..(2317)

; OTHER INFORMATION: a, c, g, t, unknown, or other

US-11-217-529-6038

Query Match 67.4%; Score 12.8; DB 7; Length 2454;

Best Local Similarity 87.5%; Pred. No. 1.4e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AACGAAAGGCTTTTC 17

|||||

Db 1041 AAGAGAAAGGCTTTTC 1026

RESULT 31

US-11-217-529-79139/c

; Sequence 79139, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 79139

; LENGTH: 2850

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-79139

Query Match 67.4%; Score 12.8; DB 7; Length 2850;

Best Local Similarity 87.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GAACGAAAGGCTTTT 16

|||||

Db 375 GAACGTAAAGGCAATT 360

RESULT 32

US-11-217-529-80319/c

; Sequence 80319, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 80319

; LENGTH: 2976

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-80319

Query Match 67.4%; Score 12.8; DB 7; Length 2976;

Best Local Similarity 87.5%; Pred. No. 1.5e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACGAAAGGCTTTTCG 18

|||||

Db 1487 ACAGAACGCGCTTTTCG 1472

RESULT 33

US-11-217-529-78066/c

; Sequence 78066, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

```

; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR FILING DATE: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78066
; LENGTH: 3267
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78066

Query Match      67.4%; Score 12.8; DB 7; Length 3267;
Best Local Similarity 87.5%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GAACGGAAGGCCTTT 16
Db      438 GTATGGAAGGCCTTT 423

RESULT 34
US-10-485-397-7/c
; Sequence 7, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 7873
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pGFPstopneo is a circular Plasmid DNA
US-10-485-397-7

Query Match      67.4%; Score 12.8; DB 6; Length 7873;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      2575 CGGTAAGACCTTTCCG 2560

RESULT 35
US-10-485-397-8/c
; Sequence 8, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7943
; TYPE: DNA
; ORGANISM: Artificial

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```

; FEATURE:
; OTHER INFORMATION: pGFPstopneoSECIS is a circular Plasmid DNA
US-10-485-397-8

Query Match      67.4%; Score 12.8; DB 6; Length 7943;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      2575 CGGTAAGACCTTTCCG 2560

RESULT 36
US-11-226-605-86/c
; Sequence 86, Application US/11226605
; Publication No. US20060088859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198US01
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 8090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pSPRT50
US-11-226-605-86

Query Match      67.4%; Score 12.8; DB 7; Length 8090;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4 CGGAAAGGCCTTTCCG 19
Db      1650 CGGTAAGACCTTTCCG 1635

RESULT 37
US-11-264-784-222/c
; Sequence 222, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 222
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```

```
; OTHER INFORMATION: Primer D8-7A
US-11-264-784-222

Query Match          66.3%; Score 12.6; DB 7; Length 95;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
    ||||| ||||| ||||| |||||
Db 41 GAACTGAATGAGCTTTCGG 23

RESULT 38
US-11-264-784-223
; Sequence 223, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 223
; LENGTH: 95
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer D8-7B
US-11-264-784-223

Query Match          66.3%; Score 12.6; DB 7; Length 95;
Best Local Similarity 78.9%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
    ||||| ||||| ||||| |||||
Db 59 GAACTGAATGAGCTTTCGG 77

RESULT 39
US-11-264-784-246/c
; Sequence 246, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; ;
```

```
; SEQ ID NO 246
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 264 bp XhoI/SacI fragment of pT8 (7-9)
US-11-264-784-246

Query Match          66.3%; Score 12.6; DB 7; Length 264;
Best Local Similarity 78.9%; Pred. No. 1.4e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
    ||||| ||||| ||||| |||||
Db 37 GAACTGAATGAGCTTTCGG 19

RESULT 40
US-11-217-529-174297/c
; Sequence 174297, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 174297
; LENGTH: 483
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (433)..(433)
; OTHER INFORMATION: a, c, g, t, unknown, or other
US-11-217-529-174297

Query Match          66.3%; Score 12.6; DB 7; Length 483;
Best Local Similarity 78.9%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGGCTTTCGG 19
    ||||| ||||| ||||| |||||
Db 478 GAAAGGAAAGGACTTTGGG 460

RESULT 41
US-10-488-619-2986
; Sequence 2986, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2986
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2986
```

```
Query Match      66.3%; Score 12.6; DB 6; Length 587;
Best Local Similarity 78.9%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTTCGG 19
Db 433 GAACAGAAAGGTCTCTCAG 451

RESULT 42
US-10-488-619-2985/c
; Sequence 2985, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2985
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(687)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-2985

Query Match      66.3%; Score 12.6; DB 6; Length 637;
Best Local Similarity 78.9%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTTCGG 19
Db 505 GAACAGAAAGGTCTCTCAG 487

RESULT 43
US-11-252-080-11/c
; Sequence 11, Application US/11252080
; Publication No. US2006090217A1
; GENERAL INFORMATION:
; APPLICANT: Texas A&M University
; TITLE OF INVENTION: ISOLATION OF SUGARCANE PROTEINS INVOLVED IN POSTTRANSCRIPTIONAL G
; FILE REFERENCE: 017575.0693 (TAMUS 1743)
; CURRENT APPLICATION NUMBER: US/11/252,080
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US/10/226,715
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314863
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 829
; TYPE: DNA
; ORGANISM: Saccharum hybrid cultivar Cp72-1210
US-11-252-080-11

Query Match      66.3%; Score 12.6; DB 7; Length 829;
Best Local Similarity 78.9%; Pred. No. 1.6e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTTCGG 19
Db 588 GAAGGGAACCCCTTTTGG 570
```

```
RESULT 44
US-09-949-925-23/c
; Sequence 23, Application US/09949925
; Publication No. US20060099575A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 67 Human secreted proteins
; FILE REFERENCE: P2023P2
; CURRENT APPLICATION NUMBER: PCT/US99/01621
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/232,150
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: PCT/US99/01621
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,167
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,162
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,161
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/073,170
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 298
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 1095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (720)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-949-925-23

Query Match      66.3%; Score 12.6; DB 1; Length 1095;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGCCCTTTCGG 19
Db 516 GAACAGAAAGGTCTTTCGG 498

RESULT 45
US-11-217-529-78935
; Sequence 78935, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78935
; LENGTH: 1242
```

```
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78935

Query Match      66.3%; Score 12.6; DB 7; Length 1242;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
Db 65 GAACAGTAAGGCTTTTGG 83

RESULT 46
US-11-264-784-255/c
; Sequence 255, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 255
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-3: synthetic delta 8-desaturase gene codon-optimized for
; OTHER INFORMATION: Yarrowia lipolytica in pDMW261
US-11-264-784-255

Query Match      66.3%; Score 12.6; DB 7; Length 1269;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
Db 675 GAACGAATGAGCTTTTCGG 657

RESULT 47
US-11-264-784-209/c
; Sequence 209, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
```

```
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 209
; LENGTH: 1270
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8S-1: Synthetic gene codon-optimized for expression in Yarrowia
; OTHER INFORMATION: lipolytica
US-11-264-784-209

Query Match      66.3%; Score 12.6; DB 7; Length 1270;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
Db 668 GAACGAATGAGCTTTTCGG 650

RESULT 48
US-11-264-784-48/c
; Sequence 48, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D8SF: synthetic delta-8 desaturase (codon-optimized for Yarrowia
; OTHER INFORMATION: lipolytica)
US-11-264-784-48

Query Match      66.3%; Score 12.6; DB 7; Length 1272;
Best Local Similarity 78.9%; Pred. No. 1.7e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCTTTTCGG 19
Db 676 GAACGAATGAGCTTTTCGG 658

RESULT 49
US-11-264-784-263/c
; Sequence 263, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
```



; APPLICANT: Yadav, Narendra S.  
 ; APPLICANT: Zhang, Hongxiang  
 ; APPLICANT: Zhu, Quinn  
 ; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
 ; FILE REFERENCE: CL3136 USNA  
 ; CURRENT APPLICATION NUMBER: US/11/264,784  
 ; CURRENT FILING DATE: 2005-11-01  
 ; NUMBER OF SEQ ID NOS: 375  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 263  
 ; LENGTH: 1272  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chimeric gene  
 US-11-264-784-263

Query Match 66.3%; Score 12.6; DB 7; Length 1272;  
 Best Local Similarity 78.9%; Pred. No. 1.7e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 676 GAACGGAATGAGCTTTCGG 658

RESULT 50  
 US-11-217-529-1422/c  
 ; Sequence 1422, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1422  
 ; LENGTH: 1758  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-1422

Query Match 66.3%; Score 12.6; DB 7; Length 1758;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 285 GAACGGAATGAGCTTTCGG 267

RESULT 51  
 US-11-217-529-182/c  
 ; Sequence 182, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 182  
 ; LENGTH: 1788  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-182

Query Match 66.3%; Score 12.6; DB 7; Length 1788;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 1493 GAACGGAAGGCAATTTCGG 1475

RESULT 52  
 US-11-217-529-79690/c  
 ; Sequence 79690, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 79690  
 ; LENGTH: 1824  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-79690

Query Match 66.3%; Score 12.6; DB 7; Length 1824;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19  
 ||||| ||||| ||||| ||||| |||||  
 Db 746 GGACGGAATGACTTTCGG 728

RESULT 53  
 US-11-264-784-250/c  
 ; Sequence 250, Application US/11264784  
 ; Publication No. US20060094092A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
 ; APPLICANT: Damude, Howard Glenn  
 ; APPLICANT: Gillies, Peter John  
 ; APPLICANT: Macool, Daniel Joseph  
 ; APPLICANT: Picataggio, Stephen K.  
 ; APPLICANT: Pollak, Dana M. Walters  
 ; APPLICANT: Ragghianti, James John  
 ; APPLICANT: Xue, Zhixiong  
 ; APPLICANT: Yadav, Narendra S.  
 ; APPLICANT: Zhang, Hongxiang  
 ; APPLICANT: Zhu, Quinn  
 ; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
 ; FILE REFERENCE: CL3136 USNA

; CURRENT APPLICATION NUMBER: US/11/264,784  
 ; CURRENT FILING DATE: 2005-11-01  
 ; NUMBER OF SEQ ID NOS: 375  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 250  
 ; LENGTH: 1852  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chimeric DBS-1::XPR gene  
 US-11-264-784-250

Query Match 66.3%; Score 12.6; DB 7; Length 1852;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19  
 |||||  
 Db 1080 GAACTGAATGAGCTTTCGG 1062

RESULT 54  
 US-11-264-784-251/c  
 ; Sequence 251, Application US/11264784  
 ; Publication No. US20060094092A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: E.I. duPont de Nemours & Co., Inc.  
 ; APPLICANT: Damude, Howard Glenn  
 ; APPLICANT: Gallies, Peter John  
 ; APPLICANT: Macool, Daniel Joseph  
 ; APPLICANT: Picataggio, Stephen K.  
 ; APPLICANT: Pollak, Dana M. Walters  
 ; APPLICANT: Ragghianti, James John  
 ; APPLICANT: Xue, Zhixiong  
 ; APPLICANT: Yadav, Narendra S.  
 ; APPLICANT: Zhang, Hongxiang  
 ; APPLICANT: Zhu, Quinn  
 ; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA  
 ; FILE REFERENCE: CL3136 USNA  
 ; CURRENT APPLICATION NUMBER: US/11/264,784  
 ; CURRENT FILING DATE: 2005-11-01  
 ; NUMBER OF SEQ ID NOS: 375  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 251  
 ; LENGTH: 1898  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chimeric DBS-2::XPR gene  
 US-11-264-784-251

Query Match 66.3%; Score 12.6; DB 7; Length 1898;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19  
 |||||  
 Db 1080 GAACTGAATGAGCTTTCGG 1062

RESULT 55  
 US-11-217-529-1481  
 ; Sequence 1481, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHIISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 1481  
 ; LENGTH: 1920  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus  
 US-11-217-529-1481

Query Match 66.3%; Score 12.6; DB 7; Length 1920;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19  
 |||||  
 Db 1210 GAACTGAAAAGACTCTCGG 1228

RESULT 56  
 US-10-505-928-487/c  
 ; Sequence 487, Application US/10505928  
 ; Publication No. US20060088532A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ludwig Institute for Cancer Research et al.  
 ; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES  
 ; FILE REFERENCE: 28967/39178  
 ; CURRENT APPLICATION NUMBER: US/10/505,928  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/363,019  
 ; PRIOR FILING DATE: 2002-03-07  
 ; NUMBER OF SEQ ID NOS: 866  
 ; SOFTWARE: PatentIn 3.2  
 ; SEQ ID NO 487  
 ; LENGTH: 2208  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-505-928-487

Query Match 66.3%; Score 12.6; DB 6; Length 2208;  
 Best Local Similarity 78.9%; Pred. No. 1.8e+02;  
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAAGCGCTTTCGG 19  
 |||||  
 Db 760 GAACGGAAAGGACATTGG 742

RESULT 57  
 US-11-217-529-728/c  
 ; Sequence 728, Application US/11217529  
 ; Publication No. US20060099612A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUNTORY LIMITED  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHIISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TOMOKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: S-38-285  
 ; CURRENT APPLICATION NUMBER: US/11/217,529  
 ; CURRENT FILING DATE: 2005-09-02  
 ; PRIOR APPLICATION NUMBER: US 10/932,182  
 ; PRIOR FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 728  
 ; LENGTH: 2286  
 ; TYPE: DNA  
 ; ORGANISM: Saccharomyces pastorianus

```
US-11-217-529-728
Query Match      66.3%; Score 12.6; DB 7; Length 2286;
Best Local Similarity 78.9%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
||||| ||| ||| |||
Db 212 GAACGGATAGGACTTCG 194

RESULT 58
US-11-217-529-254
; Sequence 254, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 254
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-254

Query Match      66.3%; Score 12.6; DB 7; Length 2397;
Best Local Similarity 78.9%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
||||| ||| ||| |||
Db 403 GACGGAATGCCATTGG 421

RESULT 59
US-10-196-749-157
; Sequence 157, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250

US-11-217-529-76510
; Sequence 76510, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76510
; LENGTH: 3015
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76510

Query Match      66.3%; Score 12.6; DB 7; Length 3015;
Best Local Similarity 78.9%; Pred. No. 1.9e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GAACGGAAGCCTTCGG 19
||||| ||| ||| |||
Db 2983 GAACGTAAGTCTTCAG 3001

RESULT 61
US-10-505-928-346/c
; Sequence 346, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
```

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; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-346

Query Match      66.3%; Score 12.6; DB 6; Length 3869;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCTTTTCGG 19
Db      182 GAAATGAAGGCATTACGG 164

RESULT 62
US-10-511-937-2853
; Sequence 2853, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlseuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/511,937
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/325,899
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2853
; LENGTH: 3869
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-2853

Query Match      66.3%; Score 12.6; DB 6; Length 3869;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCTTTTCGG 19
Db      2166 GAAGGAAAGTCCATTACG 2184

RESULT 63
US-10-505-928-188
; Sequence 188, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US/10/505,928
; PRIOR FILING DATE: 2002-03-07
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-188

Query Match      66.3%; Score 12.6; DB 6; Length 4204;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCTTTTCGG 19
Db      692 GAAGGAAAGGCTGTCTG 710

RESULT 64
US-11-217-529-3246
; Sequence 3246, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIRO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3246
; LENGTH: 5223
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3246

Query Match      66.3%; Score 12.6; DB 7; Length 5223;
Best Local Similarity 78.9%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAAGGCTTTTCGG 19
Db      324 GATCGGAAATGCGTTTGG 342

RESULT 65
US-11-263-326-98
; Sequence 98, Application US/11263326
; Publication No. US20060089306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US/11/263,326
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 98
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-98
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-98

Query Match          66.3%; Score 12.6; DB 7; Length 7008;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 1750 GAGAGGAGGCGCTTTTCGG 1768

RESULT 66
US-11-263-326-104
; Sequence 104, Application US/11263326
; Publication No. US2006009306A1
; GENERAL INFORMATION:
; APPLICANT: Wallace, Robyn H
; APPLICANT: Mulley, John C
; APPLICANT: Berkovic, Samuel F
; TITLE OF INVENTION: NEW EPILEPSY MUTATIONS
; FILE REFERENCE: 1386/13/3
; CURRENT APPLICATION NUMBER: US/11/263,326
; CURRENT FILING DATE: 2005-10-31
; PRIOR APPLICATION NUMBER: US 10/482,834
; PRIOR FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PCT/AU2004/001051
; PRIOR FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 10/451,126
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 104
; LENGTH: 7008
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-263-326-104

Query Match          66.3%; Score 12.6; DB 7; Length 7008;
Best Local Similarity 78.9%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 1750 GAGAGGAGGCGCTTTTCGG 1768

RESULT 67
US-11-024-544A-129/c
; Sequence 129, Application US/11024544A
; Publication No. US20060094086A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Yadav, Narendra
; APPLICANT: Xue, Zhixiong
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: DIACYLGLYCEROL ACYLTRANSFERASES FOR ALTERATION OF POLYUNSATURATED
; FILE REFERENCE: CL2717
; CURRENT APPLICATION NUMBER: US/11/024,544A
; CURRENT FILING DATE: 2004-12-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 129
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pK02UM26E
US-11-024-544A-129

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
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```
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 1648 GAACTGAATGAGCTTTTCGG 1630

RESULT 68
US-11-190-750-112/c
; Sequence 112, Application US/11190750
; Publication No. US20060094088A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours and Company, Inc.
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Yadav, Narendra
; APPLICANT: Zhang, Hongxiang
; TITLE OF INVENTION: ACYLTRANSFERASE REGULATION TO INCREASE THE PERCENT OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN TOTAL LIPIDS AND OILS OF
; TITLE OF INVENTION: OLEAGINOUS ORGANISMS
; FILE REFERENCE: CL2718
; CURRENT APPLICATION NUMBER: US/11/190,750
; CURRENT FILING DATE: 2005-07-27
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 112
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pK02UM26E
US-11-190-750-112

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
Best Local Similarity 78.9%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTTCGG 19
Db 1648 GAACTGAATGAGCTTTTCGG 1630

RESULT 69
US-11-264-784-123/c
; Sequence 123, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 123
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDMW297
US-11-264-784-123

Query Match          66.3%; Score 12.6; DB 7; Length 10448;
```

```
;
; NAME/KEY: misc feature
; LOCATION: (10915)..(10918)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-125

Query Match
Best Local Similarity 78.9%; Score 12.6; DB 6; Length 12918;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 1648 GAACGGAATGAGCTTTCGG 1630

RESULT 70
US-10-501-834-4/c
; Sequence 4, Application US/10501834
; Publication No. US2006008828A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Peter C., Ward, Christopher J., Rossetti, Sandro, and Torres,
; APPLICANT: Vicente E.
; TITLE OF INVENTION: Polycystic Kidney Disease Nucleic Acids
; FILE REFERENCE: 07039/386U81
; CURRENT APPLICATION NUMBER: US/10/501,834
; CURRENT FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: PCT/US03/02038
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,110
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12918
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-501-834-4

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 6; Length 12918;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 3212 GAACGCAAGGCGCTGACGG 3194

RESULT 71
US-11-264-784-125
; Sequence 125, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 125
; LENGTH: 13295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pDWW314
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10915)..(10918)
; OTHER INFORMATION: n is a, c, g, or t
```

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;
; NAME/KEY: misc feature
; LOCATION: (10923)..(10923)
; OTHER INFORMATION: n is a, c, g, or t
US-11-264-784-126

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 7; Length 13295;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 3610 GAACGGAATGAGCTTTCGG 3628

RESULT 72
US-11-264-784-124
; Sequence 124, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 124
; LENGTH: 15543
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pZP2C16M899
US-11-264-784-124

Query Match
Best Local Similarity 66.3%; Score 12.6; DB 7; Length 15543;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCGCTTTCGG 19
Db 11264 GAACGGAATGAGCTTTCGG 11282

RESULT 73
US-11-264-784-127
; Sequence 127, Application US/11264784
; Publication No. US20060094092A1
; GENERAL INFORMATION:
; APPLICANT: E.I. duPont de Nemours & Co., Inc.
; APPLICANT: Damude, Howard Glenn
; APPLICANT: Gillies, Peter John
; APPLICANT: Macool, Daniel Joseph
; APPLICANT: Picataggio, Stephen K.
; APPLICANT: Pollak, Dana M. Walters
; APPLICANT: Ragghianti, James John
; APPLICANT: Xue, Zhixiong
; APPLICANT: Yadav, Narendra S.
; APPLICANT: Zhang, Hongxiang
; APPLICANT: Zhu, Quinn
; TITLE OF INVENTION: HIGH ARACHIDONIC ACID PRODUCING STRAINS OF YARROWIA LIPOLYTICA
; FILE REFERENCE: CL3136 USNA
; CURRENT APPLICATION NUMBER: US/11/264,784
```

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; CURRENT FILING DATE: 2005-11-01
; NUMBER OF SEQ ID NOS: 375
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 127
; LENGTH: 16325
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Plasmid pzKSL5598
US-11-264-784-127

Query Match          66.3%; Score 12.6; DB 7; Length 16325;
Best Local Similarity 78.9%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCCTTTTCGG 19
      ||||| ||||| ||||| |||||
Db      14743 GAACGGAAGGCCTTTTCGG 14761

RESULT 74
US-11-284-877-17/c
; Sequence 17, Application US/11284877
; Publication No. US20060095984A1
; GENERAL INFORMATION:
; APPLICANT: Hadlaczky, Gyula
; Szalay, Aladar
; TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF AND METHODS
; FOR PREPARING ARTIFICIAL CHROMOSOMES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 12390 El Camino Real
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/284,877
; FILING DATE: 21-Nov-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 10/808,689
; FILING DATE: 24-MAR-2004
; APPLICATION NUMBER: 10/219,694
; FILING DATE: 14-AUG-2002
; APPLICATION NUMBER: 10/151,081
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/151,078
; FILING DATE: 16-MAY-2002
; APPLICATION NUMBER: 10/125,767
; FILING DATE: 17-APR-2002
; APPLICATION NUMBER: 10/287,313
; FILING DATE: 01-NOV-2002
; APPLICATION NUMBER: 09/799,462
; FILING DATE: 05-MAR-2001
; APPLICATION NUMBER: 09/724,872
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,726
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 09/724,693
; FILING DATE: 28-NOV-2000
; APPLICATION NUMBER: 08/835,682
; FILING DATE: 10-APR-1997
; APPLICATION NUMBER: 08/695,191
; FILING DATE: 07-AUG-1996
; APPLICATION NUMBER: 08/682,080
; FILING DATE: 15-JUL-1996

; APPLICATION NUMBER: 08/629,822
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 17084-004018/402Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-678-4777
; TELEFAX: 202-626-7796
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42999 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-11-284-877-17

Query Match          66.3%; Score 12.6; DB 7; Length 42999;
Best Local Similarity 78.9%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCCTTTTCGG 19
      ||||| ||||| ||||| |||||
Db      17125 GAACGGAAGGCCTTTTCGG 17107

RESULT 75
US-11-217-529-103956/c
; Sequence 103956, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHITIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 103956
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-103956

Query Match          65.3%; Score 12.4; DB 7; Length 25;
Best Local Similarity 92.9%; Pred. No. 1.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ACGGAAGGCCTTT 16
      ||||| ||||| |||||
Db      19 ACGGAAGGCATTT 6

RESULT 76
US-11-217-529-81840
; Sequence 81840, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
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; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 137023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81840
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
; US-11-217-529-81840

Query Match      65.3%; Score 12.4; DB 7; Length 108;
Best Local Similarity 92.9%; Pred. No. 1.6e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GAAAGGCGCTTTCGG 19
Db      72 GAAAGGCGCTTTCGG 85

RESULT 77
US-10-488-619-319/c
; Sequence 319, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 319
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(462)
; OTHER INFORMATION: n is g, c, a or t
US-10-488-619-319

Query Match      65.3%; Score 12.4; DB 6; Length 462;
Best Local Similarity 92.9%; Pred. No. 1.9e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 GAAAGGCGCTTTCGG 19
Db      92 GAAAGGCGCTTTCGG 79

RESULT 78
US-10-488-619-2561/c
; Sequence 2561, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2561
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-2561

Query Match      65.3%; Score 12.4; DB 6; Length 526;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GAACGGAAGGCCT 14
Db      216 GAACGGAAGGACT 203

RESULT 79
US-10-488-619-1653/c
; Sequence 1653, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1653
; LENGTH: 529
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1653

Query Match      65.3%; Score 12.4; DB 6; Length 529;
Best Local Similarity 92.9%; Pred. No. 2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGGAAGGCCTTTC 17
Db      356 CGGACAGGCCTTTC 343

RESULT 80
US-10-488-619-1654
; Sequence 1654, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greenlee, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1654
; LENGTH: 786
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(786)
; OTHER INFORMATION: n is a, c, g, or t
US-10-488-619-1654

Query Match      65.3%; Score 12.4; DB 6; Length 786;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 CGGAAGGCCTTTC 17
Db      407 CGGACAGGCCTTTC 420

```



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; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-11

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCGCTTT 16
        |||||
Db      897  ACGGAAGGCGCTTT 884

RESULT 84
US-11-217-529-79938
; Sequence 79938, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79938
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79938

Query Match      65.3%; Score 12.4; DB 7; Length 1158;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  ACGGAAGGCGCTT 15
        |||||
Db      775  ACGGAAGGCGCTT 788

RESULT 85
US-11-217-529-76861/c
; Sequence 76861, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-7

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCGCTTT 16
        |||||
Db      897  ACGGAAGGCGCTTT 884

RESULT 83
US-11-226-605-11/c
; Sequence 11, Application US/11226605
; Publication No. US2006008859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198U501
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-11-226-605-7

Query Match      65.3%; Score 12.4; DB 7; Length 1003;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3  ACGGAAGGCGCTTT 16
        |||||
Db      897  ACGGAAGGCGCTTT 884

RESULT 82
US-11-226-605-7/c
; Sequence 7, Application US/11226605
; Publication No. US2006008859A1
; GENERAL INFORMATION:
; APPLICANT: Hosted, Thomas
; APPLICANT: Walker, Scott
; APPLICANT: Bayne, Marvin
; TITLE OF INVENTION: REPORTER ASSAY SCREENS FOR PROTEIN TARGETS IN SACCHAROMYCES CEREVISIAE
; FILE REFERENCE: IN06198U501
; CURRENT APPLICATION NUMBER: US/11/226,605
; CURRENT FILING DATE: 2005-09-14
; PRIOR APPLICATION NUMBER: 60/609940
; PRIOR FILING DATE: 2004-09-15
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 1003
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107

Query Match      65.3%; Score 12.4; DB 6; Length 927;
Best Local Similarity 92.9%; Pred. No. 2.1e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  GAACGGAAGGCCT 14
        |||||
Db      558  GCACGGAAGGCCT 545

RESULT 81
US-10-473-173-107/c
; Sequence 107, Application US/10473173
; Publication No. US2006008823A1
; GENERAL INFORMATION:
; APPLICANT: VAN ANDEL INSTITUTE
; TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell
; TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification
; FILE REFERENCE: 38345-170094
; CURRENT APPLICATION NUMBER: US/10/473,173
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/279,411
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 498
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 107
; LENGTH: 927
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-473-173-107
```

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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76861
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76861

Query Match      65.3%; Score 12.4; DB 7; Length 1275;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGAAGGCGCTTTCG 18
Db      599 GGAAGGCGATTTCG 586
          ||||| |||||
          ||||| |||||

RESULT 86
US-11-217-529-4877/c
; Sequence 4877, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4877
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-4877

Query Match      65.3%; Score 12.4; DB 7; Length 1377;
Best Local Similarity 92.9%; Pred. No. 2.2e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACGGAAGCGCTT 15
Db      81 AACGAAAGCGCTT 68
          ||||| |||||
          ||||| |||||

RESULT 87
US-11-217-529-79055
; Sequence 79055, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79055
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79055

Query Match      65.3%; Score 12.4; DB 7; Length 1695;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 AACGGAAGCGCTT 15
Db      1468 AACGGAAGGCTCTT 1481
          ||||| |||||
          ||||| |||||

RESULT 88
US-11-217-529-78343
; Sequence 78343, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78343
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78343

Query Match      65.3%; Score 12.4; DB 7; Length 1731;
Best Local Similarity 92.9%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 GGAAGGCGCTTTCG 18
Db      901 GGAAGGCTCTTCG 914
          ||||| |||||
          ||||| |||||

RESULT 89
US-11-217-529-77238/c
; Sequence 77238, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77238
; LENGTH: 2646
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-77238

Query Match      65.3%; Score 12.4; DB 7; Length 2646;
Best Local Similarity 92.9%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 ACGGAAAGGCCTTT 16
Db 2161 ACGGAAAGGCATTT 2148

RESULT 90
US-11-217-529-76779/c
; Sequence 76779, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76779
; LENGTH: 2871
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-76779

Query Match 65.3%; Score 12.4; DB 7; Length 2871;
Best Local Similarity 92.9%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCT 14
Db 1185 GAACGGAAGGCCT 1172

RESULT 91
US-11-181-115-36
; Sequence 36, Application US/11181115
; Publication No. US20060088511A1
; GENERAL INFORMATION:
; APPLICANT: Dana Farber Cancer Center
; TITLE OF INVENTION: Cancer Therapy Sensitizer
; FILE REFERENCE: 7032/2072
; CURRENT APPLICATION NUMBER: US/11/181,115
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: PCT/US04/000901
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,009
; PRIOR FILING DATE: 2003-01-14
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 3669
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-181-115-36

Query Match 65.3%; Score 12.4; DB 7; Length 3669;
Best Local Similarity 92.9%; Pred. No. 2.5e+02;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTTT 16
Db 2485 ACGGAAAGGCCTTT 2498

RESULT 92
US-11-217-529-36553/c
; Sequence 36553, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36553
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-36553

Query Match 64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCG 18
Db 19 AACTGAAGGCCCTCCG 3

RESULT 93
US-11-217-529-48962/c
; Sequence 48962, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48962
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-48962

Query Match 64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGGCCTTCGG 19
Db 25 ACGGAACGGCTCTTAGG 9

RESULT 94
US-11-217-529-61824/c
; Sequence 61824, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
```

```
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 61824
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-61824

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGCCTTTCG 19
Db 23 ACAGATAGCCTTTCG 7

RESULT 95
US-11-217-529-110320
/ Sequence 110320, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 110320
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-110320

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGCCTTTCG 18
Db 9 AACGGAAGCCGGTCG 25

RESULT 96
US-11-217-529-132068
/ Sequence 132068, Application US/11217529
/ Publication No. US20060099612A1
/ GENERAL INFORMATION:
/ APPLICANT: SUNTORY LIMITED
/ APPLICANT: NAKAO, YOSHIHIRO
/ APPLICANT: NAKAMURA, NORIHISA
/ APPLICANT: KODAMA, YUKIKO
/ APPLICANT: FUJIMURA, TOMOKO
/ APPLICANT: ASHIKARI, TOSHIHIKO
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
```

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/ FILE REFERENCE: S-38-285
/ CURRENT APPLICATION NUMBER: US/11/217,529
/ CURRENT FILING DATE: 2005-09-02
/ PRIOR APPLICATION NUMBER: US 10/932,182
/ PRIOR FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 132068
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-11-217-529-132068

Query Match          64.2%; Score 12.2; DB 7; Length 25;
Best Local Similarity 82.4%; Pred. No. 1.7e+02;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACGGAAAGCCTTTCG 19
Db 7 ACGGAGAGCCTTTCG 23

RESULT 97
US-11-301-554-1419
/ Sequence 1419, Application US/11301554
/ Publication No. US20060088527A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Sleath, Paul R.
/ APPLICANT: Johnson, Jeffrey C.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Carter, Darrick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: McNabb, Andria
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.478C21
/ CURRENT APPLICATION NUMBER: US/11/301,554
/ CURRENT FILING DATE: 2005-12-13
/ PRIOR APPLICATION NUMBER: US 10/283,017
/ PRIOR FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US 10/113,872
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 10/017,754
/ PRIOR FILING DATE: 2001-10-29
/ PRIOR APPLICATION NUMBER: US 09/902,941
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: US 09/849,626
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: US 09/736,457
/ PRIOR FILING DATE: 2000-12-13
/ PRIOR APPLICATION NUMBER: US 09/702,705
/ PRIOR FILING DATE: 2000-10-30
/ PRIOR APPLICATION NUMBER: US 09/677,419
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: US 09/671,325
/ PRIOR FILING DATE: 2000-09-26
/ PRIOR APPLICATION NUMBER: US 09/658,824
/ PRIOR FILING DATE: 2000-09-08
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2157
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1419
/ LENGTH: 390
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-301-554-1419
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Query Match 64.2%; Score 12.2; DB 7; Length 390;  
Best Local Similarity 82.4%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17  
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DB 67 GAAAGGAAGTGCTTTC 83

## RESULT 98

US-11-217-529-173452  
; Sequence 173452, Application US/11217529  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIRO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 173452  
; LENGTH: 402  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-173452

Query Match 64.2%; Score 12.2; DB 7; Length 402;  
Best Local Similarity 82.4%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AACGGAAGGCCTTCG 18  
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DB 45 AACGGAAGGATTTAG 61

## RESULT 99

US-10-488-619-466/c  
; Sequence 466, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 466  
; LENGTH: 410  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(410)  
; OTHER INFORMATION: n is g, c, a or t  
US-10-488-619-466

Query Match 64.2%; Score 12.2; DB 6; Length 410;  
Best Local Similarity 82.4%; Pred. No. 2.4e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17  
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Db 184 GAACGGAACGCCTGTC 168

## RESULT 100

US-10-488-619-319  
; Sequence 319, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE REFERENCE: 98-01 WO  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 319  
; LENGTH: 462  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(462)  
; OTHER INFORMATION: n is g, c, a or t  
US-10-488-619-319

Query Match 64.2%; Score 12.2; DB 6; Length 462;  
Best Local Similarity 82.4%; Pred. No. 2.5e+02;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GAACGGAAGGCCTTTC 17  
|||||  
DB 76 GACCCCAAGGCCTTTC 92

Search completed: May 19, 2006, 05:38:22  
Job time : 13.7892 secs

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